

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 19, 2005, 20:55:30 ; Search time 8502 Seconds

(without alignments)  
1172.999 Million cell updates/sec

Title: US-10-017-407a-306

Perfect score: 1343

Sequence: 1 MTQVPRLSVPAALAGSAA.....VRVYISLLPLGDLTLAFKI 262

Scoring table:

BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DRV=xlh  
-O/cn2.1/USPTO\_spool/US10017407/runat\_19042005.142533.29458/app\_query.fasta\_1.455  
-DB=EST -QFMT=fastap -SUFFIX=rest -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1500  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10017407 @CN 1.1 4352 @runat\_19042005.142533.29458 -NCPU=6 -ICPU=3  
-NO\_WMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPOP=0.5 -FGAPOP=6  
-FGAPOP=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hgc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1330	99.0	889	4	BM451059 AGENCOURT
2	1259	93.7	814	4	BM051236 603634191
3	1228	91.4	1308	3	CR602194 full-length
4	1214	90.4	1006	2	BF663323 602144463
5	1198	88.5	921	2	BF664198 602145812
6	1186.5	88.3	772	2	BE796570 601592247
7	1155	88.0	1321	3	CR625911 full-length
8	1139	87.9	750	6	CB852718 UI-CF-FNO
9	87.6	779	2	BF663695 602145414	

10	1163	86.6	934	5	BQ931589
11	1156	86.1	919	3	AK007659 Mus muscu
12	1156	86.1	2243	3	AK054334 Mus muscu
13	1126	83.8	910	6	BY707694 BY707694
14	1111	82.7	999	3	BC019467 Mus muscu
15	1101	82.0	756	6	CA777547
16	1101	82.0	771	6	CB852030
17	1094	81.5	977	5	BU841828 AGENCOURT
18	1090	81.2	886	6	CB181160 AGENCOURT
19	1089	81.1	904	6	CB194568 AGENCOURT
20	1066	79.4	909	6	CB194405 AGENCOURT
21	1050	78.2	826	5	BP433057 BP433057
22	1049	78.1	790	4	BI411825 602966437
23	1042	77.6	753	5	BP463671 BP463671
24	1037	77.2	625	4	BM768764
25	1010	75.2	1035	5	BX339546 BX339546
26	1008	75.1	912	4	BG339399 602437508
27	1000	74.5	714	5	BM976177 UI-CF-EN1
28	996	74.2	710	5	BQ746381 UI-M-ERO-
29	981	73.0	691	2	BE279279
30	981	73.0	1122	4	BG339315 602437607
31	975	72.6	688	7	CK464189 935151 MA
32	969	72.2	1065	5	BQ072503 AGENCOURT
33	954	71.0	580	4	BM769685 K-EST0052
34	953	71.0	725	7	CN157520 946232 MA
35	945	71.0	725	7	CN159458 948536 MA
36	945	70.4	676	2	BB666437 BB666437
37	938	69.8	581	5	BP322631 BP322631
38	930	69.2	614	7	CK622065 ml32bl1.Y
39	912	67.9	581	1	AI929359 au59E03.Y
40	900	67.1	598	5	BQ918468 AGENCOURT
41	882	65.7	587	5	BP272395 BP272395
42	872	64.9	606	2	AW157329 au94F01.X
43	857	63.8	666	7	CK463833 934767 MA
44	855	63.7	710	7	CK771494 959788 MA
45	844	63.6	564	2	AW163385 946147 MA
46	843	62.8	685	7	CN159383 948451 MA
47	843	62.8	685	7	CN161942 951279 MA
48	841	62.6	675	7	CN163323 952815 MA
49	841	62.6	681	7	CK938500 UI-R-AF1-
50	841	62.6	682	7	CN166896 958978 MA
51	836	61.5	566	2	AW163525 au95H04.Y
52	823	61.3	549	2	BE014998 126934 MA
53	823	61.3	549	2	BE014998 126934 MA
54	822	61.2	589	1	AI692198 wd37h07.X
55	819	61.0	583	5	BP323071 BP323071
56	818	60.9	714	2	BF341318 602013260
57	816	60.8	573	4	BI340505 365795 MA
58	814	60.6	582	2	AW157252 au93e01.X
59	800	59.6	639	4	BG910899 602812540
60	799	59.5	556	2	BE665755 154904 MA
61	773	57.6	543	2	BE665750 154898 MA
62	773	57.6	546	2	BE237447 146741 MA
63	771	57.4	524	6	CB720369 AGENCOURT
64	769	57.3	1110	4	BI198020 602762169
65	769	57.3	550	2	BE684896 186649 MA
66	767	57.1	578	2	AW003514 wg66g10.X
67	767	57.1	579	4	BI341406 368809 MA
68	763	56.8	605	4	BG95491 358968 MA
69	762	56.7	516	6	CB716330 AGENCOURT
70	760	56.6	622	6	CD674768 f815a05.Y
71	755	56.2	695	4	BG081244 H3062H08-
72	749	55.8	572	1	AI765658 w182g12.X
73	745	55.5	513	2	BF193331 244743 MA
74	740	55.1	546	2	AW157459 au95H04.X
75	737	54.9	434	4	BM826016 K-EST0097
76	735	54.8	971	4	BG680071 602628219
77	729	54.3	2171	3	AK046931 Mus muscu
78	727	54.2	1162	2	BE797685 601584583
79	726	54.1	456	5	BQ083301 K-EST0145
80	724	53.9	517	9	CG651631 O87413096
81	724	53.9	584	7	CF360100 821402 MA
82	723	53.8	732	2	BE287985 601093725

553 2 BE286087 BE286087 601095931 156 571.5 42.6 1572 3 CR693937 Tetraodon  
580 4 BI680796 BI680796 459974 MA 157 571 42.5 453 1 AI969924 Tetraodon  
485 5 BX524890 BX524890 158 570.5 42.5 1150 3 CR684437 Tetraodon  
446 4 BM825668 BM825668 K-EST0097 159 570.5 42.5 1162 3 CR683289 Tetraodon  
620 1 AA584408 AA584408 m81b03.s 160 569.5 42.4 1244 3 CR732330 Tetraodon  
638 1 AI924025 AI924025 wnt3606.x 161 569 42.4 1186 3 CR640728 Tetraodon  
638 1 BX339545 BX339545 162 569 42.4 1208 3 CR700159 Tetraodon  
52.2 1056 5 BX339545 BX339545 163 569 42.4 1222 3 CR696179 Tetraodon  
52.1 575 1 AI810740 AI810740 t04a11.x 164 568 42.3 582 5 BQ615284 fab24d05.  
52.1 599 4 BG498801 BG498801 602544450 165 568 42.3 596 4 BM574082 f458h01.y  
51.6 970 5 BX422891 BX422891 166 568 42.3 790 4 BJ719956 BJ719956  
449 2 AW163255 AW163255 au3601.y 167 568 42.3 1228 3 CR731482 Tetraodon  
516 4 BG285119 BG285119 602409396 168 568 42.3 1243 3 CR638609 Tetraodon  
95 629 1 AI989669 AI989669 ws35a05.x 169 568 42.3 1247 3 CR727683 Tetraodon  
96 481 7 CR749077 CR749077 170 567.5 42.3 1218 3 CR727337 Tetraodon  
506 4 BI340371 BI340371 365618 MA 171 567.5 42.3 1220 3 CR682032 Tetraodon  
505 1 AA016453 AA016453 mh40c05.x 172 567 42.2 379 2 BF522579 UI-R-C3-C  
413 5 BQ082692 BQ082692 K-EST0144 173 567 42.2 746 6 CA374473 AGENCOURT  
442 7 CK457735 CK457735 922062 MA 174 566.5 42.2 1161 3 CR732881 Tetraodon  
442 7 CK458804 CK458804 923214 MA 175 566.5 42.2 1263 3 CR682009 Tetraodon  
47.7 977 4 BI198073 BI198073 602762269 176 566 41.7 724 6 CA382012 661717 NC  
474 4 BM141962 BM141962 if24h03.y 177 564 42.0 458 4 BG689814 338070 BA  
47.5 502 7 CR819655 CR819655 if22d02.y 178 563 41.9 1231 3 CR687110 Tetraodon  
47.5 411 5 BX074246 BX074246 179 562.5 41.9 1074 6 CA490947 AGENCOURT  
46.7 740 5 BF181707 BF181707 601805520 180 562 41.8 576 4 BM529070 f61f11.y  
46.7 411 5 BM768965 BM768965 K-EST0022 181 560 41.7 638 1 AI659582 tt87c02.x  
46.7 411 5 BX074246 BX074246 182 560 41.7 578 6 CA353706 625267 NC  
46.7 411 5 BF181707 BF181707 601805520 183 559.5 41.7 1143 3 CR685515 Tetraodon  
46.7 411 5 BF181707 BF181707 601805520 184 559 41.6 581 5 BQ450896 fab12d03.  
46.7 411 5 BF181707 BF181707 601805520 185 559 41.6 653 4 BM426804 p6f21.pk0  
46.7 411 5 BF181707 BF181707 601805520 186 556.5 41.4 1198 3 CR695082 Tetraodon  
46.7 411 5 BF181707 BF181707 601805520 187 553.5 41.2 871 3 CR653669 Tetraodon  
46.7 411 5 BF181707 BF181707 601805520 188 553.5 41.2 878 3 CR654482 Tetraodon  
46.7 411 5 BF181707 BF181707 601805520 189 553 41.2 428 5 BY041621 BY041621  
46.7 411 5 BF181707 BF181707 601805520 190 552.5 41.1 885 3 CR633632 Tetraodon  
46.7 411 5 BF181707 BF181707 601805520 191 551.5 41.1 1200 3 CR698066 Tetraodon  
46.7 411 5 BF181707 BF181707 601805520 192 551 41.0 569 5 BQ480163 faa86g07.  
46.7 411 5 BF181707 BF181707 601805520 193 549.5 40.9 913 3 CR638711 Tetraodon  
46.7 411 5 BF181707 BF181707 601805520 194 547 40.7 1188 3 CR690884 Tetraodon  
46.7 411 5 BF181707 BF181707 601805520 195 546.5 40.7 860 3 CR655148 Tetraodon  
46.7 411 5 BF181707 BF181707 601805520 196 546.5 40.7 861 3 CR634105 Tetraodon  
46.7 411 5 BF181707 BF181707 601805520 197 546.5 40.7 862 3 CR645383 Tetraodon  
46.7 411 5 BF181707 BF181707 601805520 198 546.5 40.7 1186 3 CR690706 Tetraodon  
46.7 411 5 BF181707 BF181707 601805520 199 545.5 40.6 860 3 CR656656 Tetraodon  
46.7 411 5 BF181707 BF181707 601805520 200 545.5 40.6 863 3 CR644752 Tetraodon  
46.7 411 5 BF181707 BF181707 601805520 201 545.5 40.6 874 3 CR651698 Tetraodon  
46.7 411 5 BF181707 BF181707 601805520 202 545.5 40.6 876 3 CR649975 Tetraodon  
46.7 411 5 BF181707 BF181707 601805520 203 545.5 40.6 881 3 CR656653 Tetraodon  
46.7 411 5 BF181707 BF181707 601805520 204 544.5 40.5 862 3 CR650550 Tetraodon  
46.7 411 5 BF181707 BF181707 601805520 205 544.5 40.5 873 3 CR733986 Tetraodon  
46.7 411 5 BF181707 BF181707 601805520 206 544 40.5 454 5 BU500439 AGENCOURT  
46.7 411 5 BF181707 BF181707 601805520 207 542.5 40.4 864 3 CR653465 Tetraodon  
46.7 411 5 BF181707 BF181707 601805520 208 542.5 40.4 884 3 CR653782 Tetraodon  
46.7 411 5 BF181707 BF181707 601805520 209 542.5 40.4 904 3 CR639009 Tetraodon  
46.7 411 5 BF181707 BF181707 601805520 210 542.5 40.4 910 3 CR637674 Tetraodon  
46.7 411 5 BF181707 BF181707 601805520 211 542.5 40.4 910 3 CR637704 Tetraodon  
46.7 411 5 BF181707 BF181707 601805520 212 542.5 40.4 924 3 CR655129 Tetraodon  
46.7 411 5 BF181707 BF181707 601805520 213 542.5 40.4 1181 3 CR692840 Tetraodon  
46.7 411 5 BF181707 BF181707 601805520 214 542 40.4 796 7 CF931709 EST0141 A  
46.7 411 5 BF181707 BF181707 601805520 215 542 40.4 905 4 BM439118 f9v8c04.y  
46.7 411 5 BF181707 BF181707 601805520 216 542 40.4 1211 3 CR698267 Tetraodon  
46.7 411 5 BF181707 BF181707 601805520 217 541.5 40.3 858 3 CR641707 Tetraodon  
46.7 411 5 BF181707 BF181707 601805520 218 541.5 40.3 863 3 CR637158 Tetraodon  
46.7 411 5 BF181707 BF181707 601805520 219 541.5 40.3 1189 3 CR734171 Tetraodon  
46.7 411 5 BF181707 BF181707 601805520 220 541 40.3 555 4 BM154433 f4v8a10.y  
46.7 411 5 BF181707 BF181707 601805520 221 541 40.3 561 4 BM186124 f9v8c04.y  
46.7 411 5 BF181707 BF181707 601805520 222 541 40.3 1188 3 CR698292 Tetraodon  
46.7 411 5 BF181707 BF181707 601805520 223 540.5 40.2 1263 3 CR727342 Tetraodon  
46.7 411 5 BF181707 BF181707 601805520 224 540 40.2 581 5 BQ783563 fab31c01.  
46.7 411 5 BF181707 BF181707 601805520 225 539 40.1 720 6 CA360096 63318 NC  
46.7 411 5 BF181707 BF181707 601805520 226 538 40.1 375 2 BE653217 UI-M-AM0-  
46.7 411 5 BF181707 BF181707 601805520 227 538 40.1 756 4 BJ739050 BJ739050  
46.7 411 5 BF181707 BF181707 601805520 228 538 40.1 764 4 BJ716953 BJ716953



229	538	40.1	765	6	CA341770	671433 NC	C 302	445	33.1	423	2	AW52701	UI-R-BJO-
230	537	40.0	553	4	BM186049	f97a10.Y	303	445	33.1	473	6	CA395926	CA395926 c870g11.Y
231	537	40.0	868	7	CK406586	AUF Iflvr	C 304	445	33.1	600	6	C23352	C23352 C23352 Japa
232	537	40.0	869	7	CK409595	AUF Iflvr	305	444	33.1	469	4	BJ010311	BJ010311
233	537	40.0	943	7	CK409493	AUF Iflvr	306	444	33.1	566	7	CK885643	CK885643 SGP166021
234	535	39.8	1215	3	CR726092	Tetraodon	307	444	33.1	781	5	BU296625	BU296625 603733078
235	532	39.6	688	6	CA350955	621897 NC	308	443	33.0	362	5	BY045218	BY045218 BY045218
236	531.5	39.6	583	9	CG567423	Q8T193749	309	441	32.8	344	5	BY057551	BY057551 BY057551
237	530	39.5	426	2	BE233897	BE233897	310	441	32.8	543	6	C23048	C23048 C23048 Japa
238	529	39.4	479	2	AW251950	UI-R-BJO-	C 311	438	32.6	370	1	AI341293	AI341293 q85d06.x
239	528	39.3	855	7	CK985363	58335 126	312	437.5	32.6	917	7	CK406909	CK406909 AUF Iflvr
240	527	39.2	537	4	BM534699	fx70d07.Y	313	436	32.5	808	7	CK977279	CK977279 27484 125
241	526	39.2	918	7	CK409380	AUF Iflvr	314	434	32.3	336	5	BY048400	BY048400 BY048400
242	525	39.1	921	7	CK406607	AUF Iflvr	C 315	433	32.2	413	2	AW523346	AW523346 UI-R-BJO-
243	524	39.0	400	5	BY050241	BY050241	C 316	432	32.2	499	2	AL919863	AL919863 AL919863
244	524	39.0	854	3	CR651708	Tetraodon	317	431	32.1	613	7	CK896516	CK896516 SGP159062
245	524	39.0	934	7	CK406893	AUF Iflvr	C 318	430	32.0	298	2	AW664650	AW664650 h184b01.x
246	522	38.9	422	2	BF593185	7050a03.x	319	427	31.8	610	7	CK896728	CK896728 SGP159280
247	521	38.8	678	7	CK974704	23486 125	C 320	426	31.7	411	2	AW251159	AW251159 UI-R-BJO-
248	520	38.7	869	7	CK985211	57529 127	C 321	423	31.5	627	5	BQ036498	BQ036498 SJ5-0017
249	519	38.6	629	1	AUI79577	AUI79577	C 322	420	31.3	598	7	CK895980	CK895980 SGP158514
250	518	38.6	460	1	AI340993	q82909.x	323	420	31.3	847	7	CK175403	CK175403 AGENCOURT
251	518	38.6	614	1	AUI80003	AUI80003	324	419	31.2	616	3	CR647326	CR647326 Tetraodon
252	518	38.6	896	7	CK407472	AUF Iflvr	325	419	31.2	937	6	CA458592	CA458592 AGENCOURT
253	512	38.1	421	2	AW299522	AW299522	326	416.5	31.0	671	5	EX864474	EX864474 EX864474
254	512	38.1	645	4	BJ705610	BJ705610	C 327	416	31.0	737	2	AW012934	AW012934 Ldt-0102
255	512	38.1	660	4	BJ727162	BJ727162	C 328	413	30.8	635	8	AZ958898	AZ958898 2M026D22
256	511	38.0	902	7	CK409572	AUF Iflvr	329	409.5	30.5	720	5	CK989253	CK989253 56281 125
257	511	38.0	956	7	CK406337	AUF Iflvr	330	408	30.4	416	5	BQ479917	BQ479917 faa8a07.
258	509.5	37.9	691	4	BJ708514	BJ708514	331	408	30.4	439	5	BY447416	BY447416 BY447416
259	509	37.9	448	1	AI349083	q83909.x	332	407.5	30.3	766	5	BU010720	BU010720 QGJ14E17.
260	509	37.9	643	6	CB512007	sealrgb53	333	407	30.3	539	6	CA333551	CA333551 haa85C09.
261	509	37.9	722	5	BQ208081	UI-R-EP0-	334	406	30.2	526	5	BY468703	BY468703 BY468703
262	509	37.9	837	6	C23373	C23373 Japa	335	404	30.1	531	5	BY085557	BY085557 BY085557
263	508.5	37.9	1205	3	AA062934	Tetraodon	336	404	30.1	808	7	CK991683	CK991683 68533 125
264	507	37.8	384	1	AA068794	mm60d11.x	C 337	403	30.0	406	4	BI288752	BI288752 UI-R-EP0-
265	504	37.5	415	2	AW299513	AW299513	338	403	30.0	599	1	AI981881	AI981881 pat.pK006
266	504	37.5	923	3	CK407551	AUF Iflvr	339	403	30.0	635	7	CK984429	CK984429 53247 126
267	503	37.5	612	4	BI304044	UI-R-DR0-	340	401.5	29.9	753	6	CA782445	CA782445 8at2H08.
268	503	37.5	875	7	CK978664	29797 125	341	401	29.9	243	4	BI032844	BI032844 603082670
269	495	36.9	415	1	AI340991	q82907.x	C 342	401	29.9	878	7	CK036616	CK036616 RTK1 29.A
270	495	36.9	638	4	BJ711589	BJ711589	C 343	399	29.7	262	2	BF509580	BF509580 UI-H-BI-
271	494	36.8	905	7	CK407588	AUF Iflvr	344	398	29.6	882	7	CK605765	CK605765 gmrhrw6-
272	492	36.6	670	6	CA355616	627543 NC	C 345	398	29.6	1045	3	CN80A6FG	CN80A6FG
273	490	36.5	731	4	BJ722907	BJ722907	C 346	397	29.6	341	1	AI650609	AI650609 w501F04.x
274	490	36.5	866	7	CK175149	AGENCOURT	347	397	29.6	857	7	CK172476	CK172476 AGENCOURT
275	489	36.4	587	7	CK986420	SGP158963	348	396.5	29.5	779	4	BG647257	BG647257 EST508886
276	488	36.3	642	1	AI477552	f858904.Y	C 349	396	29.5	759	9	CL975287	CL975287 O8IFCC027
277	486	36.2	401	6	CB698999	AMGNNUC.N	C 350	396	29.5	826	7	CK189143	CK189143 EST778458
278	485.5	36.0	527	5	BQ615750	f814b01.	351	396	29.5	866	6	CB650869	CB650869 OSJNEB15J
279	484	36.0	371	5	BY048974	BY048974	352	396	29.5	873	7	CK189144	CK189144 EST778459
280	481	35.8	704	2	BF228537	EST00248	C 353	395	29.4	365	6	CB050636	CB050636 NISC GJ18
281	479	35.7	434	2	BB787832	BB787832	354	395	29.4	365	6	CB050637	CB050637 NISC GJ18
282	478	35.6	405	1	AI912836	t286c05.x	355	395	29.4	635	6	C23181	C23181 C23181 Japa
283	477	35.5	374	5	BY037587	BY037587	C 356	394.5	29.4	720	7	C0532807	C0532807 3530 121
284	477	35.5	579	7	CK995655	SGP158175	357	394	29.3	398	4	BM573972	BM573972 fx57d11.Y
285	477	35.5	874	7	CK169125	AGENCOURT	358	394	29.3	593	7	CK888688	CK888688 SGP160680
286	476	35.4	513	5	BO783421	fab29f02.	359	394	29.3	1064	7	CK163121	CK163121 FCAS01573
287	471.5	35.1	1206	3	CR641100	Tetraodon	C 360	393	29.3	683	2	BE594747	BE594747 BE594747
288	471	35.1	360	5	BY057583	BY057583	361	392.5	29.2	818	7	CF203341	CF203341 RR890915N
289	470	35.0	746	7	CK988270	64067 125	C 362	392	29.2	419	7	CK542838	CK542838 UI-R-EAO-
290	468	34.8	436	2	AW251225	UI-R-BJO-	363	392	29.2	465	4	BJ498661	BJ498661 BJ498661
291	464	34.5	598	7	CK995107	SGP154357	364	392	29.2	499	4	BJ527812	BJ527812 BJ527812
292	463	34.5	661	4	BI468189	EST00596	365	392	29.2	515	4	BJ490344	BJ490344 BJ490344
293	461	34.3	551	7	CK986911	SGP159468	366	392	29.2	562	4	BJ496988	BJ496988 BJ496988
294	459.5	34.2	1211	3	CK863715	Tetraodon	367	391.5	29.2	833	7	CF215293	CF215293 CAST0001
295	458	34.1	372	5	BO742000	BO742000	368	391.5	29.2	924	7	CF652643	CF652643 68-L02013
296	457.5	34.1	812	7	CO804908	AGENCOURT	369	391.5	29.2	942	7	CF516928	CF516928 CAP0004_I
297	454	33.8	292	4	BM856156	K-EST0139	370	391.5	29.2	1003	3	CN80A315	CN80A315
298	453.5	33.8	644	6	CA333572	haa85h10.	371	391.5	29.2	1024	3	CN80A355	CN80A355
299	453	33.7	503	4	BG669239	DRN1G10.R	372	391	29.1	370	5	BY398856	BY398856
300	451	33.6	375	5	BY041991	BY041991	373	390.5	29.1	810	7	CF213611	CF213611 CGF100079
301	451	33.6	963	7	CK409756	AUF_iphdk	374	390	29.0	488	6	CD737778	CD737778 4023355 1



[illegible]

667	339.5	25.3	658	7	CK240496	VRJ324T7	740	333	24.8	738	7	CK861883	CK861883 33001 In
668	339.5	25.3	676	4	BI263612	WF089A09P	c 741	333	24.8	743	4	BJ252414	BJ252414 BJ252414
669	339.5	25.3	721	5	B0838009	NH2805E	742	333	24.8	766	7	CJ173178	CJ173178 NDLL 34 B
c 670	339.5	25.3	802	9	CC615544	CGWD123TV	743	333	24.8	882	7	CN201625	CN201625 Tor1590 G
671	339.5	25.3	807	2	BF259949	HVSMER002	744	332.5	24.8	645	2	BF642662	BF642662 NF070H07I
672	339	25.2	808	6	CD827397	BN25.067F	745	332.5	24.8	671	4	BM063898	BM063898 KS01060G0
673	339	25.2	889	6	CA159865	SCJFRZ3C0	746	332.5	24.8	725	6	CD823678	CD823678 BN25.049J
674	338.5	25.2	601	2	BE998051	EST429774	747	332.5	24.8	726	7	CN190771	CN190771 UCRCS06 0
675	338.5	25.2	662	2	BE610562	sg7H11 Y	748	332.5	24.8	739	7	CK932928	CK932928 CGF100434
676	338.5	25.2	666	4	BI265049	NF004C10I	749	332.5	24.8	817	7	CK197926	CK197926 FGAS00640
c 677	338.5	25.2	818	6	CD575294	UCRPT01 0	750	332	24.7	208	2	BE853865	BE853865 ux22508.Y
c 678	338	25.2	797	6	CD868553	AZ02.109E	751	332	24.7	867	7	CO102007	CO102007 GR EB002
679	337.5	25.1	548	4	BM527768	sa165f09.	752	331.5	24.7	511	4	BG653155	BG653155 sadB2f01.
680	337.5	25.1	637	2	BF520898	EST458371	753	331.5	24.7	600	7	CO909118	CO909118 BJ0204080
681	337.5	25.1	651	4	BI270050	NF003E10F	754	331.5	24.7	649	6	CD879761	CD879761 AZ04.106E
682	337.5	25.1	673	7	CN190619	UCRCS06 0	755	331.5	24.7	665	1	AI898029	AI898029 EST267472
683	337.5	25.1	674	2	AW560150	EST315198	756	331.5	24.7	681	5	BQ875399	BQ875399 QSI8A03.Y
684	337.5	25.1	683	2	BF520049	EST457517	757	331.5	24.7	681	5	BQ987553	BQ987553 QGF12119.
685	337.5	25.1	683	6	CD930335	GR45.110P	758	331.5	24.7	683	2	AW030736	AW030736 EST273991
686	337.5	25.1	699	5	BO624767	USDA-FP 0	759	331.5	24.7	683	4	BI922821	BI922821 EST542725
687	337.5	25.1	718	6	CD938268	OV.109I23	760	331.5	24.7	714	6	CA918225	CA918225 EST642372
c 688	337.5	25.1	718	6	CD938289	OV.109K04	761	331.5	24.7	726	5	BQ838107	BQ838107 WHE2806 F
c 689	337.5	25.1	746	7	CK215205	FGAS02715	762	331.5	24.7	750	7	CF921444	CF921444 gmrHrw3-
690	337	25.1	629	6	CF478576	eca01-14m	763	331	24.6	606	2	BE021597	BE021597 sm0804.Y
691	337	25.1	732	7	CF438087	EST674432	c 764	331	24.6	946	6	CA270677	CA270677 SCRUIB206
692	337	25.1	779	5	BI115361	EST600937	765	330.5	24.6	519	2	BF636493	BF636493 NF088G06D
693	336.5	25.1	543	1	AI939180	sc67h02.Y	766	330.5	24.6	596	2	BE403578	BE403578 WHE0434 C
694	336.5	25.1	617	2	BE405650	WHE1209 G	767	330.5	24.6	631	2	BF473218	BF473218 WHE09222 H
695	336.5	25.1	618	2	BE801899	sr20h08.Y	768	330.5	24.6	648	7	CN192437	CN192437 UCRCS06 0
696	336.5	25.1	653	4	BI957460	HVSMEn000	769	330.5	24.6	652	7	CF836276	CF836276 UCRCS03 0
697	336.5	25.1	704	6	CD817128	BN20.040N	770	330.5	24.6	658	7	CN191414	CN191414 UCRCS06 0
698	336.5	25.1	786	7	CN137489	OX1 57 D0	771	330.5	24.6	731	1	AJ803420	AJ803420 AJ803420
699	336.5	25.1	797	7	CK193882	FGAS00228	772	330.5	24.6	772	6	CD839679	CD839679 RF02.116D
c 700	336	25.0	442	7	CN967735	14632.100	773	330.5	24.6	1121	6	CK131093	CK131093 SCBFT106
c 701	336	25.0	646	4	BJ466490	BJ466490	774	330	24.6	569	7	CK439809	CK439809 G00021B.B
702	336	25.0	675	4	BM814917	EST593011	c 775	330	24.6	706	7	CF517412	CF517412 CAP0005.1
703	336	25.0	733	5	BQ838231	WHE2908 A	776	330	24.6	712	7	CF389766	CF389766 RTDR2 5 A
c 704	336	25.0	750	6	CD898674	G174.105L	777	330	24.6	712	7	CF473897	CF473897 RTW2 19
c 705	336	25.0	776	5	BO418942	RN0SF01F0	778	330	24.6	718	7	CF478998	CF478998 RTW2 21-
c 706	335.5	25.0	530	6	CB9395923	OSTRI63G7	779	330	24.6	747	7	CF396117	CF396117 RTDS2 13-
707	335.5	25.0	529	2	AW102353	sd86f04.Y	780	329.5	24.5	562	2	BF484304	BF484304 WHE2321 F
708	335.5	25.0	623	8	BZ641943	OGAMK72TC	781	329.5	24.5	606	2	BE205077	BE205077 EST397753
c 709	335.5	25.0	731	7	CK240495	VRJ324 V1	782	329.5	24.5	638	4	BG453560	BG453560 NF096D07L
c 710	335.5	25.0	737	2	AW340485	GM210002B	783	329.5	24.5	639	4	BI959367	BI959367 HVSMEn001
711	335.5	25.0	747	7	CF474427	RTW2 20	784	329.5	24.5	651	2	AW094365	AW094365 EST287545
712	335	24.9	337	2	AW356352	38646 MAR	785	329.5	24.5	666	1	AL504625	AL504625 AL504625
713	335	24.9	744	7	CF478537	RTW3 20	786	329.5	24.5	672	2	AW442463	AW442463 EST307393
714	334.5	24.9	531	4	BI426741	sa906G09.	787	329.5	24.5	684	4	BM110489	BM110489 EST558025
715	334.5	24.9	598	4	BI321639	sa915G02.	788	329.5	24.5	693	2	BE208886	BE208886 GF-FV-P3C
716	334.5	24.9	644	6	CD930761	GR45.112E	789	329	24.5	631	4	BM284958	BM284958 Kh93a08.Y
717	334.5	24.9	646	5	BQ838318	WHE2909 A	790	329	24.5	672	2	BF473981	BF473981 WHE0839 F
718	334.5	24.9	724	7	CF921036	gmrHrw3-	791	328.5	24.5	640	2	AW218547	AW218547 EST303730
719	334	24.9	656	5	BP176248	BP176248	792	328.5	24.5	646	2	AW625527	AW625527 EST319434
720	334	24.9	659	1	AJ615423	AJ615423	793	328.5	24.5	649	7	CF227474	CF227474 Ptad6D590
721	334	24.9	661	4	BJ247474	BJ247474	794	328.5	24.5	655	4	BI960120	BI960120 HVSMEn002
722	334	24.9	692	6	CD868552	AZ02.109E	c 795	328.5	24.5	762	7	CO171539	CO171539 NDLL 22 C
723	333.5	24.8	630	4	BG449728	NF007D11I	c 796	328.5	24.5	797	7	CF838015	CF838015 UCRCS03 0
724	333.5	24.8	632	2	BE325133	NF087F045	c 797	328.5	24.5	799	7	CF833359	CF833359 UCRCS02 0
725	333.5	24.8	654	6	CA131555	SCBGR104	c 798	328.5	24.5	800	7	CF833320	CF833320 UCRCS02 0
726	333.5	24.8	682	2	BF597864	su89C03.Y	c 799	328.5	24.5	859	6	CB823461	CB823461 EST 4685
727	333.5	24.8	682	2	BF641947	NF011B12I	800	328	24.4	743	6	CA180815	CA180815 SCACST316
728	333.5	24.8	684	5	BUR75316	V005C03 P	801	327.5	24.4	621	5	BQ743179	BQ743179 WHE4101 C
729	333.5	24.8	694	5	BUR77332	V032G08 P	802	327.5	24.4	623	6	CA821361	CA821361 RSH01H05
730	333.5	24.8	699	1	AJ615461	AJ615461	803	327.5	24.4	635	1	AJ560090	AJ560090 AJ560090
731	333.5	24.8	708	7	CN184479	UCRCS04 0	804	327.5	24.4	637	4	BF960118	BF960118 HVSMEn002
732	333.5	24.8	709	5	BQ752659	WHE4117 F	805	327.5	24.4	654	7	CF236064	CF236064 PtadXT003
733	333.5	24.8	716	5	BUR74994	V001B12 P	806	327.5	24.4	721	6	CD839960	CD839960 RF02.117E
734	333.5	24.8	722	5	BQ789135	WHE4158 A	807	327	24.3	667	6	CA196132	CA196132 SCSCBAD108
735	333.5	24.8	756	2	BF630744	HVSMEn001	808	327	24.3	676	7	CV006380	CV006380 CS gill 12
c 736	333	24.8	417	1	AI477667	fb59G04.x	809	327	24.3	762	7	CF472622	CF472622 RTDS1 10
737	333	24.8	650	7	CV093856	FAMU USDA	810	326.5	24.3	629	4	BI959561	BI959561 HVSMEn002
738	333	24.8	664	5	BP184560	BP184560	811	326.5	24.3	636	6	CA020338	CA020338 HZ36A04 R
739	333	24.8	667	4	BI957447	HVSMEn000	812	326.5	24.3	637	5	BQ623195	BQ623195 USDA-FP 0

813	326.5	24.3	643	5	BU977235	HAL1B05r	BU977235	HAL1B05r	886	320.5	23.9	681	4	BI959659	HVSMEN002
814	326.5	24.3	648	7	BI959235	HVSMEN001	BI959235	HVSMEN001	c 887	320.5	23.9	744	4	BM408348	EST502675
815	326.5	24.3	650	7	CK987645	SP7-A3(P1	CK987645	SP7-A3(P1	888	320.5	23.9	904	4	BF972265	602240747
816	326.5	24.3	656	7	CK987647	PI-A3-rev	CK987647	PI-A3-rev	889	320	23.8	712	5	BU672830	NL 6 90 D
817	326.5	24.3	669	7	CV459741	ram01-lme	CV459741	ram01-lme	890	320	23.8	770	3	CNS0AEB3	BM18064 Arabidop
818	326.5	24.3	675	7	CF932162	PI-A4 A s	CF932162	PI-A4 A s	891	320	23.8	835	4	BM407184	EST501511
819	326.5	24.3	712	6	CD841037	RFO2.121J	CD841037	RFO2.121J	892	320	23.8	901	7	CV1130539	BSPSP03e08
820	326.5	24.3	719	6	CD840175	RFO2.118E	CD840175	RFO2.118E	893	319.5	23.8	605	1	AI486500	EST244821
821	326.5	24.3	719	7	CF833209	UCRCS02.0	CF833209	UCRCS02.0	894	319.5	23.8	662	6	CA916813	EST640960
822	326.5	24.3	774	6	CA605807	SCHFAID104	CA605807	SCHFAID104	895	319.5	23.8	664	7	CV298172	EST886631
823	326.5	24.3	791	2	BF638077	NF041H0BP	BF638077	NF041H0BP	896	319.5	23.8	666	6	CB869763	HC12G06W
824	326.5	24.3	823	2	BF264389	HV CFa000	BF264389	HV CFa000	897	319.5	23.8	670	4	BG455746	NF066H01P
825	326.5	24.3	1086	7	CK213734	FGAS02564	CK213734	FGAS02564	898	319.5	23.8	740	7	CNO11226	WHE3881 F
826	326	24.3	336	5	BY998827	BY398227	BY998827	BY398227	899	319.5	23.8	748	5	BU635690	004G05 In
827	326	24.3	660	6	CD899633	GI74.113A	CD899633	GI74.113A	900	319.5	23.8	789	5	BU894945	X017B10 P
828	326	24.3	817	7	CK194117	FGAS00253	CK194117	FGAS00253	901	319	23.8	644	1	AI895091	EST264534
829	325.5	24.2	543	4	BI788368	ea69h09.	BI788368	ea69h09.	902	319	23.8	675	6	CA209393	SCCST3C1
830	325.5	24.2	574	4	BM731352	sal70h05.	BM731352	sal70h05.	903	319	23.8	684	1	AL821924	AL821924
831	325.5	24.2	610	5	BQ467961	HR01H17r	BQ467961	HR01H17r	c 904	319	23.8	711	4	BU253542	BU253542
832	325.5	24.2	624	6	CA021273	HZ39021r	CA021273	HZ39021r	c 905	319	23.8	756	6	CB680447	OSJNEF05C
833	325.5	24.2	630	7	CNO10185	WHE3867 G	CNO10185	WHE3867 G	906	319	23.8	756	7	CF428636	PH1 9 G09
834	325.5	24.2	647	4	BI960119	HVSMEN002	BI960119	HVSMEN002	907	319	23.8	819	7	CN127149	RHOH1 21
835	325.5	24.2	660	7	CF418675	USDA-FP 1	CF418675	USDA-FP 1	908	319	23.8	853	2	BF256079	HVSMER000
836	325.5	24.2	681	1	AV782400	AV782400	AV782400	AV782400	909	318.5	23.7	549	4	BG155028	8ab40b01
837	325.5	24.2	698	5	BU896211	X037C08 P	BU896211	X037C08 P	910	318.5	23.7	570	6	CA279207	SCFBF2209
838	325.5	24.2	714	1	AJ778942	AJ778942	AJ778942	AJ778942	911	318.5	23.7	582	7	CV297680	EST886057
839	325.5	24.2	734	9	CG327759	CGXFO38TH	CG327759	CGXFO38TH	912	318.5	23.7	608	7	CK750439	pa001-6ms
840	325.5	24.2	788	7	CF669731	RTCNT1 45	CF669731	RTCNT1 45	913	318.5	23.7	609	4	BM065108	K501075A0
841	325	24.2	684	6	CA142702	CMCMT210	CA142702	CMCMT210	914	318.5	23.7	623	4	BM111532	EST559068
842	325	24.2	757	7	CF395287	RTDS2 110	CF395287	RTDS2 110	915	318.5	23.7	687	6	CA192398	SCCST3C0
843	324.5	24.2	557	2	BE404145	WHE1201 G	BE404145	WHE1201 G	c 916	318.5	23.7	694	4	BU261281	BU261281
844	324.5	24.2	591	5	BQ753204	WHE4124 C	BQ753204	WHE4124 C	c 917	318.5	23.7	745	6	CA918812	EST636530
845	324.5	24.2	624	5	BQ744417	WHE4115 D	BQ744417	WHE4115 D	918	318.5	23.7	753	7	CF436915	EST673260
846	324.5	24.2	627	5	BQ788936	WHE4155 E	BQ788936	WHE4155 E	919	318.5	23.7	856	7	CK202105	FGAS01062
847	324.5	24.2	628	5	BQ744183	WHE4112 F	BQ744183	WHE4112 F	920	318	23.7	695	5	BX252395	BX252395
848	324.5	24.2	664	6	CD079415	MA3-9999U	CD079415	MA3-9999U	921	318	23.7	720	6	CA2221618	SCSGFLA03
849	324.5	24.2	680	4	BI179085	EST520030	BI179085	EST520030	c 922	318	23.7	787	5	BQ515541	EST622956
850	324.5	24.2	694	4	BG564645	EST508064	BG564645	EST508064	923	317.5	23.6	510	2	AW424002	8H59C10.Y
851	324.5	24.2	707	4	BG587428	EST489200	BG587428	EST489200	924	317.5	23.6	711	5	BQ139680	NF023A10P
852	324.5	24.2	719	7	CNI146340	WOUNDI 39	CNI146340	WOUNDI 39	c 925	317.5	23.6	720	7	CF921163	gm1rhw3-
853	324	24.1	588	2	BE493950	WHE1276 H	BE493950	WHE1276 H	c 926	317.5	23.6	756	6	CD849237	DH0AC0172
854	324	24.1	624	5	BP184421	BP184421	BP184421	BP184421	927	317	23.6	468	7	CK895492	SGP158009
855	324	24.1	640	5	BQ743388	WHE4103 D	BQ743388	WHE4103 D	928	317	23.6	605	6	CA155532	SCACR2310
856	324	24.1	641	4	BM813932	EST592025	BM813932	EST592025	929	317	23.6	663	6	CA280962	SCRFSD101
857	324	24.1	649	6	CA290596	SCUTSD102	CA290596	SCUTSD102	c 930	317	23.6	681	4	BM267355	MEST365-F
858	324	24.1	791	3	CNS0A0B15	Arabidop	BM18211	Arabidop	931	317	23.6	893	4	BI952091	HVSMEM000
859	323.5	24.1	546	4	BG096397	EST460916	BG096397	EST460916	932	316.5	23.6	515	7	CK864045	35355 In
860	323.5	24.1	664	5	BQ762267	EBr001 SQ	BQ762267	EBr001 SQ	933	316.5	23.6	559	2	BE802841	sr45d12.y
861	323.5	24.1	669	6	CD073690	MA3-0001U	CD073690	MA3-0001U	934	316.5	23.6	566	2	BE942838	EST422417
862	323.5	24.1	669	7	CF507287	USDA-FP 1	CF507287	USDA-FP 1	935	316.5	23.6	571	7	CNO08321	WHE2639 H
863	323.5	24.1	709	6	CA146291	SCVPRT207	CA146291	SCVPRT207	936	316.5	23.6	578	2	AW695176	NF092D12S
864	323.5	24.1	796	2	BE034896	ML05H01 M	BE034896	ML05H01 M	937	316.5	23.6	580	7	CN517425	G00092.B3
865	323.5	24.1	846	7	CK195394	FGAS00393	CK195394	FGAS00393	938	316.5	23.6	590	2	BF006247	EST434745
866	322.5	24.0	803	7	CK200865	FGAS00920	CK200865	FGAS00920	939	316.5	23.6	595	7	CF092647	QHN12P02.
867	322.5	24.0	633	7	CF418893	USDA-FP 1	CF418893	USDA-FP 1	940	316.5	23.6	598	2	BE124003	EST394128
868	322.5	24.0	674	7	CK739670	USDA-FP 6	CK739670	USDA-FP 6	941	316.5	23.6	637	5	BQ765794	EBr003 SQ
869	322.5	24.0	840	7	CO234257	WS0261 B2	CO234257	WS0261 B2	942	316.5	23.6	643	7	CF518411	CAP0007 I
870	322	24.0	640	6	CA191213	SCCCT2C0	CA191213	SCCCT2C0	943	316	23.5	669	6	CA187131	SCUTST308
871	322	24.0	649	6	CD904272	G356.112P	CD904272	G356.112P	944	316	23.5	691	1	AJ613139	AJ613139
872	322	24.0	716	4	BI960085	HVSMEN001	BI960085	HVSMEN001	c 945	315.5	23.5	836	9	CG323590	CGWIE57TV
873	322	24.0	736	2	BF630555	HVSMEM002	BF630555	HVSMEM002	c 946	315.5	23.5	862	6	CF059783	QCS16904.
874	322	24.0	807	7	CF443345	EST679690	CF443345	EST679690	947	315.5	23.5	539	2	AW980337	EST931490
875	321.5	23.9	647	7	CNO12727	WHE3952 B	CNO12727	WHE3952 B	948	315.5	23.5	561	4	BM732615	sal79d10.
876	321.5	23.9	686	7	CF833210	UCRCS02.0	CF833210	UCRCS02.0	949	315.5	23.5	631	2	AW776700	EST335765
877	321.5	23.9	754	4	BG584701	EST486462	BG584701	EST486462	950	315.5	23.5	668	7	CV299158	EST887617
878	321.5	23.9	770	4	BI967327	GM830001B	BI967327	GM830001B	951	315.5	23.5	702	6	CA179873	SCCST200
879	321	23.9	616	4	BJ259369	BJ259369	BJ259369	BJ259369	952	315	23.5	442	7	CN966263	13760 100
880	321	23.9	678	6	CA071322	SCACAM107	CA071322	SCACAM107	953	315	23.5	660	5	BQ806305	WHE3577 C
881	321	23.9	737	7	CF397756	RTDS3 1 C	CF397756	RTDS3 1 C	954	315	23.5	739	9	CNO13071	WHE3956 D
882	321	23.9	795	7	CK123412	OSTR30010	CK123412	OSTR30010	c 955	315	23.5	852	9	CG320079	CG320079
883	321	23.9	881	7	CK196097	FGAS00454	CK196097	FGAS00454	956	315	23.5	880	9	CG229531	CG229531
884	320.5	23.9	637	7	CNI89395	UCRCS06.0	CNI89395	UCRCS06.0	957	314.5	23.4	540	4	BG789661	8ae53e08.
885	320.5	23.9	643	2	AW695080	NF091D11S	AW695080	NF091D11S	958	314.5	23.4	562	2	AW683492	NF012H09L

959	314.5	23.4	598	5	BU008292	QGH7C13.Y	1032	307.5	22.9	772	7	CF229531	PtAXM0026
960	314.5	23.4	616	5	BO788665	WHE4152.E	1033	307.5	22.9	775	6	CD839277	RFO2.114K
961	314.5	23.4	625	5	AW034347	EST2779I8	1034	307	22.9	776	6	CD895487	G174.001P
962	314.5	23.4	708	7	CF213537	CSF100060	1035	306.5	22.8	503	1	AI898952	EST268395
963	314.5	23.4	776	7	CN987035	62721.125	1036	306.5	22.8	534	2	AE287882	N100726e
964	314.5	23.4	684	2	BF627066	HVSMBS000	1037	306.5	22.8	535	2	BE574803	H20.Triph
965	313.5	23.3	472	5	BQ640884	HE01017r	1038	306.5	22.8	546	1	AL827353	AL827353
966	313.5	23.3	573	2	BE998050	EST429773	1039	306.5	22.8	580	1	AU261430	AU261430
967	313.5	23.3	605	5	BQ970451	QHB42822.	1040	306.5	22.8	618	4	BG453059	NF089H11L
968	313.5	23.3	612	5	BQ699842	NARV122.D	C1041	306.5	22.8	664	4	BI308484	EST529894
969	313.5	23.3	635	5	BQ888753	P012B02.P	1042	306.5	22.8	668	5	BU887057	R054A07.P
970	313	23.3	486	3	CR640865	Tetraodon	C1043	306.5	22.8	694	4	BJ265176	BJ265176
971	313	23.3	679	6	CA262688	ScpILB202	1044	306	22.8	626	5	BM895773	952065C05
972	313	23.3	702	4	BI073165	PIP2A.F04	1045	306	22.8	636	7	CV502501	68895.1.M
973	313	23.3	881	7	CK202172	FGAS01069	1046	306	22.8	664	1	AJ802646	AJ802646
974	312.5	23.3	539	7	COA15038	Mdfw2041m	1047	306	22.8	692	6	CA168805	SCERQB101
975	312.5	23.3	540	4	BI788174	8867F01.	1048	306	22.8	698	1	AJ803239	AJ803239
976	312.5	23.3	545	2	AW620537	8106G09.Y	1049	306	22.8	727	6	CA219139	SCRAD111
977	312.5	23.3	577	5	BQ490451	24-E01178	1050	306	22.8	805	8	BZ533265	OQAES43TC
978	312.5	23.3	606	7	CF807049	d8HB019xK	C1051	306	22.8	884	7	CV270100	WS0151.B2
979	312.5	23.3	656	2	BF650456	NF097D11E	1052	305.5	22.7	454	4	BM136098	WHE2602.F
980	312.5	23.3	670	5	BU816246	NO62C10.P	1053	305.5	22.7	476	6	CA117774	SCBGR104
981	312.5	23.3	676	6	CD817919	EN20.043K	1054	305.5	22.7	544	4	BM527684	8a164f09.
982	312.5	23.3	704	5	BU814263	NO27B09.P	1055	305.5	22.7	561	1	AL819807	AL819807
983	312.5	23.3	706	7	CF233163	PtAJX0002	1056	305.5	22.7	564	4	BM085705	8a128d08.
984	312.5	23.3	719	7	CV226183	WS0163.B2	1057	305.5	22.7	572	5	BQ473426	8a112g01.
985	312.5	23.3	754	1	AJ806917	AJ806917	1058	305.5	22.7	596	6	CA085150	SCEZAM206
986	312.5	23.3	815	2	BE642551	Cri2.6_F2	1059	305.5	22.7	802	6	CA180913	SCACST336
987	312.5	23.3	817	7	CK193931	FGAS00235	1060	305.5	22.7	851	7	CK201455	FGAS00997
988	312	23.2	517	4	BG935465	SL1-0818	1061	305	22.7	646	7	CK860977	32005.In
989	312	23.2	647	4	BJ764257	BJ764257	1062	305	22.7	713	6	CA221136	SCEZFL404
990	312	23.2	726	6	CA158055	SCEZRR2305	1063	304.5	22.7	569	2	AW736350	EST332269
991	312	23.2	816	8	BZ541105	OQAET437C	1064	304.5	22.7	594	7	CK319292	X9P09b04
992	312	23.2	929	7	CV266697	WS0203.B2	1065	304.5	22.7	745	7	CF397680	RIDS.1.C
993	311.5	23.2	605	6	CA733178	wlpLC.pk0	1066	304.5	22.7	768	6	CD839106	RFO2.114A
994	311.5	23.2	611	4	BI957501	HVSMEn000	1067	304.5	22.7	831	7	CK201781	FGAS01030
995	311.5	23.2	622	7	CF395203	RTDS.10	1068	304	22.6	302	2	BF605771	272357.MA
996	311	23.2	742	6	CA146092	SCVPRRT207	1069	304	22.6	592	4	BM660366	952037B06
997	310.5	23.1	559	4	BI894075	8a159g06.	1070	304	22.6	622	6	CA182599	SCCST314
998	310.5	23.1	608	7	CK318739	X9P02911	1071	304	22.6	647	6	CA285613	SCEZSD107
999	310.5	23.1	616	5	BQ139156	NF011F12P	1072	304	22.6	661	6	CA107862	SCSBHR105
1000	310.5	23.1	624	7	CF417506	USDA-FP.1	1073	304	22.6	677	4	BG905724	TaLr1141H
1001	310.5	23.1	638	4	BI957710	HVSMEn001	1074	304	22.6	685	6	CA121225	SCEQR109
1002	310.5	23.1	650	2	BF646063	NF066E10E	1075	303.5	22.6	511	7	CF603338	BACCA01.0
1003	310.5	23.1	725	5	BU835879	T079G08.P	1076	303.5	22.6	618	7	CN010871	WHE3877.C
1004	310.5	23.1	756	7	CK215844	FGAS02781	1077	303.5	22.6	632	1	AI486948	EST245270
1005	310	23.1	447	7	CK879029	SGP143200	1078	303	22.6	609	1	AU263882	AU263882
1006	310	23.1	654	6	CA175542	SCJLST101	1079	303	22.6	679	6	CD823836	FN25.050C
1007	310	23.1	699	5	BX251392	EX251392	1080	303	22.6	814	7	CK201094	FGAS00961
1008	309.5	23.1	802	2	BF261040	HVSMF002	1081	302.5	22.5	577	2	AW703717	sk23e07.Y
1009	309.5	23.0	505	4	BG835402	354322.NA	1082	302.5	22.5	588	1	AL808354	AL808354
1010	309.5	23.0	565	2	AW625126	EST313943	1083	302.5	22.5	659	6	CA089962	SCSGAM207
1011	309.5	23.0	613	4	BI309404	EST30814	1084	302	22.5	636	4	BJ259464	BJ259464
1012	309.5	23.0	691	7	CN524624	Q0815M16.	1085	302	22.5	670	6	CA151503	SCJFRZ201
1013	309.5	23.0	756	6	CD842250	RFO2.126L	1086	302	22.5	674	5	BX251216	BX251216
1014	309.5	23.0	781	5	BU895241	X021B11.P	1087	302	22.5	674	5	BX254999	BX254999
1015	309	23.0	489	7	CF931812	EST0244.A	1088	302	22.5	689	5	BX250520	BX250520
1016	309	23.0	536	2	BF484461	WHE2309.A	1089	302	22.5	692	6	CA142664	SCMCRF210
1017	309	23.0	638	7	CN975309	25032.125	1090	302	22.5	784	6	CD840817	RFO2.120M
1018	309	23.0	718	6	CD888511	G118.108E	1091	302	22.5	814	7	CK202356	CK202356
1019	308.5	23.0	507	7	CF972935	PSU.2blon	1092	301.5	22.4	548	1	AI899227	EST268670
1020	308.5	23.0	685	2	AW690185	NF029D09S	1093	301.5	22.4	588	1	AL822798	AL822798
1021	308.5	23.0	712	7	CO361980	NDL2.8.G1	1094	301.5	22.4	643	5	BU880080	UM41TB11
1022	308.5	23.0	759	6	CD879592	AZO4.105M	C1095	301.5	22.4	707	7	CV254061	CV254061
1023	308.5	23.0	772	7	CF233249	PtAJX0002	1096	301	22.4	600	2	AW306980	9f51C05.Y
1024	308.5	23.0	834	7	CO489149	Q00258.B7	1097	301	22.4	622	4	BI679740	BI679740
1025	308	22.9	520	1	AU164541	AU164541	1098	301	22.4	652	6	CD847394	DH0AB582H
1026	308	22.9	626	2	BE423372	WHE0065.D	1099	301	22.4	666	7	CO532808	3530.1.21
1027	307.5	22.9	535	5	BQ624278	USDA-FP.0	C1100	301	22.4	702	7	CO230270	WS0011.B
1028	307.5	22.9	598	2	AW707192	sk28a02.Y	1101	300.5	22.4	560	5	BM885724	sam04d08.
1029	307.5	22.9	673	5	BQ991852	QGF24A02.	1102	300.5	22.4	578	4	BM068669	WHE3461.D
1030	307.5	22.9	698	7	CV128456	Mdftr31088	1103	300.5	22.4	591	1	AA660318	00189.MCR
1031	307.5	22.9	765	2	BE705618	Sc01_0391	1104	300.5	22.4	600	4	BI422587	EST533253



c1105	300.5	22.4	636	7	CK606552	gmrhrrw6-	ck178	293.5	21.9	630	7	CO174797	CO174797 NDLL1_46_G
c1106	300.5	22.4	637	6	CD904273	G356.112P	c1179	293.5	21.9	681	7	CF213698	CF213698 CGF100079
c1107	300.5	22.4	661	7	CK987646	SP7-B5 (P1	1180	293.5	21.9	697	7	CK863140	CK863140 34357 In
c1108	300.5	22.4	690	7	CF233271	PcaJXO002	c1181	293.5	21.9	785	4	BG320047	BG320047 2m01_01c0
c1109	300.5	22.4	720	7	CV272291	WS0157.B2	c1182	293	21.8	781	7	CO174891	CO174891 NDLL1_46_H
c1110	300.5	22.4	800	5	BQ518761	EST626176	1183	292.5	21.8	489	2	BE500470	BE500470 WHE05870
c1111	300	22.3	550	6	CA107671	SCRURH107	1184	292.5	21.8	496	2	BE330982	BE330982 BG92a07.y
c1112	300	22.3	679	6	CA253440	SCJLFL410	1185	292.5	21.8	496	5	BQ347189	BQ347189 TAE15028C
c1113	300	22.3	685	5	BU103556	SCCCHR100	1186	292.5	21.8	518	4	BG300054	BG300054 HVSMBO01
c1114	300	22.3	685	6	CA102750	SCCCHR100	1187	292.5	21.8	549	5	BQ080249	BQ080249 san30e12
c1115	299.5	22.3	516	4	BM402624	SLA006D04	1188	292.5	21.8	573	2	BF065160	BF065160 HV CBb002
c1116	299.5	22.3	551	1	AI828595	AL828595	1189	292.5	21.8	573	6	CD877125	CD877125 AS04_100B
c1117	299.5	22.3	584	1	AI898101	EST267544	1190	292.5	21.8	588	1	AA660308	AA660308 AO178 MBR
c1118	299.5	22.3	603	7	CF446610	EST682955	1191	292.5	21.8	590	4	BI779395	BI779395 EBR001.SQ
c1119	299.5	22.3	605	7	CF445936	EST682281	1192	292.5	21.8	617	5	BQ611858	BQ611858 esp66b11
c1120	299.5	22.3	627	4	BG299397	HVSMBO01	1193	292	21.7	628	6	CD909626	CD909626 G468.113C
c1121	299.5	22.3	699	7	CF653377	USDA-PP.0	cl194	292	21.7	647	6	CD898525	CD898525 G174.109E
c1122	299	22.2	689	7	CN991252	67764.125	1195	292	21.7	724	6	CD824049	CD824049 BN25.050N
c1123	298.5	22.2	531	2	BE124333	EST393368	cl196	291.5	21.7	551	6	CA039685	CA039685 esalnwh01
c1124	298.5	22.2	534	1	AI443130	sa84901.y	1197	291.5	21.7	580	4	BM100502	BM100502 EBRa01.SQ
c1125	298.5	22.2	590	5	BU577914	sa94d04.	1198	291.5	21.7	660	4	BI957746	BI957746 HVSMBO01
c1126	298.5	22.2	600	9	CR180853	Forward.s	1199	291	21.7	820	7	CO365680	CO365680 RTK1.18.C
c1127	298.5	22.2	612	7	CK745975	eca01-12c	cl200	291	21.7	849	7	CO368463	CO368463 RTK1_40_F
c1128	298.5	22.2	637	6	CA835476	MCS017E02	1201	291	21.7	879	7	CO366519	CO366519 RTK1_28_H
c1129	298.5	22.2	640	2	AW684885	NFO22F07N	1202	291	21.7	900	7	CO365078	CO365078 RTK1_23_B
c1130	298.5	22.2	766	7	CF236578	PtaJXT4B5	1203	290.5	21.6	483	5	BQ123267	BQ123267 EST608843
c1131	298.5	22.2	805	2	AW350997	GM210010A	cl204	290.5	21.6	525	6	CB395921	CB395921 OSTR163G4
c1132	298.5	22.2	823	2	BF256995	HVSMBO01	1205	290.5	21.6	561	2	BE474577	BE474577 BP66a08.y
c1133	298.5	22.2	1049	7	CK163799	FGAS01643	1206	290.5	21.6	625	6	CD813970	CD813970 BN15.021J
c1134	298	22.2	592	4	BI478930	949071A06	1207	290.5	21.6	654	4	BI957613	BI957613 HVSMBO01
c1135	298	22.2	673	6	CA234708	SCJLSB106	1208	290.5	21.6	674	2	BF649235	BF649235 NFO64A08E
c1136	298	22.2	724	4	BJ572947	BJ572947	cl209	290.5	21.6	706	7	CA921232	CA921232 EST638950
c1137	297.5	22.2	509	4	BJ549094	EST85213	cl210	290.5	21.6	711	6	CA921232	CA921232 RTK1.48.B
c1138	297.5	22.2	515	7	CV296836	EST85213	1211	290.5	21.6	765	7	CO369642	CO369642 RTK1.48.B
c1139	297.5	22.2	561	2	BE450736	EST401623	1212	290.5	21.6	820	7	CF443771	CF443771 EST650116
c1140	297.5	22.2	636	6	CD934106	GR45.123A	1213	290	21.6	648	5	BQ743293	BQ743293 WHE4102.D
c1141	297.5	22.2	659	2	BF646182	NFO68A08E	1214	290	21.6	655	4	BI960535	BI960535 HVSMBO02
c1142	297.5	22.2	688	1	AV821843	AV821843	1215	290	21.6	673	6	CA220527	CA220527 SCRULF402
c1143	297.5	22.2	713	7	CN146262	WOUND1.39	1216	290	21.6	679	6	CA141617	CA141617 SCJLRT205
c1144	297.5	22.2	744	6	CD430320	ETH1.17.C	1217	290	21.6	706	2	AW278810	AW278810 f69806.y
c1145	297	22.1	622	6	CA137725	SCCFT200	1218	290	21.6	707	7	CN988152	CN988152 63924.125
c1146	297	22.1	673	4	BM371957	EBMa08.SQ	1219	290	21.6	759	7	CV501184	CV501184 65678.1.M
c1147	297	22.1	736	7	CV248404	WS01120.B	1220	289.5	21.6	561	4	BM269671	BM269671 BAK02904.
c1148	297	22.1	927	7	CO480346	QO01BM14.	1221	289.5	21.6	890	7	CO488997	CO488997 QO02510.B
c1149	296.5	22.1	477	1	AU262139	AU262139	1222	289	21.5	646	7	CO529747	CO529747 3530.1.19
c1150	296.5	22.1	537	2	BE490625	WHE0370.D	1223	289	21.5	650	2	BF260414	BF260414 HVSMBO02
c1151	296.5	22.1	586	7	CF419317	USDA-PP.1	1224	289	21.5	676	7	CF671538	CF671538 RHCNT1.57
c1152	296.5	22.1	664	1	AL820289	AL820289	1225	289	21.5	702	7	CN123933	CN123933 RHOH1.D
c1153	296.5	22.1	687	6	CD820187	BN20.0511	1226	289	21.5	732	3	CNS0A750	BN42420 Arabidops
c1154	296.5	22.1	834	7	CO369560	RTK1.48.B	1227	289	21.5	826	7	CN128942	CN128942 RHOH1.32
c1155	296	22.0	646	2	AW695899	NF100E02S	1228	288.5	21.5	540	4	BI779178	BI779178 EBR001.SQ
c1156	296	22.0	670	5	BU998750	HI12A22R	1229	288.5	21.5	559	1	AU263008	AU263008 AU263008
c1157	296	22.0	691	6	CA182059	SCBGS7310	1230	288.5	21.5	636	6	CD932185	CD932185 GR45.117C
c1158	296	22.0	742	5	BQ634193	NARV064.H	1231	288	21.4	690	6	CD918343	CD918343 G608.109A
c1159	296	22.0	1090	7	CK216386	FGAS02837	1232	288	21.4	696	6	CA280310	CA280310 SCVPLB2C0
c1160	295.5	22.0	510	7	CV169700	remex1.01	cl233	287.5	21.4	510	4	BM357022	BM357022 151V-H8.T
c1161	295.5	22.0	511	4	BG262486	WHE0936.E	1234	287.5	21.4	550	2	AW278618	AW278618 f646h04.y
c1162	295.5	22.0	529	2	BF598865	sv2q10.y	1235	287.5	21.4	554	5	BX682301	BX682301 BX682301
c1163	295.5	22.0	564	2	BE398854	EST430377	1236	287.5	21.4	577	4	BM086141	BM086141 sah36a07.
c1164	295.5	22.0	589	6	CA018785	HV09K09R	1237	287.5	21.4	634	6	CA136726	CA136726 SCQSKT103
c1165	295.5	22.0	605	2	AW776435	EST335500	1238	287.5	21.4	634	6	CA823264	CA823264 R23C02.tw
c1166	295.5	22.0	641	1	AL827928	AL827928	1239	287.5	21.4	643	9	CL561927	CL561927 OB_Ba002
c1167	295.5	22.0	654	7	CF575000	MCSA142A0	cl240	287.5	21.4	655	5	B0750517	B0750517 EST633253
c1168	295.5	22.0	672	6	CD825507	BN25.060P	cl241	287.5	21.4	703	4	BM407958	BM407958 EST582285
c1169	295	22.0	571	6	CB399845	OSTF16367	1242	287.5	21.4	777	5	BP133315	BP133315 BP133315
c1170	295	22.0	670	7	CF433879	NIT1.30.C	1243	287	21.4	593	5	BU579330	BU579330 sar57a02.
c1171	295	22.0	701	4	BI569035	HVSMBO01	1244	287	21.4	630	6	CA191567	CA191567 SCCRT2C0
c1172	294.5	21.9	803	4	BI956671	HVSMBO00	1245	287	21.4	691	5	BQ840928	BQ840928 WHE4205.B
c1173	294	21.9	571	1	AU246119	AU246119	1246	287	21.4	729	8	BZ635220	BZ635220 OGCAG32TC
c1174	294	21.9	613	6	CD911360	G550.110P	1247	287	21.4	753	7	CF471006	CF471006 RTDS1.15
c1175	294	21.9	692	4	BI978962	2B11.Old	cl248	287	21.4	774	6	CB651301	CB651301 OSJNED16D
c1176	294	21.9	722	2	BJ576352	EST76352	cl249	287	21.4	795	7	CO176253	CO176253 NDLL1_60_G
c1177	293.5	21.9	556	2	BE124175	EST394300	1250	287	21.4	807	7	CF663779	CF663779 RTCNT1_5_



1251	287	21.4	860	7	CO365601	RTK1_18_C	1324	281.5	21.0	569	5	BQ839243	WHE4163_H
1252	287	21.4	919	9	CG235840	QG3AC56TV	1325	281.5	21.0	683	4	BG370011	HVSM810D2
1253	286.5	21.3	584	5	BQ623631	USDA_PP_0	1326	281.5	21.0	748	7	CF663501	RFCNTL_3
1254	286.5	21.3	595	6	CB075138	IX15902_b	1327	281.5	21.0	749	7	CF671166	RFCNTL_55
1255	286.5	21.3	623	6	CAB21671	RSH06A03	1328	281.5	21.0	761	7	CF395084	RIDS2_9_C
1256	286	21.3	387	1	AUI179319	AUI79319	1329	281.5	21.0	814	7	CO362000	NDL2_8_BO
1257	286	21.3	438	6	C23182	C23182_Japa	1330	281	20.9	577	5	BP184433	BP184433
1258	286	21.3	568	1	AU267141	AU267141	1331	281	20.9	587	6	CD899632	GI74_113A
1259	286	21.3	569	1	AU270834	AU270834	1332	281	20.9	711	5	BO533731	NHRV060_A
1260	286	21.3	577	1	AU264259	AU264259	1333	280.5	20.9	501	2	BE586643	WHE0509_C
1261	286	21.3	582	4	BI432495	EST535256	1334	280.5	20.9	509	7	CA190343	MgfW2016F
1262	286	21.3	609	6	CA139015	SCQRT209	1335	280.5	20.9	519	7	CF439324	EST675669
1263	286	21.3	649	6	CA120549	SCCCLR107	1336	280.5	20.9	523	1	AV770739	AV770739
1264	286	21.3	668	4	BI959395	HVSMEN001	1337	280.5	20.9	670	6	CA836696	MCU010A09
1265	286	21.3	668	7	CF667338	RFCNTL_29	1338	280.5	20.9	672	6	CA166266	SCUTR2310
1266	285.5	21.3	517	4	BI205825	EST523865	1339	280	20.8	509	2	BE050599	za67f09.9
1267	285.5	21.3	540	6	CD878426	AZ04_102L	1340	280	20.8	580	2	AM686370	NP04UG10N
1268	285.5	21.3	555	5	BM885163	sa195f06	1341	280	20.8	590	5	BU579089	sa65902
1269	285.5	21.3	581	6	CB878369	HP08B22T	1342	280	20.8	613	6	CA276256	SCEP8D200
1270	285.5	21.3	745	7	CF203406	CF203406	1343	280	20.8	638	6	CA208994	SCEZAD1C0
1271	285	21.2	566	7	CV511753	kc47c06.y	1344	280	20.8	656	4	BG836117	Zm06_08E1
1272	285	21.2	641	6	CB651300	OSJNED16D	1345	280	20.8	929	3	CNS0AAMA	AB17367
1273	285	21.2	850	7	CO174878	NDL1_46_G	1346	279.5	20.8	578	2	AW707224	sk22c12.y
1274	284.5	21.2	508	1	AI974778	T113251e	1347	279.5	20.8	725	6	CD842282	RFO2_1260
1275	284.5	21.2	519	2	BE203574	EST396250	1348	279.5	20.8	761	7	CV502602	69004_1_M
1276	284.5	21.2	532	2	BE361185	DGL_70_D1	1349	279.5	20.8	843	2	BE640750	Cr12_1_F1
1277	284.5	21.2	551	1	AI775483	EST256583	1350	279	20.8	516	7	CO531897	3530_1_20
1278	284.5	21.2	551	2	BE202817	EST402839	1351	279	20.8	614	6	CA137607	SCAGRT204
1279	284.5	21.2	616	6	CD830642	BN40_046E	1352	279	20.8	625	7	CN771644	tad92e03
1280	284.5	21.2	654	4	BI967946	GM830003B	1353	279	20.8	636	6	CA133289	SCEQRT103
1281	284.5	21.2	789	7	CA048696	GQ0224_B7	1354	279	20.8	748	6	CA146644	SCVPRT208
1282	284.5	21.2	850	7	CK204382	FGAS01291	1355	278.5	20.7	438	6	CA190352	SCCPR1C0
1283	284.5	21.2	881	7	CK204040	FGAS01257	1356	278.5	20.7	510	5	BM895774	952065C05
1284	284	21.1	567	6	CD879591	AZ04_105M	1357	278.5	20.7	582	7	CN495499	Mdfw20201
1285	284	21.1	619	5	BU030545	OHJ15L05	1358	278.5	20.7	667	6	CD841580	RFO2_123L
1286	284	21.1	692	7	CK099634	A078P58_5	1359	278.5	20.7	710	6	CA919819	EST637537
1287	284	21.1	813	4	BG321263	Zm04_0300	1360	278.5	20.7	767	6	CD838198	RFO2_110F
1288	284	21.1	885	7	CO798751	AGENCOURT	1361	278.5	20.7	1002	9	CN80579X	Tetraodon
1289	283.5	21.1	408	2	BE361254	DGL_70_D1	1362	278	20.7	440	6	CD808702	LcA0A705c
1290	283.5	21.1	444	2	AW559274	EST306110	1363	278	20.7	631	4	BI960531	HVSM8n002
1291	283.5	21.1	463	7	CV297681	EST86058	1364	278	20.7	631	6	CD278486	TI43C0228
1292	283.5	21.1	471	1	AI488060	EST246382	1365	278	20.7	651	4	BJ572893	BJ572893
1293	283.5	21.1	473	4	BI893815	sa93c09	1366	278	20.7	654	6	CA069091	SCSBAD105
1294	283.5	21.1	509	4	BG314500	WHE2495_E	1367	278	20.7	681	6	CD430207	ETH1_17_H
1295	283.5	21.1	525	4	BI317613	sa9f0d05	1368	278	20.7	687	7	CF227858	PtaXMO005
1296	283.5	21.1	541	2	AW256836	EST304973	1369	278	20.7	812	6	CA183398	SCQST312
1297	283.5	21.1	548	2	AW733300	sk71f10.y	1370	277.5	20.7	705	7	CF232502	PcauX0001
1298	283.5	21.1	559	7	CF807795	psHB028XE	1371	277	20.6	552	6	CA017209	HV14G11u
1299	283.5	21.1	578	6	CB870318	HC13P20w	1372	277	20.6	738	7	CO168725	NDL1_2_Do
1300	283.5	21.1	588	1	AI166314	xylem.est	1373	277	20.6	774	4	BI421792	EST532458
1301	283.5	21.1	670	6	CA298654	SCSFL804	1374	276.5	20.6	343	1	AA899498	UI-R-E0-d
1302	283	21.1	507	6	CD971462	QAD9602_s	1375	276.5	20.6	409	5	BQ471953	HV03P16r
1303	283	21.1	522	7	CF243853	3530_1_24	1376	276.5	20.6	632	6	CB077276	h551n02.g
1304	283	21.1	582	6	CD869339	AZ02_111G	1377	276.5	20.6	657	4	BI943810	BI943810.y
1305	283	21.1	649	5	BU998774	HI12C04r	1378	276.5	20.6	717	6	CD839418	RFO2_115D
1306	283	21.1	652	4	BI957644	HVSMEN001	1379	276.5	20.6	763	6	CD845034	RFO2_141F
1307	283	21.1	666	5	BQ468365	HW01A23T	1380	276	20.6	629	7	CO523183	3530_1_15
1308	282.5	21.0	419	2	BF483204	WHE1787_B	1381	276	20.6	645	7	CF471822	RTDS1_6_C
1309	282.5	21.0	457	2	BF519907	EST457372	1382	276	20.6	665	2	BE821841	GM700015B
1310	282.5	21.0	464	2	BE125749	DGL_55_H1	1383	275.5	20.5	561	6	CA019093	HV10M04r
1311	282.5	21.0	507	6	CA181402	SCBFT313	1384	275.5	20.5	590	6	CD825329	BN25_060H
1312	282.5	21.0	572	4	BG448465	NF036C01R	1385	275	20.5	477	4	BI468157	EST00564
1313	282.5	21.0	636	6	CB090660	9Y78f07.9	1386	275	20.5	599	6	CD898673	GI74_108L
1314	282.5	21.0	656	4	BU564155	BU564155	1387	275	20.5	626	1	AI776146	EST257234
1315	282.5	21.0	751	7	CF667253	RTCNT1_29	1388	275	20.5	659	6	CD845342	RFO2_142M
1316	282	21.0	469	6	CA497305	WHE3225	1389	275	20.5	701	7	CN975504	25361_125
1317	282	21.0	509	2	BF519941	EST457409	1390	274.5	20.4	454	6	CA006913	CA006913
1318	282	21.0	594	7	CO502679	59952_1_I	1391	274.5	20.4	575	4	BM407644	EST561971
1319	282	21.0	621	6	CA222822	SCBZFL404	1392	274.5	20.4	718	6	CD839061	RFO2_113M
1320	282	21.0	737	6	CA216695	SCCST3C1	1393	274.5	20.4	748	6	CD839811	RFO2_116L
1321	282	21.0	798	7	CV036558	RTNACL1_6	1394	274	20.4	644	2	BB635220	BB635220
1322	281.5	21.0	300	2	BE393514	601310205	1395	274	20.4	650	1	AJ432275	AJ432275
1323	281.5	21.0	543	2	AW704578	sk38h08.y	1396	274	20.4	651	2	BE590347	SB87_Suga



Average insert size 1.75 kb. Library constructed by Life Technologies."

ORIGIN									
Alignment Scores:									
Pred. No.:	2,986-125	Length:	889						
Score:	1330.00	Matches:	262						
Percent Similarity:	99.62%	Conservative:	0						
Best Local Similarity:	99.62%	Mismatches:	0						
Query Match:	99.03%	Indels:	1						
DB:	4	Gaps:	0						
US-10-017-407A-306 (1-262) x BM451059 (1-889)									
Qy	1	MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla	20						
Db	13	ATGACCCAGCGGTGCCCGCTCTCCGTGCCCGCGCTGGCGCTGGCGCTGACCGCA	72						
Qy	21	LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgCysProProTrpArgGly	40						
Db	73	CTGGCGCGCCCTTCGCCACTGGCTCTCTCTGGGGAGGCGGTGCCCGCCATGGCGAGGC	132						
Qy	41	ArgArgGluGlnCysLeuLeuProProGluAspSerArgLeuTrpGlnTyrIleLeuSer	60						
Db	133	CGGCGAGAGCAGTGCCTCTTCCCGCCGAGGACAGCCGCTGTGGCAGTATCTTCTGAGC	192						
Qy	61	ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuLeuThrLeuGluGlnPro	80						
Db	193	CGCTCCATCGGGAGCACCCGGCGCTGGAGACCTTGAGGCTGCTGACCTGGAGCAGCGG	252						
Qy	81	GlnGlyAspSerMetMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeu	100						
Db	253	CAGGGGATTCTATGATGACCTGCAGCAGGCGCCAGCTCTTGCGCCAACTGGCGGGCTC	312						
Qy	101	IleGlnAlaLysLeuAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeu	120						
Db	313	ATCCAGGCCCAAGAGCGCTGGACCTTGGACACTTTCACGGGTACTTCCGCCCTGGCCCTG	372						
Qy	121	AlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnProPro	140						
Db	373	GCCTCTGGCGCTCCCGCGGACGGGCGCTGGTGTACTCTGCAGGTGAGCGCGAGCCCGG	432						
Qy	141	GluLeuGlyArgProLeuTrpArgGlnAlaGluAlaGluHisLysIleAspLeuArgLeu	160						
Db	433	GAGCTGGAGCGGCCCTCTGTGGAGGAGCGCGGAGGCGGAGCACAGATCGACCTCCGGCTG	492						
Qy	161	LysProAlaLeuGluThrLeuAspGluLeuLeuAlaAlaGlyGluAlaGlyThrPheAsp	180						
Db	493	AAGCCCGCTTGGAGACCTTGAGCAGCTGTCTGGCGGGCGGCGCGGCGGACCTTCGAC	552						
Qy	181	ValAlaValValAspAlaAspLysGluAsnCysSerAlaTyrTyrGluArgCysLeuGln	200						
Db	553	GTGGCCGTGGTGGATGCGGACAAAGAGAACTGCTCCGCCCTACTACGAGCGCTGCCCTGAG	612						
Qy	201	LeuLeuArgProGlyGlyIleLeuAlaValLeuArgValLeuTrpArgGlyLysValLeu	220						
Db	613	CTGCTGCGACCCGAGGACATCTCTCGCCCTCTCAGAGTCTCTGTGGCGGGAGGTGCTG	672						
Qy	221	GlnProProLysGlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArgIleArg	240						
Db	673	CAACCTCCGAAAGGGAGCGTGGCGCGCGAGTGTGTGCGAAACCTAAACGACGATCCGG	732						
Qy	241	ArgAspValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeu-AlaPhe	260						
Db	733	CGGAGCGTCAGGGTCTACATCAGCTCTCTGCCCTTGGGGGATGGACTCACCTTGGGCTT	792						
Qy	260	eLysile	262						
Db	793	CAAGATC	799						
RESULT 2									
BM051236									
LOCUS									
814 bp mRNA linear EST 07-NOV-2001									
BM051236									

DEFINITION 603634191F1 NIH\_MGC\_43 Homo sapiens cDNA clone IMAGE:5424766 5', mRNA sequence.

ACCESSION BM051236

VERSION BM051236.1 GI:16780503

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 814)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: LfCM1886 row: e column: 23

High quality sequence stop: 811.

Location/Qualifiers

1..814

source

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5424766"

/tissue\_type="normal pigmented retinal epithelium"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH MGC 43"

/note="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 4,74e-118 Length: 814

Score: 1259.00 Matches: 259

Percent Similarity: 97.74% Conservative: 0

Best Local Similarity: 97.74% Mismatches: 1

Query Match: 93.75% Indels: 5

DB: 4 Gaps: 0

US-10-017-407A-306 (1-262) x BM051236 (1-814)

Qy 3 GlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAlaLeuGly 22

Db 4 CAGCGGTGCCCGGCTCTCCGTGGCGCGCGCTGGCGCTGGCGCTGACCGCCTGGGC 63

Qy 23 AlaAlaPheAlaThrGlyLeuPheLeuGlyArgCysProProTrpArgGlyArgArg 42

Db 64 GCCGCTTTCGCCACATGGCTCTTCTGGGGAGCGGTGCCCGCCCAITGGGAGCGCGCA 123

Qy 43 GluGlnCysLeuLeuProGluAspSerArgLeuTrpGlnTyrLeuLeuSerArgSer 62

Db 124 GAGCAGTGCCTGCTTCCCCCGGAGCAGCGCCCTGTGGCAGTATCTTCTGAGCGCTCC 183

Qy 63 MetArgGluHisProAlaLeuArgSerLeuArgLeuLeuThrLeuGluGlnProGlnGly 82

Db 184 ATCGGAGACACCGCGCGCTGCGAAGCCTGAGGCTGTGACCTCGAGCAGCGCGGG 243

Qy 83 AspSerMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeuIleGln 102

Db 244 GATTCTATGATGACCTGGAGCAGGCCCGAGCTTCTTGGCCACCTGGCGCGGCTCATCCAG 303



```

QY      212 ----- 212
Db      906 GCTCTGGTCACTCTCTGCGCGGCACCTCCCTCGAGGCGCGCCTCCCGCCAGACACC 965
QY      212 ----- 212
Db      966 TCCCTCCGAGACCCCGCCTTCCTGTCGGGACCTCCCTCCAAGACCCCGCCTCCCGCCG 1025
QY      212 ----- 212
Db      1026 GGCACCTCCCTCCAGTCCCGCGCCTTCCTCCGCGAGACACCTCCCTCCGAAGCCCGCCCTC 1085
QY      213 -----ValLeuTPrArgGlyLysValLeuGlnPr 222
Db      1086 CCACGGCCGGTTGGCGCGCCCTCCCGCAGGTCTGTGGCGGGAGAGTGTCTGCAACC 1145
QY      222 oProlysGlyAspValAlaAlaGluCysValArgAsnLeuAenGluUArgGlyAeArgAs 242
Db      1146 TCCGAAGGGGACGTGGCGCGCGAGTGTGTGCGAACCCTAAGCAACGCATCCGGCGCGGA 1205
QY      242 pValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPheIysI 262
Db      1206 CGTCAAGGTCTACATCAGCCTCTCGCCCTGGGCGATGGACTCAGCTTGGCCTTCAAGAT 1265
QY      262 e 262
Db      1266 C 1266

RESULT 4
BF663323
LOCUS      602144463F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297911 5',
DEFINITION mRNA sequence.
ACCESSION BF663323
VERSION    1
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1006)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCW1152 row: m column: 16
High quality sequence stop: 745.
FEATURES             Location/Qualifiers
     source           1..1006
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4297911"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_48"
     note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
     Site 2: EcoRI; cDNA made by oligo-dT priming.
     Directionally cloned into EcoRI/XhoI sites using the
     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
     for average insert size 1.8kb. Library constructed by Ling
     Hong in the laboratory of Gerald M. Rubin (University of
     California, Berkeley) using ZAP-cDNA synthesis kit
     (Stratagene) and Superscript II RT (Life Technologies).
     Note: this is a NIH_MGC Library."

```

```

ORIGIN
Alignment Scores:      2,53e-113      Length:      1006
Pred. No.:            1214.00      Matches:      251
Score:                96.56%      Conservative: 2
Best Local Similarity: 95.80%      Mismatches: 5
Query Match:          90.39%      Indels:      5
DB:                   2           Gaps:          0

US-10-017-407A-306 (1-262) x BF663323 (1-1006)
QY      1 MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla 20
Db      7 ATGACCCAGCCGGTGGCCCGGCTCTCCGTGCGCGCGCGCTGGCCCTGGGCTCAGCCGCA 66
QY      21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgGlyArgGlyProProTrpArgGly 40
Db      67 CTGGCGCGCGCTTCCGACATGGCTCTTCTTGGGAGGCGGTGCCCCCATGGCGAGGC 126
QY      41 ArgArgGluGlnCysLeuLeuProGluAspSerArgLeuTrpGlyTyrLeuLeuSer 60
Db      127 CGCGGAGAGCAAGTGCCTTCCCGCGGAGGACAGCGCGCTGTGGCAGTATCTTCTGAGC 186
QY      61 ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuLeuThrLeuGlnPro 80
Db      187 CGCTCCATCGGGAGACACCGCGCGCTGGAGGCTGAGGCTGCTGACCTTGGAGGAGCGCG 246
QY      81 GlnGlyAspSerMetMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeu 100
Db      247 CAGGGGGATTCTATGATGACCTCGAGCAGGCGCCAGCTCTTGGCCAACTCTGGCGGGCTC 306
QY      101 IleGlnAlaLysLysAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeu 120
Db      307 ATCCAGGCGCAAGCGCGCTGGACCTGGCGACCTTTCACGGGCTACTCCGCGCTGGCCCTG 366
QY      121 AlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnProPro 140
Db      367 GCCCTGGGCGTCCCGCGAGCGGGCGGTGGTGACCTGGAGGTGGAGCGGCGAGGCCCGCG 426
QY      141 GluLeuGlyArgProLeuTrpArgGlnAlaGluAlaGluHisLysIleAspLeuArgLeu 160
Db      427 GAGCTGGGACGCGCCCTGTGGAGGCGGCGCGAGGCGGAGCACAGATCGACCTCGCGCTG 486
QY      161 LysProAlaLeuGluThrLeuAspGluLeuLeuAlaGlyGluAlaGlyThrPheAsp 180
Db      487 AAGCCCGCTTGGAGACCTCGACGAGCTGTGGCGGGCGGCGGCGGCGGCGGCGGCGGCGG 546
QY      181 ValAlaValAlaAspAlaAspLysGluAsnCysSerAlaTyrTyrGluArgCysLeuGln 200
Db      547 GTGGCGGTGGTGGATGGGACGAGGAGGAGAACTGCTCGGCTACTACGAGCGCTGTCTGCAG 606
QY      201 LeuLeuArgProGlyGlyIleLeuAlaValLeuArgVal-LeuTrpArgGlyLysValLeu 220
Db      607 CTGCTGCGACCGGAGGCGATCTCGCGCTCTCTCAGAGTCTTGTGGCGCGGAGAGGTGCT 666
QY      220 uGlnProProLysGlyAspValAlaAlaGluCysValArgAsnLeu-AsnGluArgGly 239
Db      667 GAAACT-CCGAAGGGGACGTGGCGCGCGAGTGTGTGGGAAACCTAAACAAACGAGCATC 725
QY      240 ArgArgAspValArgValTyrIleSerLeuLeu-ProLeuGlyAspGlyLeuThrLeu 258
Db      726 CGCGGGGAGCGGAGGCTTACATCAGGCTTCTGGGCGCTTGGGCGGATGAGATCACCCTT 783

RESULT 5
BF664198
LOCUS      602145812F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4309298 5',
DEFINITION mRNA sequence.
ACCESSION BF664198
VERSION    1
KEYWORDS   EST.
SOURCE     Homo sapiens (human)

```

ORGANISM	Homo sapiens	Db	367	GCCTGGCGCTGCCCGGACGGCGGTGGTACCTGGAGGTGACGGCGACGCC-CCG	425
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Qy	141	GLuLeuGlyValArgProLeuTrpArgGlnAlaGluAlaGluHisLysIleAspLeuArgLeu	160
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .	Db	426	GAGCTGGGACGGCCCTGTGGAGCGAGCGCGGAGCGGACCAAGATCGACCTCCGGCTG	485
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	Qy	161	LysProAlaLeuGluThrLeuAspGluLeuLeuAlaAlaGlyGluAlaGlyThrPheAsp	180
JOURNAL	Unpublished (1999)	Db	486	AAGCCCGCCTTGGAGACCCCTGGACGAGCTGCTGGCGCGGCGGAGCGCGACCTTCGAC	545
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs-r@mail.nih.gov Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: Ling Hong/Rubin Laboratory DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LLCM182 row: h column: 03 High quality sequence stop: 726.	Qy	181	ValAlaValValAspAlaAspLysGluAsnCyseSerAlaTyrTyrGluArgCysLeuGln	200
		Db	546	GTGGCGTGGTGGATCCGACCAAGGAGAACTGCTCCGC-TACTACGAGCGCTCCCTGCAG	604
		Qy	201	LeuLeuArgProGlyGlyIleLeuAlaValLeuArgValLeuTrpArgGlyLysValLeu	220
		Db	605	CTGCTCGACCCCGAGGATCTCTCGCGTCTCAGAGTCTCTGGCGGGAAGGTGCTG	664
		Qy	221	GlnProProLysGlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArgGileArg	240
		Db	665	CAACCTCCGAAAGGGGACGTCGGCGCGAGTGTGCGACACCT-AACGGAACGCATCCGG	723
		Qy	241	ArgAspValArgValTyrIleSerLeuLeuPro 251	
		Db	724	CGGAGCTCAGGCTCTACATCAGCCTCTTCCCT 756	
FEATURES	Location/Qualifiers				
source	1..921				
	/organism="Homo sapiens"				
	/mol_type="mRNA"				
	/db_xref="taxon:9606"				
	/clone="IMAGE:4309298"				
	/tissue_type="primary B-cells from tonsils (cell line)"				
	/lab_host="DH10B (phage-resistant)"				
	/clone_lib="NIH MGC 48"				
	/notes="Organ: B-cells; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."				
ORIGIN					
Alignment Scores:					
Pred. No.:	1..02e-110	Length:	921		
Score:	1188.00	Matches:	244		
Percent Similarity:	98.01%	Conservative:	2		
Best Local Similarity:	97.21%	Mismatches:	5		
Query Match:	88.46%	Indels:	3		
DB:	2	Gaps:	0		
US-10-017-407A-306 (1-262) x BF664198 (1-921)					
Qy	1 MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla	20			
Db	7 ATGACCCAGCCGTCGCCGGCTCTCCGTGCCCGCGCGTGGCCCTGGGCTCAGCCGCA	66			
Qy	21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyValArgCysProTrpArgGly	40			
Db	67 CTGGGCGCCGCTTCGCCACTGTCCTTCTGGGAGGGGTCGCCCTCAGCGAGGC	126			
Qy	41 ArgArgGluGlnCysLeuLeuProProGluAspSerArgLeuTrpGlnTyrLeuLeuSer	60			
Db	127 CGCGGAGACAGTCTGCTTCCCCCGGAGGACGCGCTGGGAGATATCTTCTGAGC	186			
Qy	61 ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuLeuThrLeuGluGlnPro	80			
Db	187 CGCTCCATCGGAGACACCGCGCTGCGAAGCCTGAGGCTGCTGACCTCGGAGCAGCG	246			
Qy	81 GlnGlyAspSerMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeu	100			
Db	247 CAGGGGGATTCATGATGACCTCGGAGCGAGGCCACCTTGGCCCAACCTGGCGGCTC	306			
Qy	101 IleGlnAlaLysLysAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeu	120			
Db	307 ATCCAGGCCAAGAGGCGCTGACCTGGGACCTTCAGGGCTACTTCCGCCCTGGCCCTG	366			
Qy	121 AlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnProPro	140			

ORIGIN



## Alignment Scores:

Pred. No.: 1.13e-110 Length: 772  
Score: 1186.50 Matches: 245  
Percent Similarity: 94.23% Conservative: 0  
Best Local Similarity: 94.23% Mismatches: 12  
Query Match: 88.35% Indels: 4  
DB: 2 Gaps: 2

US-10-017-407A-306 (1-262) x BE796570 (11-772)

QY 1 MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla 20  
DB 2 ATGACCCAGCGTGCCTCCGCGCTCTCCGTCGCCGCGCTGGCTCGAGCGCA 61  
QY 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgCysProProThrArgGly 40  
DB 62 CTGGGGCGCGCTTCGCCATCGCTCTCTCTGGGAGGCGGTGCCCTCCATGGCGAGCG 121  
QY 41 ArgArgGluGlnCysLeuLeuProProGluAspSerArgLeuTrpGlnTyrLeuLeuSer 60  
DB 122 CGGCGAGAGAGTGCCTGCTTCCCCCGAGGACAGCGCTGTGGCAGTATCTTCTGAGC 181  
QY 61 ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuLeuThrLeuGluPro 80  
DB 182 CGCTCCATCGCGAGACACCGCGCTGCGAAGCCTGAGGCTGTGACCTCGAGCAGCGC 241  
QY 81 GlnGlyAspSerMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeu 100  
DB 242 CAGGGGATTCATGATGACCTGCGAGCAGCGCCAGCTCTTGCCCAACCTGGCGGGCTC 301  
QY 101 IleGlnAlaLysLysAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeu 120  
DB 302 ATCCAGGCCAAGAAGCGCTGGACCTGGCGCACTTCAAGGCTACTCCGCGCTGGCCCTG 361  
QY 121 AlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnProPro 140  
DB 362 GCCCTGGCGCTGCCCGCGAGCGGGCGTGTGACCTGCGAGTGGACGCGAGCGCCCGC 421  
QY 141 GluLeuGlyArgProLeuTrpArgGlnAlaGluAlaGluHisLysIleAspLeuArgLeu 160  
DB 422 GAGCTGGAGCGGCCCTGTGGAGGCGAGCGCGAGCGGAGCACAAAGATCGACCTCGGGCTG 481  
QY 161 LysProAlaLeuGluThrLeuAspGluLeuLeuAlaAlaGlyLysAlaGlyThrPheAsp 180  
DB 482 AAGCCCGCTTGGAGACCTTGGACGAGCTGTGGCGCGCGAGCGGCAC--TTCCGAC 539  
QY 181 ValAlaValAspAlaAspLysGluAenCysSerAlaTyrTrpGluArgCysLeuGln 200  
DB 540 GTGGCGTGTGGATGCGGACAAAGGAGAACTGTCTCCGCTACTACGAGCGCTGCCTGCAG 599  
QY 201 LeuLeuArgProGlyLysIleLeuAlaValLeuArgValLeuTrpArgGlyLysValLeu 220  
DB 600 CTGCTGCGACCGGAGGATCTCTCGCGCTCTCAGAGTCTGTGGCGCGGGAAGGTGCTG 659  
QY 221 Gln-ProProLysGlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArgIleAr 240  
DB 660 CAAACCTCCGAAGGGAGCTGGCGCGCGAGTGTGCGAARCTAAAGAACCGCAT---CG 716  
QY 240 gArgAspValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAla 259  
DB 717 GCGGGACGTGACG---TCTACATCAGCTCTCTGCTGGCGGATGGACTCACCTGGCT 771

## RESULT 7

LOCUS CR625911 1321 bp mRNA linear HTC 21-JUL-2004  
DEFINITION full-length cDNA clone CS0DN002YB07 of Adult brain of Homo sapiens (human).  
ACCESSION CR625911  
VERSION CR625911.1 GI:50506718  
KEYWORDS HTC; CDSLT\_cDNA.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

## REFERENCE

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
REMARK Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

## REFERENCE

2 (bases 1 to 1321)

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

## FEATURES

source

1..1321  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0DN002YB07"  
/tissue\_type="Adult brain"  
/plasmid="pCMVSPORT\_6"

## ORIGIN

## Alignment Scores:

Pred. No.: 7.78e-110 Length: 1321  
Score: 1181.50 Matches: 255  
Percent Similarity: 65.38% Conservative: 0  
Best Local Similarity: 65.38% Mismatches: 0  
Query Match: 87.97% Indels: 135  
DB: 3 Gaps: 3

US-10-017-407A-306 (1-262) x CR625911 (1-1321)

QY 1 MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla 20  
DB 155 ATGACCCAGCGTGCCTCCGCGCTCTCCGTCGCCGCGCTGGCTCGAGCGCA 214  
QY 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeu----- 31  
DB 215 CTGGCGCGCGCTTTCGCCACTGGCCTCTTCTGGGTGAGCAGGACCTGTGTCGGCGGCG 274  
QY 31 ----- 31  
DB 275 GGGTGGCGGGCGCAGAGTAGGGCGCGGCTGGCTCAGGTTAATCCAAACACCTCTCCCC 334  
QY 32 ---GlyArgArgCysProProTrpArgGlyArgGluGlnCysLeuLeuProGln 50  
DB 335 GTACAGGAGGGGTGCTCCCATGCGAGGCGGCGGAGCAGTGCCTGCTTCCCCCGA 394  
QY 50 uAspSerArgLeuTrpGlnTyrLeuLeuSerArgSerMetArgGluHisProAlaLeuAr 70  
DB 395 GGACAGCGCGCTGTGGCAGTATCTTCTGAGCGGCTCCATGCGGAGACCCCGCGCTGCG 454  
QY 70 gSerLeuArgLeu----- 74  
DB 455 AAGCCTGAGGTGTGTGTCAGCAGGGCGCGGACGGAACCGGGGTCTCCTCTCGACCCCTGCG 514  
QY 74 ----- 74  
DB 515 GGTCCACAGTGGCTGTGTGACCTTGGGTGGGCCCTTGGCCCTCCTGGGCTTCCGGCTTC 574  
QY 74 ----- 74  
DB 575 CTTGGGCGGGTGGTGGGTGCGGTTCGGAAGGGCCAGTCCCCCAGGCGCAGCCAGAACCG 634  
QY 74 ----- 74



```
Db 635 CGCCCCCTGGGGCTTGGGAGACCCCGAGGCGAAGTGGGTGACCTGACCTGCTGTGTCACAC 694
Qy 75 -----LeuThrLeuGluGlnProGlnGlyAspSerMetThrCysGly 89
Db 695 CTCCTCTTTCCAGCAGCTGACCTGAGCAGCGCGCAGGGGGGATTCATGATGACCTGGCA 754
Qy 89 uGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeuIleGlnAlaLysAlaLeuAspLe 109
Db 755 GCAGGCCACAGCTCTTGGCCAACTGGCGCGGTCTCATCCAGGCCAAGAGCGCTGGACCT 814
Qy 109 uGlyThrPheThrGlyTyrSerAlaLeuAlaLeuAlaLeuAlaLeuProAlaAspGlyAr 129
Db 815 GGGCACCTTCACGGGTACTTCGGCCCTGCGCCCTGGCGCTGCGCGCTGCCCGGACGGCG 874
Qy 129 gValValThrCysGluValAlaAspAlaGlnProGluLeuGlyArgProLeuTrpArg-- 148
Db 875 CGTGGTGACTGCGAGGTGAGCGGAGCGGCCCGCGAGCTGGGACGCCCTCTGGAGGCA 934
Qy 148 ----- 148
Db 935 GGTGAGCGCCCGCCCTAGCTCTGCAGCCCCCAGCGGGGGCGCAACGGCTGACCCGCTCC 994
Qy 149 -----GlnAlaGluAlaGluHisLysIleAspLeuArgLeuLysProAlaLeuGluThrL 167
Db 995 CTCGCGAGCGCGAGCGGAGCACAAGATCGACCTCCGGCTGAAGCCCGCCCTTGGAGACC 1054
Qy 167 euAspGluLeuLeuAlaAlaGlyGluAlaGlyThrPheAspValAlaValAlaAspAlaA 187
Db 1055 TGGACGAGCTGTGGCGGGCGGAGCGCGCACCTTCACGCTGGCGCTGGTGATCGCG 1114
Qy 187 sPlysGluAsnCysSerAlaTyrTyrGluArgCysLeuGlnLeuLeuArgProGlyGlyI 207
Db 1115 ACAAGAGAACTGCTCCGCTACTACGAGCGCTGCTGCGAGCTGCTGCGACCGGAGGCA 1174
Qy 207 leuAlaValLeuArgValLeuTrpArgLysValLeuGlnProProLysGlyAspV 227
Db 1175 TCCTCGCCCTCTCAGAGTCTCTGTGGCGGGGAAGGTGCTGCACACTCCGAAAGGGGACG 1234
Qy 227 alAlaAlaGluCysValArgAsnLeuAsnGluArgIleArgArgAspValArgValTyrI 247
Db 1235 TGGCGGCCGAGTGTGTGCANACCTTAACGACGCATCCGGCGGACGTCAGGGTCTACA 1294
Qy 247 leSerLeuLeuProLeuGlyAspGly 255
Db 1295 TCAGCCTCTGCGCCCTGGCGATGA 1320

RESULT 8
CB852718 750 bp mRNA linear EST 22-APR-2003
LOCUS UI-CF-FN0-afl-p-08-0-UI.s1 UI-CF-FN0 Homo sapiens cDNA clone
DEFINITION UI-CF-FN0-afl-p-08-0-UI 3', mRNA sequence.
ACCESSION CB852718
VERSION CB852718.1 GI:30047716
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 750)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
8889548
Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
```

```
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.reagen.com) or from Open Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD
POLYA=No.

FEATURES
            Location/Qualifiers
    source          1..750
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="UI-CF-FN0-afl-p-08-0-UI"
                    /tissue_type="Human Lung Epithelial cells"
                    /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                    /clone_lib="UI-CF-FN0"
                    /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                    modified polylinker; Site 1: EcoR I; Site 2: Not I;
                    UI-CF-FN0 is a subtracted cDNA library derived from two
                    normal human lung epithelial cell libraries (EN1 and
                    DUI). The library was subtracted according to according to
                    Ronaldo, Lennon and Soares, Genome Research, 6:791-806,
                    1996. For additional information, contact:
                    bento-soares@uiowa.edu
                    TAG_SEQ=None found"

ORIGIN
Alignment Scores:
Pred. No.:      5e-110      Length:      750
Score:          1180.00     Matches:    228
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:      87.86%     Indels:      0
DB:               6         Gaps:         0

US-10-017-407A-306 (1-262) x CB852718 (1-750)

Qy 32 GlyArgCysProProTrpArgGlyArgArgGluGlnCysLeuLeuProGluAsp 51
Db 30 GGGAGGGGTGCCCCCATGGCGAGCGCGCGAGAGCAGTGTCTTCCCCCGAGGAC 89
Qy 52 SerArgLeuTrpGlnTyrLeuLeuSerArgSerMetArgGluHisProAlaLeuArgSer 71
Db 90 AGCGCGCTGTGCAGTATCTTCTGAGCGCTCATGCGGGAGCACCGCGCTGCCAAGC 149
Qy 72 LeuArgLeuLeuThrLeuGlnProGlnGlyAspSerMetThrCysGluGlnAla 91
Db 150 CTGAGGCTGCTGACCTGGAGCAGCGCGAGGGGGATTCTATGATGACCTGCCGAGCGGCC 209
Qy 92 GlnLeuLeuAlaAsnLeuAlaArgLeuIleGlnAlaLysAlaLeuAspLeuGlyThr 111
Db 210 CAGCTTTGGCCAACTGGCGGGCTCATCCAGGCCAAGAGCGCTGACCTGGGCACC 269
Qy 112 PheThrGlyTyrSerAlaLeuAlaLeuAlaLeuAlaLeuProAlaAspGlyArgValVal 131
Db 270 TTTACGGGCTACTCCGCCCTGGCCCTGGCGCTGCGCGCTGCCCGACGGCGCGTGGTG 329
Qy 132 ThrCysGluValAlaAspAlaGlnProGluLeuGlyArgProLeuTrpArgGlnAlaGlu 151
Db 330 ACCTCGAGGTGGAAGCGCGAGCGCCCGAGCTGGGACCGGCCCTGTGGAGGGCAGGCCGAG 389
Qy 152 AlaGluHisLysIleAspLeuArgLeuLysProAlaLeuGluThrLeuAspGluLeuLeu 171
Db 390 GGGGAGCACAGATCGACCTCGGGCTGAAGCCCGCTTGGAGACCTTGGACGAGCTGCTG 449
Qy 172 AlaAlaGlyGluAlaGlyThrPheAspValAlaValAlaAspAlaAspLysGluAsnCys 191
Db 450 GCGCGGGCGAGCGCGGACCTTCGACGTGGCGCTGGTGGATCGGACAAAGAGAACTGC 509
Qy 192 SerAlaTyrTyrGluArgCysLeuGlnLeuLeuArgProGlyGlyIleAlaValLeu 211
Db 510 TCCGCTACTACGAGCGCTGCGCTGACGTGCTGCCAGCCCGAGGCATCTCCCGCTCTC 569
```

```
cdna Library preparation: Dr. M. Bento Soares, University of Iowa
cdna Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.reagen.com) or from Open Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD
POLYA=No.

FEATURES
            Location/Qualifiers
    source          1..750
                    /organism="Homo sapiens"
                    /mol_type="mRNA"
                    /db_xref="taxon:9606"
                    /clone="UI-CF-FN0-afl-p-08-0-UI"
                    /tissue_type="Human Lung Epithelial cells"
                    /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                    /clone_lib="UI-CF-FN0"
                    /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                    modified polylinker; Site 1: EcoR I; Site 2: Not I;
                    UI-CF-FN0 is a subtracted cDNA library derived from two
                    normal human lung epithelial cell libraries (EN1 and
                    DUI). The library was subtracted according to according to
                    Ronaldo, Lennon and Soares, Genome Research, 6:791-806,
                    1996. For additional information, contact:
                    bento-soares@uiowa.edu
                    TAG_SEQ=None found"
```



http://image.llnl.gov  
 Plate: LfCM2613 row: e column: 24  
 High quality sequence stop: 532.  
 Location/Qualifiers  
 1. .934  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6427775"  
 /issue\_type="epidermoid carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 101"  
 /note="Organ: lung; Vector: pOTB7; Site\_1: EcoRI; Site\_2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
 Pred. No.: 3 71e-108 Length: 934  
 Score: 1163.00 Matches: 246  
 Percent Similarity: 94.36% Conservative: 5  
 Best Local Similarity: 92.48% Mismatches: 8  
 Query Match: 86.60% Indels: 8  
 DB: 5 Gaps: 2

US-10-017-407A-306 (1-262) x BQ931589 (1-934)

QY 2 ThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAlaLeu 21  
 DB 1 ACCGACCGGTGGCTTCTCCGTGCGCGCGCGCTGGCCCTGGGCTACGCCGACTG 60  
 QY 22 GlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgArgCysProProTrpArgGlyArg 41  
 DB 61 GCGCGCGCTTCGCCACTGCGCTCTTCTTGGGAGCGGTGCCCCCATATGGGCGGCGG 120  
 QY 42 ArgGluGlnCysLeuLeuProGluAspSerArgLeuTrpGlnTyrLeuLeuSerArg 61  
 DB 121 CGAGAGCAGTGGCTGCTTCCCCCGAGGACCGCGCTGTGGCAGTATCTTCTGAGCCGC 180  
 QY 62 SerMetArgGluHieProAlaLeuArgSerLeuArgLeuLeuThrLeuGluGlnProGln 81  
 DB 181 TCCATGCGGAGACCCCGCGCTGCGAAGCCTGAG---CTGACCTCGGAGCGCGCAG 236  
 QY 82 GlyAspSerMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeuLeu 101  
 DB 237 GGGGATTCTATGATGACCTCGCAGCAGGCGCCAGCTCTTGGCCAACTGGCGGGCTCATC 296  
 QY 102 GlnAlaLeuLeuAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeuAla 121  
 DB 297 CAGGCCAAGAGCGCTGGACCTGGGCACCTTACGGGGCTACTTCGGCCCTGGCCCTGGCC 356  
 QY 122 LeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnProProGlu 141  
 DB 357 CTGGCGCTCCCGCGGACGGCGCTGGTGAGCTCGGAGTGGAGCGGAGCCCGCGAG 416  
 QY 142 LeuGlyArgProLeuTrpArgGlnAlaGluAlaGluHisLeuLeuAspLeuArgLeuLeu 161  
 DB 417 CTGGGACGGCCCTGTGGAGGAGCGCGGAGGCGGAGCAAGATCGACCTCGGCTGAAG 476  
 QY 162 ProAlaLeuGluThrLeuAspGluLeuLeuAlaAlaGlyGluAlaGlyThrPheAspVal 181  
 DB 477 CCGCGCTTGGAGACCTTGGACGAGCTGTCTGGCGGGCGGCGGCGGCGGCGGCGGCG 536  
 QY 182 AlaValAspAlaAspLysGluAsnCysSerAlaTyrTyrGluArgCysLeuGlnLeu 201  
 DB 537 GCGGTGGTGGATGCGGACGAGGAGAACTGCTCCGCTACTACGAGCGCTGCTGAGCTG 596  
 QY 202 LeuArgProGlyGlyLeuAlaValLeuArgValLeuTrpArgGlyLysValLeuGln 221

Db 597 CTGCGACCGGAGGCGATCTCGCGCTCAGAGTCTGTGGCGGGAGGTGCTGCAG 656  
 QY 222 ProProLysGlyAspValAlaAlaGluCysVal---ArgAsnLeuAsnGluArg-1leAr 240  
 Db 657 CTCCCAAGGGGAACTTGGCGCGCGATGTGTGCAAAACCTAAACGACGACCATCCG 716  
 QY 240 gArg-AspValArg-ValTyrIleSerLeu-LeuProLeuGlyAsp-GlyLeuThrLeuA 259  
 Db 717 GCGGGGACGTACGGGTCTACATCAGCTCCCGGCCCTGGGCGAAGGAGACTCACCTTGG 776  
 QY 259 laPheLys 261  
 Db 777 CCCTTCAA 784

## RESULT 11

## AK007659

## LOCUS

## DEFINITION

AK007659 919 bp mRNA linear HTC 03-APR-2004  
 Mus musculus 10 day old male pancreas cDNA, RIKEN full-length  
 enriched library, clone:1810030M08 product:weakly similar to  
 PUTATIVE O-METHYLTRANSFERASE (FRAGMENT) (Rhodothermus marinus),  
 full insert sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## REFERENCE

## AUTHORS

## TITLE

Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.  
 Direct Submission  
 Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@sc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)  
 Please visit our web site (http://genome.gsc.riken.jp/) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGATCCAGAGCTCTTTTCTTTTNN 3'], cDNA was prepared by using trihalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of subtraction to Rot = 20.0. Second strand cDNA was prepared with the primer adapter of sequence[5' GAGAGAGAGCGCCGAATTAATTCGAGTTAATTAATTAATTCCTCCCTCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI. Host: SOLR.

## FEATURES

## Location/Qualifiers

1..919  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="FANTOM DB:1810030M08"  
 /db\_xref="taxon:10090"  
 /clone="1810030M08"  
 /sex="male"  
 /tissue\_type="pancreas"  
 /clone\_lib="RIKEN full-length enriched mouse cDNA library"  
 /dev\_stage="10 day old"  
 1..919  
 /note="weakly similar to PUTATIVE O-METHYLTRANSFERASE (FRAGMENT) [Rhodothermus marinus] (SPRF|Q9XCB3, evidence: FASTY, 55.5%id, 97.3%length, match=331)"

## misc\_feature

## ORIGIN

Alignment Scores:  
 Pred. No.: 1,88e-107 Length: 919  
 Score: 1156.00 Matches: 224  
 Percent Similarity: 92.37% Conservative: 18  
 Best Local Similarity: 85.50% Mismatches: 20  
 Query Match: 86.08% Indels: 0  
 DB: 3 Gaps: 0

US-10-017-407A-306 (1-262) x AK007659 (1-919)

Qy 1 MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla 20  
 Db 37 ATGGCTCAGCCGCTCCCTCGCTATCTATCCAGCGGCACCTGCGGCTCGGCGCG 96  
 Qy 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgArgCysProTrpArgGly 40  
 Db 97 CTGGGCGCGCTCGCTCTCTGCTCTGGGAAACGCTGGGCTCCATGGGGGTCC 156  
 Qy 41 ArgArgGlnGlnCysLeuLeuProGluAspSerArgLeuTrpGlnTrpArgLeuSer 60  
 Db 157 AGCGGCGAGAGCGCTGCTGCGACCTGAGGACATCCCTGTGGCAGTATCTGCTGAC 216  
 Qy 61 ArgSerMetArgGlnHisProAlaLeuArgSerLeuArgLeuLeuThrLeuGlnPro 80  
 Db 217 CGCTCCATGAGAGAGACCGCGCGCTGCGAGGCTGCGACTGCTGACCTGACCGAGCGG 276

Qy 81 GlnGlyAspSerMetMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeu 100  
 Db 277 CAGGGGGATTCATGATGACCTGTGACAGGCCAGCTTCTGCCACACTTGGCGGCTC 336  
 Qy 101 IleGlnAlaLysLeuAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeu 120  
 Db 337 ATTAAGGCCCAAGAAAGCTCTGGATCTGGGTACTTTTCAGGGGTACTTCGGCCCTT 396  
 Qy 121 AlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValValAspAlaGlnProPro 140  
 Db 397 GCCTTTGGCGCTTCCCGAGGCTGCGCGCTGTGTGACCTGCGAGGTTGACGACGAGCCCG 456  
 Qy 141 GlnLeuGlyArgProLeuTrpArgGlnAlaGluAlaGluHisLysIleAspLeuArgLeu 160  
 Db 457 AAGCTGGGACGCCCATGTGGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 516  
 Qy 161 LysProAlaLeuGlnThrLeuAspGluLeuLeuAlaAlaGlyGluAlaGlyThrPheAsp 180  
 Db 517 CAGCCCGCTTCACACATTTGATGAGCTCTAGCGGGGCGAGCGCGAACCCTTCGAC 576  
 Qy 181 ValAlaValValAspAlaAspLysGluAsnCysSerAlaTyrTyrGluArgCysLeuGln 200  
 Db 577 ATAGCGGTGTGGAGCGCGACAAAGAGAACTGTACCGCTTACTAGAGCGCTGTCTGCAG 636  
 Qy 201 LeuLeuArgProGlyGlyIleLeuLeuAlaValLeuArgValLeuTrpArgGlyLysValLeu 220  
 Db 637 CTCCTACGTCTCCGAGGCGTCTCTGCTACTACAGTCTGTGGCGGAGAGAGTCTG 696  
 Qy 221 GlnProProLysGlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArgLeuArg 240  
 Db 697 CAGCCTCAGCCCGAGCAAGAACTGTTGAATGTGTGGGAACCTGAACGACATCCCTG 756  
 Qy 241 ArgAspValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPhe 260  
 Db 757 AGGGAGCGCAGGGTCTACATCAGCTCTCTGCGGCTGGATGATGGCTCTCTCTGGCCTTT 816  
 Qy 261 LysIle 262  
 Db 817 AAGATC 822  
 RESULT 12  
 LOCUS AK054334  
 DEFINITION Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN full-length enriched library, clone:B330016L21 product:weakly similar to PUTATIVE O-METHYLTRANSFERASE (FRAGMENT) [Rhodothermus marinus], full insert sequence.  
 ACCESSION AK054334  
 VERSION AK054334.1 GI:26344156  
 KEYWORDS HTC; CAP trapper.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1  
 AUTHORS Carninci,P. and Hayashizaki,Y.  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE 99279253  
 PUBMED 10349636  
 REFERENCE 2  
 AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
 MEDLINE 20499374  
 PUBMED 11042159  
 REFERENCE 3  
 AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,

Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS

20530913  
11076861  
4  
The RIKEN Genome Exploration Research Group Phase II Team and the  
PANTOM Consortium  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS

5  
The FANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS

6 (bases 1 to 2243)  
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Iotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tegawa, A., Takahashi, F., Takaku-Akahira, S., Takada, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
Direct Submission

TITLE  
JOURNAL

Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.jp,  
URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site for further details.

URL: <http://genome.gsc.riken.jp/>  
Location/Qualifiers

FEATURES

source

1. .2243  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="FANTOM DB:E330016121"  
/db\_xref="taxon:10090"  
/clone="E330016121"  
/sex="female"  
/tissue type="ovary"  
/clone\_lib="RIKEN full-length enriched mouse cDNA library"  
/dev\_stage="2 days pregnant adult"  
40. .828  
/note="unnamed protein product; putative  
weakly similar to PUTATIVE O-METHYLTRANSFERASE (FRAGMENT)  
[Rhodothermus marinus] (SPTR|Q9XC3, evidence: FASTY,  
55.5%ID, 97.3%length, match=331)"  
/codon\_start=1  
/protein\_id="BAC35735.1"  
/db\_xref="GI:26344157"

CDS

/translation="NAQPVRLISIPAAALGSAALGAAPATGLILGKWPWPSRROE  
RLLPEDPLWYLILSRNREHPALRSLLLTLEQPGDSMTCEQAQLLANLARLIK  
AKKALDGLFTGISLALALALPEAGRVNTEVDAPPKLRPMKQAEVEQKIDRL  
QPALQTLDELLAAGEAGTFDIAVDADKENTAYYERCLQLLRPGGLVAVLRWRGE

VLQOPRNKTVCEVNLNRIERILRDARVYISLLPLDDGLSLAFKI"  
2223. .2228  
/note="putative"  
2243  
/note="putative"

polya\_signal

polya\_site

ORIGIN

Alignment Scores:

Pred. No.: 6.61e-107 Length: 2243  
Score: 1156.00 Matches: 224  
Percent Similarity: 92.37% Conservative: 18  
Best Local Similarity: 85.50% Mismatches: 20  
Query Match: 86.08% Indels: 0  
DB: 3 Gaps: 0

US-10-017-407A-306 (1-262) x AK054334 (1-2243)

QY 1 MetThrGlnProValProArgLeuSerValProAlaLeuAlaLeuGlySerAlaAla 20

DB 40 ATGGCTCAGCCCGCTCCCTCGGCTATCTATCCAGCGCAGCTGGCCCTCGGCTCGGCGCG 99

QY 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgCysProTrpArgGly 40

DB 100 CTGGGCGCGCTTCGCTACTGTCTCTTGTCTGGGGAACGCTGGCTCCATGGGGTCC 159

QY 41 ArgArgGluGlnCysLeuLeuProGluAspSerArgLeuTrpGlnTyrLeuLeuSer 60

DB 160 AGCGCGCAAGAGCGCTGCTGCACCTGAGGACAAATCCCTCTGGCAGTATCTGCTGAGC 219

QY 61 ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuLeuThrGluGlnPro 80

DB 220 CGCTCCATGAGAGACACCGCGCTGGCGAGCTCGGAGCTGCTGACCTGGAGAGCGG 279

QY 81 GlnGlyAspSerMetMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeu 100

DB 280 CAGGGGGATTCCATGATGACCTGTGACAGGCCAGCTTCTGGCCAACTCTGGCGCGCTC 339

QY 101 IleGlnAlaLysLeuAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeu 120

DB 340 ATTAAGGCCCAAGAAAGCTCTGGATCTGGGTACTTTTCACGGGTACTTCGGCCCTCGGCGCTA 399

QY 121 AlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnProPro 140

DB 400 GCCTTGGCGCTTCCGAGGCTCGCGCGTGGTGACCTGCGAGGTTGACGACAGAGCCCCG 459

QY 141 GluLeuGlyArgProLeuTrpArgGlnAlaGluAlaGluHisLysIleAspLeuArgLeu 160

DB 460 AAGCTGGGACGCCCATGTGGAAGCAGGCGAAGTGGAGCAGAGATCCACCTTCGGCTG 519

QY 161 LysProAlaLeuGluThrLeuAspGluLeuLeuAlaAlaGlyGluAlaGlyThrPheAsp 180

DB 520 CAGCCCGCTCGACAGATTTGGATGAGCTCTTAGCGGGCGGAGCGCGAACCCTTCGAC 579

QY 181 ValAlaValValAspAlaAspLysGluAsnCysSerAlaTyrTrpGluArgCysLeuGln 200

DB 580 ATAGCGTGGTGGACGCGGACAAAGAACTGTACCGCTCTACTACGAGCGCTGTCTGCGAG 639

QY 201 LeuLeuArgProGlyGlyIleLeuAlaValLeuArgValLeuTrpArgGlyLysValLeu 220

DB 640 CTCCTACGTCCCGAGGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 699

QY 221 GlnProProLysGlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArgIleArg 240

DB 700 CAGCCTCAGCCCGGAGCAAGAACTGTTGAATGTGTGGGAACCTGAACGACGATCCTG 759

QY 241 ArgAspValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPhe 260

DB 760 AGGAGCGCGAGGCTCTACATCAGCTCTCTGCGCCCTGGATGATGGCTCTCTTGGCGCTTT 819

QY 261 LysIle 262

DB 820 AAGATC 825

## RESULT 13

BY707694 910 bp mRNA linear EST 16-DEC-2002  
 BY707694 RIKEN full-length enriched, 10 day old male pancreas Mus  
 musculus cDNA clone 1810030M08 5', mRNA sequence.  
 BY707694  
 EST. GI:27118872  
 Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 910)  
 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,  
 Nikaide, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,  
 Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,  
 Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,  
 Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,  
 Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,  
 Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,  
 Fletcher, C.P., Forrest, A., Frazer, K.S., Gaasterland, T.,  
 Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,  
 Gustingich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,  
 Kawai, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,  
 Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,  
 Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,  
 Numata, K., Okido, T., Pavan, W.J., Perte, G., Pesole, G.,  
 Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,  
 Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,  
 Sandelin, A., Schneider, C., Semp, C.A., Setou, M., Shimada, K.,  
 Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,  
 Verdardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,  
 Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,  
 Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,  
 Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M.,  
 Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,  
 Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,  
 Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,  
 Rogers, J., Birney, E. and Hayashizaki, Y.  
 Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)  
 22354683  
 12466851  
 Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic  
 Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/  
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,  
 Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F.,  
 Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,  
 Kondo, S., Kono, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,  
 Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N.,  
 Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,  
 Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.  
 Direct Submission  
 Computational Analysis of Full-Length Mouse cDNAs Compared with  
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new  
 genes. Genome Res. 10 (10), 1617-1630 (2000)  
 RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
 10 (11), 1757-1771 (2000)  
 Computer-based methods for the mouse full-length cDNA  
 encyclopedia: real-time sequence clustering for construction of a  
 non-redundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for  
 further details.

## FEATURES

Location/Qualifiers  
 source  
 1..910  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strains="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="1810030M08"  
 /sex="male"  
 /tissue\_type="pancreas"  
 /dev\_stage="10 day old"  
 /clone\_lib="RIKEN full-length enriched, 10 day old male  
 pancreas"

## ORIGIN

Alignment Scores:  
 Pred. No.: 2,166-104 Length: 910  
 Score: 1126.00 Matches: 222  
 Percent Similarity: 91.98% Conservative: 19  
 Best Local Similarity: 84.73% Mismatches: 21  
 Query Match: 83.84% Indels: 1  
 DB: 6 Gaps: 0

US-10-017-407A-306 (1-262) x BY707694 (1-910)

QY 1 MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla 20  
 DB 34 ATGGCTCAGCCCGTCCCTCGCTATCTATCCAGCGGCACCTGGCCCTCGGCTCGCCCGG 93  
 QY 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgArgCysProProTrpArgGly 40  
 DB 94 CTGGCGCG-GCCTTCGCTACTGTCTCTTGTCTGGGAAACGGTGGCCCTCCATGGGGGTCC 152  
 QY 41 ArgArgGluGlnCysLeuLeuProGluAspSerArgLeuTrpGlnTrpLeuLeuSer 60  
 DB 153 AGCGCGAAGAGCGCGCTGCTGCCACCTGAGGACAAATCCCTGTGGCAGTATCTGTGAGC 212  
 QY 61 ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuLeuGluGlnPro 80  
 DB 213 CGCTCCATGAGAGACACCGCGCGCTCGCGACCTGCTGACCTGAGCAGCG 272  
 QY 81 GlnGlyAspSerMetMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeu 100  
 DB 273 CAGGGGGATTCCATGATGACCTGTGAACAGGCCACAGCTTCTGSCCAACCTGGCGGGTTC 332  
 QY 101 IleGlnAlaLysLeuAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeu 120  
 DB 333 ATTAAGGCCAGAAAGCTCTGGATCTGGGTACTTTTCAGGGGTACTTCGGCCCTGGCCCTA 392  
 QY 121 AlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnProPro 140  
 DB 393 GCCTTGGCGCTTCGGAGGCTGGCCGCTGTGTGACCTGCGAGGTTTGACGACAGCCCGC 452  
 QY 141 GluLeuGlyArgProLeuTrpArgGlnAlaGluAlaGluHisLysIleAspLeuArgLeu 160  
 DB 453 AAGCTGGGACGCCCATGTGGAAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 512  
 QY 161 LysProAlaLeuGluThrLeuAspGluLeuLeuAlaAlaGlyGluAlaGlyThrPheAsp 180  
 DB 513 CAGCCCGCGCTCGACAGCAATGGATGAGTCTTAGCGGGGGGAGGCGGAGGAGGAGGAGGAG 572  
 QY 181 ValAlaValAlaAspAlaAspLysGluAsnCysSerAlaTyrTyrGluArgCysLeuGln 200  
 DB 573 ATAGCGGTGGTGGACCGCGCAAAAGAGAACTGTACCGCTACTACGAGCGCTGTCTGCAG 632  
 QY 201 LeuLeuArgProGlyGlyIleLeuAlaValLeuArgValLeuTrpArgGlyLysValLeu 220  
 DB 633 CTCCTACGCTCCCGGAGGCGTGTCTGCTGCTACTCAGAGTCTGTGGCGGAGGAGGAGTGT 692



QY 221 GlnProProLyGlyAspValAlaGluCysValArgAsnLeuAsnGluArg 240  
 |||||  
 |||||  
 Db 693 CAGCCTCAGCCAGCAAGACTGTGAATGTGTGGCAACTGAACGACGATCCTG 752  
 |||||  
 QY 241 ArgAspValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPhe 260  
 |||||  
 |||||  
 Db 753 AGGAGCGCCAGGGTCTACATCAGCCTCTGCGCCCTCGATGATGGCGTCTCTTGGCCTTT 812  
 |||||  
 QY 261 LysIle 262  
 |||||  
 Db 813 AGATC 818  
 |||||

RESULT 14  
 BC019467  
 LOCUS  
 DEFINITION Mus musculus catechol-O-methyltransferase domain containing 1, mRNA  
 (CDNA clone IMAGE:4036276), containing frame-shift errors.  
 BC019467  
 HTG  
 ACCESSION BC019467.1 GI:18043387  
 VERSION Mus musculus (house mouse)  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCE  
 AUTHORS

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
 Schetz, T.E., Brownstein, M.J., Udgin, T.B., Toshiyuki, S.,  
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,  
 Abramson, R.D., Mullaly, S.J., Bosak, S.A., McSwan, P.J.,  
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,  
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
 Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,  
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,  
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,  
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.B.,  
 Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
 Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 12477932

2 (bases 1 to 999)  
 Strausberg, R.  
 Direct Submission  
 TITLE  
 JOURNAL

Submitted (19-DEC-2001) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 1A03, Bethesda, MD 20892-2590,  
 USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgapsb@mail.nih.gov](mailto:cgapsb@mail.nih.gov)  
 Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys  
 cDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Baylor College of Medicine Human Genome  
 Sequencing Center  
 Center code: BCM-HGSC  
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
 Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,  
 Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,  
 A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAC Plate: 37 Row: a Column: 14

This clone was selected for full length sequencing because it  
 passed the following selection criteria: Similarity but not  
 identity to protein  
 This clone has the following problem: frame shifted.

FEATURES  
 source  
 Location/Qualifiers  
 1..999  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="mix FVB/N, C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:4036276"  
 /tissue\_type="Mammary tumor. WAP-TGF alpha model. 7 months  
 old, gross tissue."  
 /clone\_lib="NCI\_CGAP\_Mam5"  
 /lab\_host="DH10B"  
 /note="Vector: pCMV-SPORT6"

ORIGIN  
 Alignment Scores:  
 Pred. No.: 8,41e-103 Length: 999  
 Score: 1111.00 Matches: 224  
 Percent Similarity: 83.97% Conservative: 17  
 Best Local Similarity: 78.05% Mismatches: 21  
 Query Match: 82.73% Indels: 26  
 DB: 3 Gaps: 1

US-10-017-407A-306 (1-262) x BC019467 (1-999)  
 QY 1 MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla 20  
 |||||  
 |||||  
 Db 23 ATGGCTCAGCCCGCTCCCTCGGTATCTATCCAGCGCGCACTGGCCCTGGGCTCGGCCGCG 82  
 |||||  
 QY 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgCysProProTrpArgGly 40  
 |||||  
 |||||  
 Db 83 CTGGCGCGCGCTCTCGCTACTGTCTCTGTGGGGAACGCTGGCGCTCCATGGGGGTCC 142  
 |||||  
 QY 41 ArgArgGluGlnCysLeuLeuProGluAspSerArgLeuTrpGlnTyrLeuLeuSer 60  
 |||||  
 |||||  
 Db 143 AGCGCGCAAGAGCGCTGCTGCGCACCTGAGGACAAATCCCTCTGGCAGTATCTGTGAGC 202  
 |||||  
 QY 61 ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuThrLeuGlnPro 80  
 |||||  
 |||||  
 Db 203 CCGCTCATGAGAGAGACCGCGCGCTGCGGAGCGCTGCGGACTGTGACCTGAGAGAGCG 262  
 |||||  
 QY 81 GlnGlyAspSerMetMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeu 100  
 |||||  
 |||||  
 Db 263 CAGGGGGATTCATGATGACCTGTGAACAGGCCAGCTTCTGCCCAACCTGGCGCGCTC 322  
 |||||  
 QY 101 IleGlnAlaLysIleAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeu 120  
 |||||  
 |||||  
 Db 323 ATTAAGGCCCAAGAAAGCTCTGGATCTGGGTACTTTTACCGGGTACTTCGGCCCTGGCCCTA 382  
 |||||  
 QY 121 AlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnProPro 140  
 |||||  
 |||||  
 Db 383 GCCTTGGCGCTTCCGAGGCTGCGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 442  
 |||||  
 QY 141 GluLeuGlyArgProLeuTrpArg-----148  
 |||||  
 |||||  
 Db 443 AGCTGGGAGCGGCCCATGTGGAA- GCAGGTGAGAGCCCCACACCTCGCGCGCTCGGGCT 501  
 |||||  
 QY 149 -----GlnAlaGluAlaGluHisLys 155  
 |||||  
 |||||  
 Db 502 CCGGCTCGGGGCGGTGCCCGCTGACCGGCTCTTCCGAGGACAGAGTGGAGCAAG 561  
 |||||  
 QY 156 IleAspLeuArgLeuLysProAlaLeuGluThrLeuAspGluLeuAlaGlyGlu 175  
 |||||  
 |||||  
 Db 562 ATCGACCTTCGGCTCGAGCCCGCTGACAGCATTTGGATGAGCTCTACGGCGGCGGAG 621  
 |||||  
 QY 176 AlaGlyThrPheAspValAlaValValAspAlaAspLysGluAsnCysSerAlaTyr 195  
 |||||  
 |||||  
 Db 622 GCGGGAACCTTCGACATAGCCCTGTGTGGAGCGGACAAAGAGACTGTACCGCTACTAC 681  
 |||||  
 QY 196 GluArgCysLeuGlnLeuLeuArgProGlyGlyIleLeuAlaValLeuArgValLeuTrp 215  
 |||||



Db 682 GAGCGCTGCTCAGCTCTACGTCGCGAGGGTCTCGCTACTCAGAGTCTGTGG 741  
 QY 216 ArgGlyLysValLeuGlnProProLysGlyAspValAlaAlaGluCysValArgAsnLeu 235  
 Db 742 CGCGGAGAAGTGTGCGAGCTCAGCCAGGAACAAGACTGTTGAATGTGTGCGGAACCTG 801  
 QY 236 AsnGluArgIleArgAspValArgValTyrIleSerLeuLeuProLeuGlyAspGly 255  
 Db 802 AACGAACGATCTCTGAGGAGCGCCAGGGTCTACATCAGGCTCTCGCCCTGGATGATGC 861  
 QY 256 LeuThrLeuAlaPheLysile 262  
 Db 862 CTCCTCTGGCCTTAAAGATC 882

RESULT 15  
 CA777547/c  
 LOCUS  
 DEFINITION  
 ip21q07.x1 HR85 islet Homo sapiens cDNA clone IMAGE:6217933 3',  
 similar to TR:085769 085769 HYPOTHETICAL 24.8 KD PROTEIN. ;, mRNA  
 sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

CA777547 756 bp mRNA linear EST 03-DEC-2002  
 ip21q07.x1 HR85 islet Homo sapiens cDNA clone IMAGE:6217933 3',  
 similar to TR:085769 085769 HYPOTHETICAL 24.8 KD PROTEIN. ;, mRNA  
 sequence.  
 CA777547  
 CA777547.1 GI:26015422  
 EST.  
 Homo sapiens (human)  
 Homo sapiens

REFERENCE  
 AUTHORS

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 756)  
 Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,  
 Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,  
 Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,  
 Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,  
 Cardenas,M., Gibbons,Y., McCann,R., Cole,R., Tsagareishvili,R.,  
 Williams,T., Jackson,Y. and Bowers,Y.

Endocrine Pancreas Consortium  
 Unpublished (2000)  
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
 Endocrine Pancreas Consortium  
 Harvard University, Howard Hughes Medical Institute  
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
 MA 02138

Tel: 617-495-1812  
 Fax: 617-495-8557  
 Email: dmelton@biohp.harvard.edu  
 Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:  
 Washington University Genome Sequencing Center For information on  
 obtaining a clone please contact: Dr. Hiroshi Inoue  
 (hinoue@im.wustl.edu)

Seq primer: -40UP from Gibco  
 High quality sequence stop: 462.

FEATURES  
 source

1..756  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6217933"  
 /tissue\_type="Purified pancreatic islet"  
 /lab\_host="DH10B"  
 /clone\_lib="HR85 islet"  
 /note="Organ: Pancreas; Vector: pBluescript SK(-); Site\_1:  
 NotI; Site\_2: XhoI; cDNA made by oligo-dT priming. -1kb. 5'  
 Size selected on agarose gel. Average insert size ~1kb. 5'  
 XhoI site was destroyed after directional cloning.  
 Amplified once. Contact information: Hiroshi Inoue, MD,  
 Metabolism Div. (Alan Permutt Lab), Washington University  
 School of Medicine, Box 8127, 660 South Euclid Ave., St.  
 Louis, MO 63110. E-mail: hinoue@imgate.wustl.edu, Tel:  
 314-362-1916, Fax: 314-747-2692."

ORIGIN

Alignment Scores:  
 Pred. No.: 5.98e-102 Length: 756

Score: 1101.00 Matches: 216  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 81.98% Indels: 0  
 DB: 6 Gaps: 0

US-10-017-407A-306 (1-262) x CA777547 (1-756)

QY 47 LeuProGluUAspSerArgLeuTyrGlnTyrLeuLeuSerArgSerMetArgGluHis 66  
 Db 756 CTTTCCCGGAGGAGGAGCGGCTGTGGCAGTATCTTTTGAAGCGCTCCATGCGGAGCAC 697  
 QY 67 ProAlaLeuArgSerLeuArgLeuLeuThrLeuGluGlnProGlnGlyAspSerMetMet 86  
 Db 696 CCGGCGCTCGGAGGCTGAGGCTGCTGACCTTGGAGAGCGCCGAGGGGATTTCTATGATG 637  
 QY 87 ThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeuIleGlnAlaLysAla 106  
 Db 636 ACCTCGAGGAGGCGGCTCTTGGCCAACTTGGCGCGCTCATCCAGGCCAAGAAGGCG 577  
 QY 107 LeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeuAlaLeuAlaLeuProAla 126  
 Db 576 CTGGACCTGGGCGACCTTTCAGCGGCTACTCGGCCCTGGGCCCTGGCGCTGGCCCGG 517  
 QY 127 AspGlyArgValValThrCysGluValAspAlaGlnProProGluLeuGlyArgProLeu 146  
 Db 516 GACGGGCGGCTGGTACCTTGGAGGTGAGCGGCGAGCCCCCGAGCTGGGACGGGCCCTG 457  
 QY 147 TrpArgGlnAlaGluAlaGluHisLysIleAspLeuArgLeuLysProAlaLeuGluThr 166  
 Db 456 TGGAGGCGAGGCGGAGCGGAGCACAAGATCGACCTCGGCTGAAGCCGCGCTTGGAGACC 397  
 QY 167 LeuAspGluLeuLeuAlaAlaGlyGluAlaGlyThrPheAspValAlaValValAspAla 186  
 Db 396 CTGGACGAGCTGCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 337  
 QY 187 AspLysGluAsnCysSerAlaTyrTyrGluArgCysLeuGlnLeuLeuArgProGlyGly 206  
 Db 336 GACAGGAGGAACTGCTCGGCTACTACGAGCGCTGCTGCGAGCTGCTGCGAGCGG 277  
 QY 207 IleLeuAlaValLeuArgValLeuTrpArgGlyLysValLeuGlnProProLysGlyAsp 226  
 Db 276 ATCTCTCGCGCTCTCAGAGTCTCTGTGGCGCGGGAAGGTGCTGCAACCTCCGAAAGGGGAC 217  
 QY 227 ValAlaAlaGluCysValArgAsnLeuAsnGluArgIleArgArgAspValArgValTyr 246  
 Db 216 GTGGCGCGGAGTGTGCGGAAACCTAAACGAAACGATCCCGCGGAGCGTCAGGGTCTAC 157  
 QY 247 IleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPheLysile 262  
 Db 156 ATCAGCCTCTCTGGCCCTGGGCGATGGACTCACCTTGGGCTTCAAGATC 109

Search completed: April 20, 2005, 01:05:10  
 Job time : 8586 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 19, 2005, 20:52:38 ; Search time 622 Seconds  
(without alignments)  
2555.431 Million cell updates/sec

Perfect score: 1343  
Sequence: 1 WTQVPRLSVPAALGSA.....VRVYISLLPLDGLTLAFKI 262

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 5622541 seqs, 303335566 residues

Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Command line parameters:

-Q=/cgn2\_1/USPTO.spool/US10017407/runat.19042005.142440.29067/app.query.fasta\_1.455  
-DB=Published Applications NA -QFWT=fastap -SUFFI=rnpb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bts -START=1 -END=1 -MORIX=blosum62  
-TRANS=human40.cdi -LIST=1500 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=0 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USRP=US10017407 @CNG 1.1 699 @runat.19042005.142440.29067  
-NCPUS=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq\*
- 13: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq\*
- 17: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq\*
- 18: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq\*
- 19: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq\*
- 20: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq\*
- 21: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUBCOMB.seq\*
- 22: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

\*

Result No.	Score	Query Match	Length	DB ID	Description
1	1343	100.0	789	9	US-09-844-468-3
35	1343	100.0	989	16	US-10-210-951-21
37	1343	100.0	989	16	US-10-211-884-21
40	1343	100.0	989	16	US-10-013-909A-305
63	1343	100.0	989	17	US-10-211-858-21
69	1343	100.0	989	17	US-10-307-817-121
70	1343	100.0	989	17	US-10-307-817-125
73	1343	100.0	1037	9	US-09-844-468-1
74	1343	98.6	967	15	US-10-106-698-521
75	884	65.8	787	17	US-10-307-817-123
76	707	52.6	620	17	US-10-240-435-182
C	509	37.9	458	10	US-09-918-995-23102
78	509	37.9	474	10	US-09-918-995-22407
79	428.5	31.9	1512	18	US-10-739-930-3516
C	425.5	31.7	84428	17	US-10-229-148B-1
81	413	30.8	849	17	US-10-425-114-25410
82	413	30.8	1159	17	US-10-425-114-2777
83	413	30.8	1218	16	US-10-361-460-77
84	411	30.6	86941	17	US-10-461-194-2
85	409.5	30.5	85692	17	US-10-461-194-1
86	407	30.3	901	17	US-10-425-114-27082
87	407	30.3	2381	18	US-10-425-115-138013
88	406	30.2	1257	18	US-10-425-115-66941
89	405.5	30.2	980	9	US-09-452-239-21
90	405.5	30.2	1508	17	US-10-424-599-18320
91	401	29.9	891	9	US-09-452-239-1
92	398.5	29.7	744	17	US-10-239-463-1
93	396	29.5	888	18	US-10-425-115-53820
94	396	29.5	1058	9	US-09-452-239-11
95	396	29.5	1060	18	US-10-437-963-62449
C	396	29.5	3759	18	US-10-437-963-23149
97	394	29.3	1078	9	US-09-452-239-41
98	392.5	29.2	962	9	US-09-452-239-23
99	392.5	29.2	1023	9	US-09-452-239-25
100	392.5	29.2	1044	17	US-10-424-599-95805
101	392.5	29.2	1051	16	US-10-289-757-146
102	392.5	29.2	1059	16	US-10-289-757-36
103	392	29.2	975	18	US-10-437-963-61696
C	391.5	29.2	1072	9	US-09-770-443-132
105	389.5	29.0	1060	17	US-10-425-114-23879
106	389.5	29.0	1377	18	US-10-425-115-138007
107	389	29.0	997	18	US-09-452-239-13
108	387.5	28.9	991	18	US-10-425-115-53827
109	387	28.8	953	9	US-09-452-239-45
110	387	28.8	1152	17	US-10-425-114-26100
111	387	28.8	1152	18	US-10-425-115-53821
112	387	28.8	1443	18	US-10-767-701-14336
113	386	28.7	1012	15	US-10-174-693-94
114	386	28.7	1026	15	US-10-174-693-6
115	386	28.7	1088	17	US-10-425-114-12284
116	386	28.7	1097	17	US-10-425-114-4691
117	386	28.7	1118	9	US-09-452-239-37
118	386	28.7	1146	9	US-09-452-239-3
119	386	28.7	1160	16	US-10-361-460-31
120	385.5	28.7	931	9	US-09-452-239-17
121	385.5	28.7	1063	16	US-10-289-757-37
122	385.5	28.7	1287	18	US-10-425-115-113175
123	385.5	28.7	1423	17	US-10-424-599-75405
124	385	28.7	1097	17	US-10-425-114-16291
125	385	28.7	1200	18	US-10-425-115-138010
126	385	28.7	1506	18	US-10-425-115-113176
127	385	28.7	1890	18	US-10-739-930-2642
128	383.5	28.6	1003	16	US-10-361-460-33
129	383.5	28.6	1030	17	US-10-425-114-2377
130	383.5	28.6	1057	9	US-09-452-239-5
131	383.5	28.6	1089	17	US-10-425-114-2526
132	382.5	28.5	929	9	US-09-452-239-19
133	382	28.4	617	18	US-10-021-323-15391
134	381	28.4	876	18	US-10-437-963-41905
135	381	28.4	1049	9	US-09-452-239-43

136	380.5	28.3	1114	17	US-10-425-114-3140	Sequence 3140, Ap	209	174	13.0	296	15	US-10-174-693-195	Sequence 195, App
137	378	28.1	944	16	US-10-361-460-32	Sequence 32, Appl	210	173.5	12.9	584	18	US-10-425-115-53810	Sequence 53810, A
138	378	28.1	1066	18	US-10-425-115-179664	Sequence 179664, A	211	172.5	12.8	522	15	US-10-156-761-3105	Sequence 3105, Ap
139	377.5	28.1	905	18	US-10-431-963-41715	Sequence 41715, A	212	172	12.8	2355	17	US-10-424-599-18324	Sequence 18324, A
140	377	28.0	1233	9	US-10-767-799-6335	Sequence 6335, Ap	213	172	12.8	2256646	18	US-10-470-565-1	Sequence 1, Appl
141	376	28.0	923	9	US-09-452-239-7	Sequence 7, Appl	214	171.5	12.8	562	15	US-10-174-693-53	Sequence 53, Appl
142	376	28.0	1006	17	US-10-425-114-27818	Sequence 27818, A	215	170	12.7	447	11	US-09-732-627A-4334	Sequence 4334, Ap
143	374	27.8	1146	18	US-10-425-115-53825	Sequence 53825, A	216	170	12.7	75216	15	US-10-080-170-646	Sequence 646, App
144	373	27.8	1281	18	US-10-425-115-138015	Sequence 138015, A	217	170	12.7	75216	18	US-10-080-170-646	Sequence 646, App
145	372.5	27.7	1090	18	US-10-767-701-12827	Sequence 12827, A	218	170	12.7	75216	18	US-10-468-356-646	Sequence 646, App
146	369	27.5	966	18	US-10-739-930-382	Sequence 382, App	219	169	12.6	1289	17	US-10-398-221-1713	Sequence 1713, Ap
147	368.5	27.4	1018	9	US-09-452-239-35	Sequence 35, Appl	220	168	12.5	2233	17	US-10-398-221-1713	Sequence 3545, Ap
148	366.5	27.3	995	18	US-10-767-795-3303	Sequence 3303, Ap	221	164	12.2	399	15	US-10-174-693-193	Sequence 193, App
149	366	27.3	326	9	US-09-880-107-632	Sequence 632, App	222	164	12.2	495269	17	US-10-398-221-8	Sequence 8, Appl
150	360	26.8	729	9	US-09-938-842A-2400	Sequence 2400, App	223	164	12.2	3011208	17	US-10-398-221-2058	Sequence 2058, Ap
151	360	26.8	729	11	US-09-938-842A-2400	Sequence 2400, App	224	160	11.9	554	17	US-10-425-114-17961	Sequence 17961, A
152	356.5	26.5	1057	17	US-10-425-114-24738	Sequence 24738, A	225	159.5	11.9	415	9	US-09-770-423-481	Sequence 481, App
153	356.5	26.5	1107	18	US-10-425-115-138003	Sequence 138003, A	226	159.5	11.7	345	18	US-10-425-115-53808	Sequence 53808, A
154	354	26.4	840	18	US-10-425-115-138002	Sequence 138002, A	227	156	11.6	19024	9	US-09-070-927A-179	Sequence 179, Appl
155	354	26.4	912	9	US-09-452-239-27	Sequence 27, Appl	228	149.5	11.1	508	9	US-09-452-239-15	Sequence 15, Appl
156	351.5	26.2	813	18	US-10-425-115-108865	Sequence 108865, A	229	143	10.6	593	18	US-10-425-115-106605	Sequence 106605, A
157	348	25.9	77536	10	US-09-940-316B-1	Sequence 1, Appl	230	142	10.6	529	18	US-10-425-115-121105	Sequence 121105, A
158	344	25.6	1079	17	US-10-424-599-98070	Sequence 98070, A	231	140.5	10.5	645	18	US-10-653-047-932	Sequence 932, App
159	343	25.5	889	17	US-10-425-114-1308	Sequence 1308, Ap	232	136	10.1	409	18	US-10-767-795-6334	Sequence 6334, Ap
160	342.5	25.5	693	18	US-10-425-114-190671	Sequence 190671, A	233	134.5	10.0	524	18	US-10-437-963-873	Sequence 873, App
161	341	25.4	982	9	US-09-452-239-31	Sequence 31, Appl	234	129	9.6	696	18	US-10-425-115-22425	Sequence 22425, A
162	336.5	25.1	1058	17	US-10-424-599-100655	Sequence 100655, A	235	128	9.5	894	17	US-10-114-270-15	Sequence 15, Appl
163	331.5	24.7	1073	18	US-10-425-115-113171	Sequence 113171, A	236	126.5	9.4	534	9	US-09-974-300-2268	Sequence 2268, Ap
164	331	24.6	997	17	US-10-424-599-71962	Sequence 71962, A	237	126	9.4	777	18	US-10-343-593-37	Sequence 37, Appl
165	320.5	23.9	972	17	US-10-424-599-133785	Sequence 133785, A	238	126	9.4	897	17	US-10-114-270-17	Sequence 17, Appl
166	320.5	23.9	985	17	US-10-425-114-23965	Sequence 23965, A	239	124.5	9.3	242	9	US-09-923-876-781	Sequence 781, App
167	320	23.8	749	18	US-10-767-795-6336	Sequence 6336, Ap	240	124.5	9.3	242	10	US-09-923-876-781	Sequence 781, App
168	317	23.6	1486	17	US-10-425-114-3685	Sequence 3685, Ap	241	122	9.1	402	14	US-10-082-727-78	Sequence 78, Appl
169	317	23.6	1582	18	US-10-425-115-138009	Sequence 138009, A	242	122	9.1	717	18	US-10-425-115-138006	Sequence 138006, A
170	314	23.4	257	15	US-10-102-524-1360	Sequence 1360, Ap	243	121.5	9.0	711	19	US-10-472-928-1931	Sequence 1931, Ap
171	311.5	23.2	699	11	US-09-938-842A-1739	Sequence 1739, Ap	244	121.5	9.0	11309	8	US-08-961-527-108	Sequence 108, App
172	311.5	23.2	699	11	US-09-938-842A-1739	Sequence 1739, Ap	245	121.5	9.0	11309	17	US-10-158-844-108	Sequence 4979, Ap
173	309	23.1	257	15	US-10-102-524-1452	Sequence 1452, Ap	246	120	8.9	3972	19	US-10-857-625-89	Sequence 89, Appl
174	306.5	22.8	792	18	US-10-425-115-140246	Sequence 140246, A	247	120	8.9	3972	19	US-10-857-625-89	Sequence 89, Appl
175	303.5	22.6	774	17	US-10-424-599-18322	Sequence 18322, A	248	119	8.9	418	17	US-10-424-599-61757	Sequence 61757, A
176	298.5	22.2	1075	15	US-10-174-693-55	Sequence 55, Appl	249	118.5	8.8	1253	13	US-10-087-192-1322	Sequence 1322, Ap
177	291	21.7	1074	15	US-10-174-693-54	Sequence 54, Appl	250	116.5	8.7	895	17	US-10-425-114-23156	Sequence 23156, A
178	286.5	21.3	109519	11	US-09-758-759-1	Sequence 1, Appl	251	116.5	8.7	900	18	US-10-425-115-144539	Sequence 144539, A
179	281.5	21.0	792	9	US-09-770-445-841	Sequence 841, Appl	252	116.5	8.7	1159	18	US-10-425-115-62761	Sequence 62761, A
180	279	20.8	651	11	US-09-758-759-84	Sequence 84, Appl	253	115	8.6	639	9	US-09-738-626-1240	Sequence 1240, Ap
181	278.5	20.7	546	18	US-10-021-323-10069	Sequence 10069, A	254	115	8.6	3309400	9	US-09-738-626-1	Sequence 1, Appl
182	276.5	20.6	343	9	US-09-917-800A-275	Sequence 275, App	255	114.5	8.5	3846	18	US-10-425-115-69524	Sequence 69524, A
183	276.5	20.6	343	17	US-10-152-319A-298	Sequence 298, App	256	114	8.5	468	17	US-10-424-599-133784	Sequence 133784, A
184	266.5	19.8	781	18	US-10-425-115-53814	Sequence 53814, A	257	112.5	8.4	371	18	US-10-437-963-67549	Sequence 67549, A
185	249.5	18.6	786	18	US-10-425-115-53809	Sequence 53809, A	258	112	8.3	2086	9	US-09-935-757-5	Sequence 5, Appl
186	231.5	17.2	1159	18	US-10-425-115-53828	Sequence 53828, A	259	111.5	8.3	602	18	US-10-425-115-172234	Sequence 172234, A
187	224.5	16.7	760	15	US-10-174-693-25	Sequence 25, Appl	260	111	8.3	13715	8	US-08-781-986A-195	Sequence 195, App
188	224	16.7	534	9	US-09-452-239-47	Sequence 47, Appl	261	111	8.3	13715	17	US-10-329-624-195	Sequence 195, App
189	220	16.4	575	18	US-10-425-115-140243	Sequence 140243, A	262	110	8.2	236	15	US-10-174-693-175	Sequence 175, App
190	219	16.3	481	18	US-10-425-115-155678	Sequence 155678, A	263	110	8.2	919	17	US-10-425-114-3232	Sequence 3232, Ap
191	216.5	16.1	578	18	US-10-767-701-26345	Sequence 26345, A	264	109	8.1	521	17	US-10-424-599-35115	Sequence 35115, A
192	215	16.0	672	15	US-10-156-761-5814	Sequence 5814, Ap	265	109	8.1	624	17	US-10-369-493-35007	Sequence 35007, A
193	215	16.0	9025608	15	US-10-156-761-1	Sequence 1, Appl	266	108.5	8.1	1545	18	US-10-425-115-51263	Sequence 51263, A
194	207	15.4	528	9	US-09-452-239-33	Sequence 33, Appl	267	107.5	8.0	1206	17	US-10-240-425-1322	Sequence 1322, Ap
195	206.5	15.4	641	18	US-10-437-963-77651	Sequence 77651, A	268	107.5	8.0	1206	18	US-10-240-425-1322	Sequence 1322, Ap
196	203	15.1	567	18	US-10-767-701-12825	Sequence 12825, A	269	107.5	8.0	1311	13	US-10-087-192-1325	Sequence 192, App
197	202	15.0	399	15	US-10-174-693-194	Sequence 194, App	270	107.5	8.0	1327	13	US-10-044-090-642	Sequence 642, App
198	200.5	14.9	632	13	US-10-194-163-655	Sequence 655, App	271	107	8.0	253	9	US-09-923-876-4875	Sequence 4875, Ap
199	194.5	14.5	525	18	US-10-021-323-10926	Sequence 10926, A	272	107	8.0	253	10	US-09-923-876-4875	Sequence 4875, Ap
200	189.5	14.1	8580	17	US-09-840-743-16	Sequence 16, Appl	273	106.5	7.9	1438	18	US-10-425-115-36031	Sequence 36031, A
201	185.5	13.8	658	17	US-10-425-114-23426	Sequence 23426, A	274	106.5	7.9	1438	17	US-10-425-114-34097	Sequence 34097, A
202	183	13.6	594	15	US-10-174-693-105	Sequence 105, App	275	106	7.9	1350	9	US-09-925-301-266	Sequence 266, App
203	181.5	13.5	505	9	US-09-452-239-29	Sequence 29, Appl	276	105.5	7.9	374	18	US-10-425-115-148943	Sequence 148943, A
204	180	13.4	607	15	US-10-174-693-23	Sequence 23, Appl	277	105.5	7.9	596	18	US-10-425-115-125234	Sequence 125234, A
205	176.5	13.1	510	9	US-09-452-239-9	Sequence 9, Appl	278	105	7.8	356	14	US-10-062-727-156	Sequence 156, App
206	176.5	13.1	600	9	US-09-452-239-39	Sequence 39, Appl	279	105	7.8	457	9	US-09-935-757-3	Sequence 3, Appl
207	176	13.1	451	14	US-10-062-727-457	Sequence 457, App	280	104.5	7.8	1593	18	US-10-437-963-40777	Sequence 40777, A
208	175.5	13.1	9025608	15	US-10-156-761-1	Sequence 1, Appl	281	104	7.7	484	18	US-10-425-115-52200	Sequence 52200, A

282	103.5	7.7	834	17	US-10-282-122A-39491	Sequence 39491, A	c 355	93.5	7.0	154746	10	US-09-827-688-8	Sequence 8, Appli
283	103	7.7	6432	17	US-10-378-083-1	Sequence 1, Appli	356	93	6.9	1524	18	US-10-425-115-114038	Sequence 114038,
284	102	7.6	328	17	US-10-425-114-6556	Sequence 6556, Ap	357	93	6.9	1508	17	US-10-369-493-33780	Sequence 33780, A
285	101.5	7.6	2505	17	US-10-303-110A-1	Sequence 1, Appli	358	93	6.9	1716	8	US-08-808-031A-1	Sequence 1, Appli
286	101.5	7.6	2505	17	US-10-303-110A-4	Sequence 4, Appli	359	93	6.9	3744	17	US-10-302-172-585	Sequence 585, App
287	101	7.5	1602	18	US-10-437-963-102014	Sequence 102014,	360	93	6.9	4018	17	US-10-172-118-308	Sequence 308, App
288	101	7.5	1786	17	US-10-302-172-657	Sequence 657, App	361	93	6.9	4018	17	US-10-342-887-308	Sequence 308, App
289	100.5	7.5	1815	16	US-10-327-813-3	Sequence 3, Appli	362	93	6.9	5032	18	US-10-473-576-26	Sequence 26, Appl
290	100.5	7.5	1815	17	US-10-329-668-3	Sequence 3, Appli	363	93	6.9	5591	17	US-10-170-385-14	Sequence 14, Appl
291	100.5	7.5	1815	18	US-10-717-049-3	Sequence 3, Appli	364	93	6.9	7788	16	US-10-329-079-8	Sequence 8, Appli
292	100	7.4	8460	14	US-10-237-271-2	Sequence 2, Appli	365	93	6.9	37360	16	US-10-329-079-6	Sequence 6, Appli
293	100	7.4	8460	17	US-10-191-997-115	Sequence 115, App	366	92.5	6.9	1107	15	US-10-156-761-6131	Sequence 6131, Ap
294	100	7.4	8460	17	US-10-274-085-4	Sequence 4, Appli	367	92.5	6.9	2433	10	US-09-864-636A-587	Sequence 587, App
295	100	7.4	8460	18	US-10-717-597-192	Sequence 192, App	368	92.5	6.9	2433	11	US-09-864-426A-587	Sequence 587, App
296	100	7.4	8460	19	US-10-278-698-161	Sequence 161, App	369	92.5	6.9	2433	16	US-10-084-839-587	Sequence 587, App
297	100	7.4	8460	19	US-10-278-698-677	Sequence 677, App	370	92.5	6.9	2445	10	US-09-864-636A-571	Sequence 571, App
298	99	7.4	2010	17	US-10-159-563-379	Sequence 379, App	371	92.5	6.9	2445	10	US-09-864-636A-575	Sequence 575, App
299	99	7.4	2010	17	US-10-418-007-3	Sequence 3, Appli	372	92.5	6.9	2445	10	US-09-864-636A-579	Sequence 579, App
300	99	7.4	2010	18	US-10-641-995-7	Sequence 7, Appli	373	92.5	6.9	2445	10	US-09-864-636A-581	Sequence 581, App
301	99	7.4	2010	18	US-10-437-963-10627	Sequence 10627, A	374	92.5	6.9	2445	11	US-09-864-426A-571	Sequence 571, App
302	99	7.4	2685	17	US-10-401-403-147	Sequence 147, App	375	92.5	6.9	2445	11	US-09-864-426A-575	Sequence 575, App
303	99	7.4	2685	17	US-10-401-403-171	Sequence 171, App	376	92.5	6.9	2445	11	US-09-864-426A-579	Sequence 579, App
304	98.5	7.3	1338	15	US-10-156-761-3240	Sequence 3240, Ap	377	92.5	6.9	2445	11	US-09-864-426A-581	Sequence 581, App
305	98.5	7.3	2384	17	US-10-104-047-567	Sequence 567, App	378	92.5	6.9	2445	16	US-10-084-839-571	Sequence 571, App
306	98.5	7.3	3147	9	US-09-741-669-216	Sequence 216, App	379	92.5	6.9	2445	16	US-10-084-839-575	Sequence 575, App
307	98.5	7.3	3147	9	US-09-815-243-5965	Sequence 5965, Ap	380	92.5	6.9	2445	16	US-10-084-839-579	Sequence 579, App
308	98.5	7.3	3147	15	US-10-301-997-84	Sequence 84, Appl	381	92.5	6.9	2445	16	US-10-084-839-581	Sequence 581, App
309	98.5	7.3	3147	17	US-10-282-122A-20260	Sequence 20260, A	382	92.5	6.9	2445	16	US-10-084-839-2818	Sequence 2818, Ap
310	98.5	7.3	3147	18	US-10-818-509-84	Sequence 84, Appl	383	92.5	6.9	2445	16	US-10-084-839-2822	Sequence 2822, Ap
311	98.5	7.3	77536	10	US-09-940-316B-1	Sequence 1, Appli	384	92.5	6.9	2445	16	US-10-084-839-2826	Sequence 2826, Ap
312	98	7.3	828	17	US-10-282-122A-31998	Sequence 31998, A	385	92.5	6.9	2445	16	US-10-084-839-2828	Sequence 2828, Ap
313	98	7.3	77294	19	US-10-729-802-1	Sequence 1, Appli	386	92.5	6.9	2493	10	US-09-864-636A-589	Sequence 589, App
314	97.5	7.3	2505	17	US-10-303-110A-2	Sequence 2, Appli	387	92.5	6.9	2493	16	US-10-084-839-589	Sequence 589, App
315	97.5	7.3	2505	17	US-10-303-110A-3	Sequence 3, Appli	388	92.5	6.9	2493	16	US-10-084-839-589	Sequence 589, App
316	97.5	7.3	2505	17	US-10-303-110A-5	Sequence 5, Appli	389	92.5	6.9	2493	16	US-10-084-839-2836	Sequence 2836, Ap
317	97.5	7.3	2505	17	US-10-303-110A-6	Sequence 6, Appli	390	92.5	6.9	2493	10	US-09-864-636A-585	Sequence 585, App
318	97.5	7.3	2505	17	US-10-303-110A-7	Sequence 7, Appli	391	92.5	6.9	2493	10	US-09-864-426A-585	Sequence 585, App
319	97.5	7.3	2505	17	US-10-303-110A-10	Sequence 10, Appl	392	92.5	6.9	2493	16	US-10-084-839-585	Sequence 585, App
320	97.5	7.3	5208	18	US-10-437-963-69592	Sequence 69592, A	393	92.5	6.9	2508	10	US-09-864-636A-401	Sequence 401, App
321	97	7.2	421	17	US-10-424-599-1595	Sequence 1595, Ap	394	92.5	6.9	2508	10	US-09-864-636A-405	Sequence 405, App
322	97	7.2	1104	17	US-10-282-122A-33573	Sequence 33573, A	395	92.5	6.9	2508	10	US-09-864-636A-407	Sequence 407, App
323	97	7.2	2867	18	US-10-437-963-195	Sequence 195, App	396	92.5	6.9	2508	10	US-09-864-636A-409	Sequence 409, App
324	96.5	7.2	1854	18	US-10-425-115-126435	Sequence 126435,	397	92.5	6.9	2508	10	US-09-864-636A-411	Sequence 411, App
325	96.5	7.2	2227	18	US-10-425-115-3967	Sequence 3967, Ap	398	92.5	6.9	2508	10	US-09-864-636A-415	Sequence 415, App
326	96.5	7.2	5397	18	US-10-437-963-69644	Sequence 69644, A	399	92.5	6.9	2508	10	US-09-864-636A-417	Sequence 417, App
327	96	7.1	1322	18	US-10-425-115-122270	Sequence 122270,	400	92.5	6.9	2508	10	US-09-864-636A-419	Sequence 419, App
328	96	7.1	15952	14	US-10-171-311-51	Sequence 51, Appl	401	92.5	6.9	2508	10	US-09-864-636A-423	Sequence 423, App
329	95.5	7.1	348	17	US-10-424-599-30454	Sequence 30454, A	402	92.5	6.9	2508	10	US-09-864-636A-426	Sequence 426, App
330	95.5	7.1	1272	17	US-10-369-493-37699	Sequence 37699, A	403	92.5	6.9	2508	10	US-09-864-636A-431	Sequence 431, App
331	95.5	7.1	1565	18	US-10-739-930-2155	Sequence 2155, Ap	404	92.5	6.9	2508	11	US-09-864-636A-439	Sequence 439, App
332	95.5	7.1	2261	18	US-10-437-963-15102	Sequence 15102, A	405	92.5	6.9	2508	11	US-09-864-426A-401	Sequence 401, App
333	95.5	7.1	2553	9	US-09-815-243-7690	Sequence 7690, Ap	406	92.5	6.9	2508	11	US-09-864-426A-405	Sequence 405, App
334	95.5	7.1	2553	17	US-10-282-122A-29994	Sequence 29994, A	407	92.5	6.9	2508	11	US-09-864-426A-407	Sequence 407, App
335	95	7.1	553	17	US-10-264-049-1169	Sequence 1169, Ap	408	92.5	6.9	2508	11	US-09-864-426A-409	Sequence 409, App
336	95	7.1	1717	15	US-10-156-761-4336	Sequence 4336, Ap	409	92.5	6.9	2508	11	US-09-864-426A-411	Sequence 411, App
337	95	7.1	1062	18	US-10-739-930-1766	Sequence 1766, Ap	410	92.5	6.9	2508	11	US-09-864-426A-415	Sequence 415, App
338	95	7.1	1948	17	US-10-282-122A-15101	Sequence 15101, A	411	92.5	6.9	2508	11	US-09-864-426A-417	Sequence 417, App
339	95	7.1	2597	17	US-10-094-749-246	Sequence 246, App	412	92.5	6.9	2508	11	US-09-864-426A-419	Sequence 419, App
340	95	7.1	4184	10	US-09-927-827-42	Sequence 42, Appl	413	92.5	6.9	2508	11	US-09-864-426A-423	Sequence 423, App
341	94.5	7.0	373	17	US-10-424-599-109508	Sequence 109508,	414	92.5	6.9	2508	11	US-09-864-426A-426	Sequence 426, App
342	94.5	7.0	1243	18	US-10-739-930-2839	Sequence 2839, Ap	415	92.5	6.9	2508	11	US-09-864-426A-431	Sequence 431, App
343	94.5	7.0	2488	19	US-10-719-024-1	Sequence 1, Appli	416	92.5	6.9	2508	11	US-09-864-426A-439	Sequence 439, App
344	94	7.0	717	17	US-10-282-122A-31785	Sequence 31785, A	417	92.5	6.9	2508	16	US-10-084-839-401	Sequence 401, App
345	94	7.0	4618	18	US-10-723-860-4935	Sequence 4935, Ap	418	92.5	6.9	2508	16	US-10-084-839-405	Sequence 405, App
346	94	7.0	14101	17	US-10-197-824-6	Sequence 6, Appli	419	92.5	6.9	2508	16	US-10-084-839-407	Sequence 407, App
347	94	7.0	17589	17	US-10-197-824-3	Sequence 3, Appli	420	92.5	6.9	2508	16	US-10-084-839-409	Sequence 409, App
348	93.5	7.0	840	15	US-10-156-761-1969	Sequence 1969, Ap	421	92.5	6.9	2508	16	US-10-084-839-411	Sequence 411, App
349	93.5	7.0	1107	15	US-10-156-761-4441	Sequence 4441, Ap	422	92.5	6.9	2508	16	US-10-084-839-415	Sequence 415, App
350	93.5	7.0	2505	17	US-10-303-110A-8	Sequence 8, Appli	423	92.5	6.9	2508	16	US-10-084-839-417	Sequence 417, App
351	93.5	7.0	2505	17	US-10-303-110A-9	Sequence 9, Appli	424	92.5	6.9	2508	16	US-10-084-839-419	Sequence 419, App
352	93.5	7.0	2505	17	US-10-303-110A-11	Sequence 11, Appl	425	92.5	6.9	2508	16	US-10-084-839-423	Sequence 423, App
353	93.5	7.0	2505	17	US-10-303-110A-12	Sequence 12, Appl	426	92.5	6.9	2508	16	US-10-084-839-426	Sequence 426, App
354	93.5	7.0	125746	15	US-10-156-761-15102	Sequence 15102, A	427	92.5	6.9	2508	16	US-10-084-839-431	Sequence 431, App

C 428	92.5	6.9	2508	16	US-10-084-839-439	Sequence 439, App	C 501	92.5	6.9	2517	16	US-10-084-839-484	Sequence 484, App
C 429	92.5	6.9	2508	16	US-10-084-839-2737	Sequence 2737, App	C 502	92.5	6.9	2517	16	US-10-084-839-495	Sequence 495, App
C 430	92.5	6.9	2508	16	US-10-084-839-2739	Sequence 2739, App	C 503	92.5	6.9	2517	16	US-10-084-839-501	Sequence 501, App
C 431	92.5	6.9	2508	16	US-10-084-839-2741	Sequence 2741, App	C 504	92.5	6.9	2517	16	US-10-084-839-509	Sequence 509, App
C 432	92.5	6.9	2508	16	US-10-084-839-2743	Sequence 2743, App	C 505	92.5	6.9	2517	16	US-10-084-839-513	Sequence 513, App
C 433	92.5	6.9	2508	16	US-10-084-839-2745	Sequence 2745, App	C 506	92.5	6.9	2517	16	US-10-084-839-517	Sequence 517, App
C 434	92.5	6.9	2508	16	US-10-084-839-2747	Sequence 2747, App	C 507	92.5	6.9	2517	16	US-10-084-839-521	Sequence 521, App
C 435	92.5	6.9	2508	16	US-10-084-839-2749	Sequence 2749, App	C 508	92.5	6.9	2517	16	US-10-084-839-525	Sequence 525, App
C 436	92.5	6.9	2508	16	US-10-084-839-2751	Sequence 2751, App	C 509	92.5	6.9	2517	16	US-10-084-839-529	Sequence 529, App
C 437	92.5	6.9	2508	16	US-10-084-839-2753	Sequence 2753, App	C 510	92.5	6.9	2517	16	US-10-084-839-533	Sequence 533, App
C 438	92.5	6.9	2508	16	US-10-084-839-2755	Sequence 2755, App	C 511	92.5	6.9	2517	16	US-10-084-839-537	Sequence 537, App
C 439	92.5	6.9	2508	16	US-10-084-839-2757	Sequence 2757, App	C 512	92.5	6.9	2517	16	US-10-084-839-541	Sequence 541, App
C 440	92.5	6.9	2508	16	US-10-084-839-2761	Sequence 2761, App	C 513	92.5	6.9	2517	16	US-10-084-839-2706	Sequence 2706, App
C 441	92.5	6.9	2511	9	US-09-777-430A-12	Sequence 12, Appl	C 514	92.5	6.9	2517	16	US-10-084-839-2779	Sequence 2779, App
C 442	92.5	6.9	2511	10	US-09-940-244-258	Sequence 258, App	C 515	92.5	6.9	2517	16	US-10-084-839-2784	Sequence 2784, App
C 443	92.5	6.9	2511	10	US-09-864-636A-262	Sequence 262, App	C 516	92.5	6.9	2517	16	US-10-084-839-2790	Sequence 2790, App
C 444	92.5	6.9	2511	11	US-09-758-282-59	Sequence 59, Appl	C 517	92.5	6.9	2517	16	US-10-084-839-2794	Sequence 2794, App
C 445	92.5	6.9	2511	11	US-09-864-426A-262	Sequence 262, App	C 518	92.5	6.9	2517	16	US-10-084-839-2796	Sequence 2796, App
C 446	92.5	6.9	2511	16	US-10-084-839-262	Sequence 262, App	C 519	92.5	6.9	2517	16	US-10-084-839-2798	Sequence 2798, App
C 447	92.5	6.9	2511	16	US-10-084-839-2715	Sequence 2715, App	C 520	92.5	6.9	2517	16	US-10-084-839-2800	Sequence 2800, App
C 448	92.5	6.9	2511	16	US-10-084-839-2834	Sequence 2834, App	C 521	92.5	6.9	2517	16	US-10-084-839-2802	Sequence 2802, App
C 449	92.5	6.9	2511	18	US-10-309-584-258	Sequence 258, App	C 522	92.5	6.9	2517	16	US-10-084-839-2804	Sequence 2804, App
C 450	92.5	6.9	2511	19	US-10-783-557-259	Sequence 259, App	C 523	92.5	6.9	2517	16	US-10-084-839-2806	Sequence 2806, App
C 451	92.5	6.9	2514	10	US-09-864-636A-133	Sequence 133, App	C 524	92.5	6.9	2517	16	US-10-084-839-2808	Sequence 2808, App
C 452	92.5	6.9	2514	10	US-09-864-636A-454	Sequence 454, App	C 525	92.5	6.9	2517	16	US-10-084-839-2856	Sequence 2856, App
C 453	92.5	6.9	2514	10	US-09-864-636A-475	Sequence 475, App	C 526	92.5	6.9	2520	10	US-09-864-636A-222	Sequence 222, App
C 454	92.5	6.9	2514	10	US-09-864-636A-499	Sequence 499, App	C 527	92.5	6.9	2520	10	US-09-864-636A-505	Sequence 505, App
C 455	92.5	6.9	2514	10	US-09-758-282-260	Sequence 260, App	C 528	92.5	6.9	2520	10	US-09-864-636A-541	Sequence 541, App
C 456	92.5	6.9	2514	11	US-09-864-426A-133	Sequence 133, App	C 529	92.5	6.9	2520	10	US-09-864-636A-543	Sequence 543, App
C 457	92.5	6.9	2514	11	US-09-864-426A-454	Sequence 454, App	C 530	92.5	6.9	2520	10	US-09-864-636A-573	Sequence 573, App
C 458	92.5	6.9	2514	11	US-09-864-426A-475	Sequence 475, App	C 531	92.5	6.9	2520	10	US-09-864-636A-577	Sequence 577, App
C 459	92.5	6.9	2514	11	US-09-864-426A-499	Sequence 499, App	C 532	92.5	6.9	2520	10	US-09-864-636A-583	Sequence 583, App
C 460	92.5	6.9	2514	16	US-10-084-839-133	Sequence 133, App	C 533	92.5	6.9	2520	10	US-09-758-282-279	Sequence 279, App
C 461	92.5	6.9	2514	16	US-10-084-839-454	Sequence 454, App	C 534	92.5	6.9	2520	11	US-09-864-426A-222	Sequence 222, App
C 462	92.5	6.9	2514	16	US-10-084-839-475	Sequence 475, App	C 535	92.5	6.9	2520	11	US-09-864-426A-505	Sequence 505, App
C 463	92.5	6.9	2514	16	US-10-084-839-499	Sequence 499, App	C 536	92.5	6.9	2520	11	US-09-864-426A-541	Sequence 541, App
C 464	92.5	6.9	2514	16	US-10-084-839-2768	Sequence 2768, App	C 537	92.5	6.9	2520	11	US-09-864-426A-543	Sequence 543, App
C 465	92.5	6.9	2514	16	US-10-084-839-2764	Sequence 2764, App	C 538	92.5	6.9	2520	11	US-09-864-426A-573	Sequence 573, App
C 466	92.5	6.9	2514	16	US-10-084-839-2775	Sequence 2775, App	C 539	92.5	6.9	2520	11	US-09-864-426A-577	Sequence 577, App
C 467	92.5	6.9	2514	16	US-10-084-839-2788	Sequence 2788, App	C 540	92.5	6.9	2520	11	US-09-864-426A-583	Sequence 583, App
C 468	92.5	6.9	2514	16	US-10-084-839-2850	Sequence 2850, App	C 541	92.5	6.9	2520	16	US-10-084-839-222	Sequence 222, App
C 469	92.5	6.9	2514	16	US-10-084-839-2852	Sequence 2852, App	C 542	92.5	6.9	2520	16	US-10-084-839-505	Sequence 505, App
C 470	92.5	6.9	2514	16	US-10-084-839-2854	Sequence 2854, App	C 543	92.5	6.9	2520	16	US-10-084-839-541	Sequence 541, App
C 471	92.5	6.9	2517	10	US-09-864-636A-69	Sequence 69, Appl	C 544	92.5	6.9	2520	16	US-10-084-839-543	Sequence 543, App
C 472	92.5	6.9	2517	10	US-09-864-636A-128	Sequence 128, App	C 545	92.5	6.9	2520	16	US-10-084-839-573	Sequence 573, App
C 473	92.5	6.9	2517	10	US-09-864-636A-484	Sequence 484, App	C 546	92.5	6.9	2520	16	US-10-084-839-577	Sequence 577, App
C 474	92.5	6.9	2517	10	US-09-864-636A-495	Sequence 495, App	C 547	92.5	6.9	2520	16	US-10-084-839-583	Sequence 583, App
C 475	92.5	6.9	2517	10	US-09-864-636A-501	Sequence 501, App	C 548	92.5	6.9	2520	16	US-10-084-839-2711	Sequence 2711, App
C 476	92.5	6.9	2517	10	US-09-864-636A-509	Sequence 509, App	C 549	92.5	6.9	2520	16	US-10-084-839-2792	Sequence 2792, App
C 477	92.5	6.9	2517	10	US-09-864-636A-513	Sequence 513, App	C 550	92.5	6.9	2520	16	US-10-084-839-2810	Sequence 2810, App
C 478	92.5	6.9	2517	10	US-09-864-636A-517	Sequence 517, App	C 551	92.5	6.9	2520	16	US-10-084-839-2812	Sequence 2812, App
C 479	92.5	6.9	2517	10	US-09-864-636A-521	Sequence 521, App	C 552	92.5	6.9	2520	16	US-10-084-839-2820	Sequence 2820, App
C 480	92.5	6.9	2517	10	US-09-864-636A-525	Sequence 525, App	C 553	92.5	6.9	2520	16	US-10-084-839-2824	Sequence 2824, App
C 481	92.5	6.9	2517	10	US-09-864-636A-529	Sequence 529, App	C 554	92.5	6.9	2520	16	US-10-084-839-2830	Sequence 2830, App
C 482	92.5	6.9	2517	10	US-09-864-636A-533	Sequence 533, App	C 555	92.5	6.9	2526	9	US-09-777-430A-14	Sequence 14, Appl
C 483	92.5	6.9	2517	10	US-09-864-636A-537	Sequence 537, App	C 556	92.5	6.9	2526	9	US-09-777-430A-19	Sequence 19, Appl
C 484	92.5	6.9	2517	10	US-09-758-282-74	Sequence 74, Appl	C 557	92.5	6.9	2526	9	US-09-777-430A-22	Sequence 22, Appl
C 485	92.5	6.9	2517	10	US-09-758-282-238	Sequence 238, App	C 558	92.5	6.9	2526	9	US-09-777-430A-25	Sequence 25, Appl
C 486	92.5	6.9	2517	11	US-09-864-426A-69	Sequence 69, Appl	C 559	92.5	6.9	2526	10	US-09-864-636A-103	Sequence 103, App
C 487	92.5	6.9	2517	11	US-09-864-426A-128	Sequence 128, App	C 560	92.5	6.9	2526	10	US-09-864-636A-104	Sequence 104, App
C 488	92.5	6.9	2517	11	US-09-864-426A-484	Sequence 484, App	C 561	92.5	6.9	2526	10	US-09-864-636A-117	Sequence 117, App
C 489	92.5	6.9	2517	11	US-09-864-426A-495	Sequence 495, App	C 562	92.5	6.9	2526	10	US-09-864-636A-118	Sequence 118, App
C 490	92.5	6.9	2517	11	US-09-864-426A-501	Sequence 501, App	C 563	92.5	6.9	2526	10	US-09-864-636A-119	Sequence 119, App
C 491	92.5	6.9	2517	11	US-09-864-426A-509	Sequence 509, App	C 564	92.5	6.9	2526	10	US-09-864-636A-132	Sequence 132, App
C 492	92.5	6.9	2517	11	US-09-864-426A-513	Sequence 513, App	C 565	92.5	6.9	2526	10	US-09-864-636A-267	Sequence 267, App
C 493	92.5	6.9	2517	11	US-09-864-426A-517	Sequence 517, App	C 566	92.5	6.9	2526	10	US-09-864-636A-273	Sequence 273, App
C 494	92.5	6.9	2517	11	US-09-864-426A-521	Sequence 521, App	C 567	92.5	6.9	2526	10	US-09-864-636A-349	Sequence 349, App
C 495	92.5	6.9	2517	11	US-09-864-426A-525	Sequence 525, App	C 568	92.5	6.9	2526	10	US-09-864-636A-373	Sequence 373, App
C 496	92.5	6.9	2517	11	US-09-864-426A-529	Sequence 529, App	C 569	92.5	6.9	2526	10	US-09-864-636A-375	Sequence 375, App
C 497	92.5	6.9	2517	11	US-09-864-426A-533	Sequence 533, App	C 570	92.5	6.9	2526	10	US-09-864-636A-379	Sequence 379, App
C 498	92.5	6.9	2517	11	US-09-864-426A-537	Sequence 537, App	C 571	92.5	6.9	2526	10	US-09-864-636A-383	Sequence 383, App
C 499	92.5	6.9	2517	16	US-10-084-839-69	Sequence 69, Appl	C 572	92.5	6.9	2526	10	US-09-864-636A-387	Sequence 387, App
C 500	92.5	6.9	2517	16	US-10-084-839-128	Sequence 128, App	C 573	92.5	6.9	2526	10	US-09-864-636A-391	Sequence 391, App

C 574	92.5	6.9	2526	10	US-09-864-636A-395	Sequence 395, App	C 647	92.5	6.9	2526	16	US-10-084-839-2725	Sequence 2725, Ap
C 575	92.5	6.9	2526	10	US-09-864-636A-399	Sequence 399, App	C 648	92.5	6.9	2526	16	US-10-084-839-2727	Sequence 2727, Ap
C 576	92.5	6.9	2526	10	US-09-864-636A-452	Sequence 452, App	C 649	92.5	6.9	2526	16	US-10-084-839-2729	Sequence 2729, Ap
C 577	92.5	6.9	2526	10	US-09-864-636A-455	Sequence 455, App	C 650	92.5	6.9	2526	16	US-10-084-839-2731	Sequence 2731, Ap
C 578	92.5	6.9	2526	10	US-09-864-636A-459	Sequence 459, App	C 651	92.5	6.9	2526	16	US-10-084-839-2733	Sequence 2733, Ap
C 579	92.5	6.9	2526	10	US-09-864-636A-471	Sequence 471, App	C 652	92.5	6.9	2526	16	US-10-084-839-2735	Sequence 2735, Ap
C 580	92.5	6.9	2526	10	US-09-864-636A-497	Sequence 497, App	C 653	92.5	6.9	2526	16	US-10-084-839-2763	Sequence 2763, Ap
C 581	92.5	6.9	2526	10	US-09-864-636A-558	Sequence 558, App	C 654	92.5	6.9	2526	16	US-10-084-839-2765	Sequence 2765, Ap
C 582	92.5	6.9	2526	10	US-09-758-282-60	Sequence 60, Appl	C 655	92.5	6.9	2526	16	US-10-084-839-2767	Sequence 2767, Ap
C 583	92.5	6.9	2526	10	US-09-758-282-74	Sequence 74, Appl	C 656	92.5	6.9	2526	16	US-10-084-839-2773	Sequence 2773, Ap
C 584	92.5	6.9	2526	10	US-09-758-282-162	Sequence 162, App	C 657	92.5	6.9	2526	16	US-10-084-839-2786	Sequence 2786, Ap
C 585	92.5	6.9	2526	10	US-09-758-282-165	Sequence 165, App	C 658	92.5	6.9	2526	16	US-10-084-839-2832	Sequence 2832, Ap
C 586	92.5	6.9	2526	10	US-09-758-282-211	Sequence 211, App	C 659	92.5	6.9	2526	16	US-10-084-839-2838	Sequence 2838, Ap
C 587	92.5	6.9	2526	10	US-09-758-282-213	Sequence 213, App	C 660	92.5	6.9	2526	16	US-10-084-839-2840	Sequence 2840, Ap
C 588	92.5	6.9	2526	10	US-09-758-282-215	Sequence 215, App	C 661	92.5	6.9	2526	16	US-10-084-839-2842	Sequence 2842, Ap
C 589	92.5	6.9	2526	10	US-09-758-282-258	Sequence 258, App	C 662	92.5	6.9	2526	16	US-10-084-839-2844	Sequence 2844, Ap
C 590	92.5	6.9	2526	11	US-09-864-426A-103	Sequence 103, App	C 663	92.5	6.9	2526	16	US-10-084-839-2846	Sequence 2846, Ap
C 591	92.5	6.9	2526	11	US-09-864-426A-104	Sequence 104, App	C 664	92.5	6.9	2526	16	US-10-084-839-2848	Sequence 2848, Ap
C 592	92.5	6.9	2526	11	US-09-864-426A-117	Sequence 117, App	C 665	92.5	6.9	2532	10	US-09-864-636A-463	Sequence 463, App
C 593	92.5	6.9	2526	11	US-09-864-426A-118	Sequence 118, App	C 666	92.5	6.9	2532	10	US-09-864-636A-467	Sequence 467, App
C 594	92.5	6.9	2526	11	US-09-864-426A-119	Sequence 119, App	C 667	92.5	6.9	2532	11	US-09-864-426A-463	Sequence 463, App
C 595	92.5	6.9	2526	11	US-09-864-426A-132	Sequence 132, App	C 668	92.5	6.9	2532	11	US-09-864-426A-467	Sequence 467, App
C 596	92.5	6.9	2526	11	US-09-864-426A-267	Sequence 267, App	C 669	92.5	6.9	2532	16	US-10-084-839-463	Sequence 463, App
C 597	92.5	6.9	2526	11	US-09-864-426A-273	Sequence 273, App	C 670	92.5	6.9	2532	16	US-10-084-839-467	Sequence 467, App
C 598	92.5	6.9	2526	11	US-09-864-426A-349	Sequence 349, App	C 671	92.5	6.9	2532	16	US-10-084-839-2769	Sequence 2769, Ap
C 599	92.5	6.9	2526	11	US-09-864-426A-373	Sequence 373, App	C 672	92.5	6.9	2532	16	US-10-084-839-2771	Sequence 2771, Ap
C 600	92.5	6.9	2526	11	US-09-864-426A-375	Sequence 375, App	C 673	92.5	6.9	2532	10	US-09-864-636A-563	Sequence 563, App
C 601	92.5	6.9	2526	11	US-09-864-426A-379	Sequence 379, App	C 674	92.5	6.9	2619	11	US-09-864-426A-563	Sequence 563, App
C 602	92.5	6.9	2526	11	US-09-864-426A-383	Sequence 383, App	C 675	92.5	6.9	2619	16	US-10-084-839-563	Sequence 563, App
C 603	92.5	6.9	2526	11	US-09-864-426A-387	Sequence 387, App	C 676	92.5	6.9	2619	16	US-10-084-839-2816	Sequence 2816, Ap
C 604	92.5	6.9	2526	11	US-09-864-426A-391	Sequence 391, App	C 677	92.5	6.9	2643	10	US-09-864-636A-559	Sequence 559, App
C 605	92.5	6.9	2526	11	US-09-864-426A-395	Sequence 395, App	C 678	92.5	6.9	2643	11	US-09-864-426A-559	Sequence 559, App
C 606	92.5	6.9	2526	11	US-09-864-426A-399	Sequence 399, App	C 679	92.5	6.9	2643	16	US-10-084-839-559	Sequence 559, App
C 607	92.5	6.9	2526	11	US-09-864-426A-452	Sequence 452, App	C 680	92.5	6.9	2643	16	US-10-084-839-2814	Sequence 2814, Ap
C 608	92.5	6.9	2526	11	US-09-864-426A-455	Sequence 455, App	C 681	92.5	6.9	3135	10	US-09-864-636A-481	Sequence 481, App
C 609	92.5	6.9	2526	11	US-09-864-426A-459	Sequence 459, App	C 682	92.5	6.9	3135	11	US-09-864-426A-481	Sequence 481, App
C 610	92.5	6.9	2526	11	US-09-864-426A-471	Sequence 471, App	C 683	92.5	6.9	3135	16	US-10-084-839-481	Sequence 481, App
C 611	92.5	6.9	2526	11	US-09-864-426A-497	Sequence 497, App	C 684	92.5	6.9	3135	16	US-10-084-839-2777	Sequence 2777, Ap
C 612	92.5	6.9	2526	11	US-09-864-426A-558	Sequence 558, App	C 685	92	6.9	813	17	US-10-369-439-33103	Sequence 33103, A
C 613	92.5	6.9	2526	16	US-10-084-839-103	Sequence 103, App	C 686	92	6.9	942	10	US-09-942-025-8	Sequence 8, Appli
C 614	92.5	6.9	2526	16	US-10-084-839-104	Sequence 104, App	C 687	92	6.9	1130	17	US-10-282-122A-19437	Sequence 19437, A
C 615	92.5	6.9	2526	16	US-10-084-839-117	Sequence 117, App	C 688	92	6.9	1932	17	US-10-267-502-88	Sequence 88, Appl
C 616	92.5	6.9	2526	16	US-10-084-839-118	Sequence 118, App	C 689	92	6.9	67311	10	US-09-942-025-1	Sequence 1, Appli
C 617	92.5	6.9	2526	16	US-10-084-839-119	Sequence 119, App	C 690	91.5	6.8	903	15	US-10-156-761-642	Sequence 642, App
C 618	92.5	6.9	2526	16	US-10-084-839-132	Sequence 132, App	C 691	91.5	6.8	1092	18	US-10-437-963-97637	Sequence 97637, A
C 619	92.5	6.9	2526	16	US-10-084-839-267	Sequence 267, App	C 692	91.5	6.8	1116	17	US-10-282-122A-32148	Sequence 32148, A
C 620	92.5	6.9	2526	16	US-10-084-839-273	Sequence 273, App	C 693	91.5	6.8	1149	15	US-10-156-761-5745	Sequence 5745, Ap
C 621	92.5	6.9	2526	16	US-10-084-839-349	Sequence 349, App	C 694	91.5	6.8	1896	15	US-10-156-761-5658	Sequence 5658, Ap
C 622	92.5	6.9	2526	16	US-10-084-839-373	Sequence 373, App	C 695	91.5	6.8	2253	17	US-10-282-122A-30610	Sequence 30610, A
C 623	92.5	6.9	2526	16	US-10-084-839-375	Sequence 375, App	C 696	91.5	6.8	2499	10	US-09-864-636A-79	Sequence 79, Appl
C 624	92.5	6.9	2526	16	US-10-084-839-379	Sequence 379, App	C 697	91.5	6.8	2499	10	US-09-758-282-94	Sequence 94, Appl
C 625	92.5	6.9	2526	16	US-10-084-839-383	Sequence 383, App	C 698	91.5	6.8	2499	11	US-09-864-426A-79	Sequence 79, Appl
C 626	92.5	6.9	2526	16	US-10-084-839-387	Sequence 387, App	C 699	91.5	6.8	2499	16	US-10-084-839-79	Sequence 79, Appl
C 627	92.5	6.9	2526	16	US-10-084-839-391	Sequence 391, App	C 700	91.5	6.8	2499	16	US-10-084-839-2682	Sequence 2682, Ap
C 628	92.5	6.9	2526	16	US-10-084-839-395	Sequence 395, App	C 701	91.5	6.8	2505	10	US-09-864-636A-155	Sequence 155, App
C 629	92.5	6.9	2526	16	US-10-084-839-399	Sequence 399, App	C 702	91.5	6.8	2505	10	US-09-758-282-266	Sequence 266, App
C 630	92.5	6.9	2526	16	US-10-084-839-452	Sequence 452, App	C 703	91.5	6.8	2505	11	US-09-864-426A-155	Sequence 155, App
C 631	92.5	6.9	2526	16	US-10-084-839-455	Sequence 455, App	C 704	91.5	6.8	2505	16	US-09-864-839-155	Sequence 155, App
C 632	92.5	6.9	2526	16	US-10-084-839-459	Sequence 459, App	C 705	91.5	6.8	2505	16	US-10-084-839-2709	Sequence 2709, Ap
C 633	92.5	6.9	2526	16	US-10-084-839-471	Sequence 471, App	C 706	91.5	6.8	2511	9	US-09-777-430A-9	Sequence 9, Appli
C 634	92.5	6.9	2526	16	US-10-084-839-497	Sequence 497, App	C 707	91.5	6.8	2511	10	US-09-864-636A-244	Sequence 244, App
C 635	92.5	6.9	2526	16	US-10-084-839-558	Sequence 558, App	C 708	91.5	6.8	2511	11	US-09-758-282-3	Sequence 3, Appli
C 636	92.5	6.9	2526	16	US-10-084-839-2701	Sequence 2701, App	C 709	91.5	6.8	2511	11	US-09-864-426A-244	Sequence 244, App
C 637	92.5	6.9	2526	16	US-10-084-839-2702	Sequence 2702, App	C 710	91.5	6.8	2511	16	US-10-084-839-244	Sequence 244, App
C 638	92.5	6.9	2526	16	US-10-084-839-2703	Sequence 2703, App	C 711	91.5	6.8	2511	16	US-10-084-839-2713	Sequence 2713, Ap
C 639	92.5	6.9	2526	16	US-10-084-839-2704	Sequence 2704, App	C 712	91.5	6.8	2553	18	US-10-469-858-1	Sequence 1, Appli
C 640	92.5	6.9	2526	16	US-10-084-839-2705	Sequence 2705, App	C 713	91.5	6.8	2731748	18	US-10-297-465A-1	Sequence 1, Appli
C 641	92.5	6.9	2526	16	US-10-084-839-2707	Sequence 2707, App	C 714	91.5	6.8	2731748	18	US-10-297-465A-1	Sequence 1, Appli
C 642	92.5	6.9	2526	16	US-10-084-839-2716	Sequence 2716, App	C 715	91	6.8	798	18	US-10-425-115-60646	Sequence 60646, A
C 643	92.5	6.9	2526	16	US-10-084-839-2718	Sequence 2718, App	C 716	91	6.8	846	17	US-10-282-122A-23727	Sequence 23727, A
C 644	92.5	6.9	2526	16	US-10-084-839-2720	Sequence 2720, App	C 717	91	6.8	1209	17	US-10-425-114-16417	Sequence 16417, A
C 645	92.5	6.9	2526	16	US-10-084-839-2721	Sequence 2721, App	C 718	91	6.8	1400	17	US-10-437-963-42255	Sequence 22555, A
C 646	92.5	6.9	2526	16	US-10-084-839-2723	Sequence 2723, App	C 719	91	6.8	1590	17	US-10-282-122A-41291	Sequence 41291, A



c 720	91	6.8	2064	15	US-10-156-761-2302	Sequence 2902, Ap	1394	88.5	6.6	1392	15	US-10-156-761-6437	Sequence 6437, Ap
c 721	91	6.8	2299	18	US-10-466-531-49	Sequence 49, Appl	1395	88.5	6.6	1437	17	US-10-369-493-31948	Sequence 31948, A
c 722	91	6.8	2454	15	US-10-156-761-2410	Sequence 2410, Ap	1396	88.5	6.6	1566	18	US-10-437-963-1947	Sequence 1947, Ap
c 754	91	6.8	2749	10	US-09-591-428-516	Sequence 516, App	1397	88.5	6.6	1696	17	US-10-120-988-151	Sequence 151, App
844	91	6.8	2749	14	US-10-167-747-215	Sequence 215, App	1398	88.5	6.6	2038	18	US-10-739-930-4499	Sequence 4499, Ap
969	91	6.8	2749	15	US-10-223-085-59	Sequence 59, Appl	1399	88.5	6.6	2413	9	US-09-931-087A-2	Sequence 2, Appl
973	91	6.8	2749	15	US-10-223-084-59	Sequence 59, Appl	1400	88.5	6.6	2413	16	US-10-062-923-2	Sequence 2, Appl
974	91	6.8	2749	15	US-10-223-088-59	Sequence 59, Appl	1401	88.5	6.6	2454	14	US-10-198-846-13360	Sequence 13360, A
975	91	6.8	2749	15	US-10-223-090-59	Sequence 59, Appl	1402	88.5	6.6	3060	18	US-10-837-318-46	Sequence 46, Appl
976	91	6.8	2749	15	US-10-223-087-59	Sequence 59, Appl	1403	88.5	6.6	3060	18	US-10-836-063A-69	Sequence 69, Appl
978	91	6.8	2749	15	US-10-223-083-59	Sequence 59, Appl	1404	88.5	6.6	3060	19	US-10-926-223-56	Sequence 56, Appl
979	91	6.8	2749	15	US-10-223-089-59	Sequence 59, Appl	1405	88.5	6.6	3289	18	US-10-723-860-6374	Sequence 6374, A
1151	91	6.8	2749	16	US-10-223-081-59	Sequence 59, Appl	1406	88.5	6.6	3413	17	US-10-424-599-52304	Sequence 52304, A
1171	91	6.8	2749	16	US-10-223-082-59	Sequence 59, Appl	1407	88.5	6.6	22459	11	US-09-973-278-883	Sequence 883, App
1240	91	6.8	2749	17	US-10-170-481A-215	Sequence 215, App	1408	88.5	6.6	30350	13	US-10-118-328-3	Sequence 3, Appl
1242	91	6.8	2749	17	US-10-210-028-215	Sequence 215, App	1409	88.5	6.6	30350	18	US-10-694-438-3	Sequence 3, Appl
1302	91	6.8	2749	17	US-10-163-521A-215	Sequence 215, App	1410	88.5	6.6	37116	17	US-10-107-431-279	Sequence 279, App
1311	91	6.8	2749	17	US-10-305-654-59	Sequence 59, Appl	1411	88.5	6.6	84428	17	US-10-229-148B-1	Sequence 1, Appl
1324	91	6.8	2749	19	US-10-081-056-59	Sequence 59, Appl	1412	88.5	6.6	109519	11	US-09-758-759-1	Sequence 1, Appl
1339	91	6.8	2749	19	US-10-918-851-215	Sequence 215, App	1413	88.5	6.6	160361	17	US-10-235-192A-35	Sequence 35, Appl
1340	91	6.8	2749	19	US-10-931-886-385	Sequence 385, App	1414	88	6.6	813	17	US-10-369-493-33037	Sequence 33037, A
1341	91	6.8	2749	19	US-10-805-667-215	Sequence 215, App	1415	88	6.6	852	17	US-10-389-647-34	Sequence 34, Appl
1342	91	6.8	2749	19	US-10-897-359-215	Sequence 215, App	1416	88	6.6	931	18	US-10-767-701-2040	Sequence 2040, Ap
1344	91	6.8	2749	17	US-10-369-493-31552	Sequence 31552, A	1417	88	6.6	1043	18	US-10-425-115-143306	Sequence 143306, A
1345	90.5	6.7	1023	18	US-10-437-963-96859	Sequence 96859, A	1418	88	6.6	1087	18	US-10-425-115-140838	Sequence 140838, A
c1346	90.5	6.7	1248	15	US-10-156-761-1741	Sequence 1741, Ap	1419	88	6.6	1281	17	US-10-369-493-44499	Sequence 44499, A
c1347	90.5	6.7	1611	17	US-10-260-138-1334	Sequence 1334, Ap	1420	88	6.6	1461	15	US-10-156-761-1666	Sequence 1666, Ap
1348	90.5	6.7	1820	18	US-10-437-963-49451	Sequence 49451, A	1421	88	6.6	1464	17	US-10-424-599-128274	Sequence 128274, A
c1349	90.5	6.7	2526	10	US-09-864-636A-102	Sequence 102, App	1422	88	6.6	1694	18	US-10-437-963-97638	Sequence 97638, A
c1350	90.5	6.7	2526	10	US-09-758-282-159	Sequence 159, App	1423	88	6.6	2006	18	US-10-437-963-18431	Sequence 18431, A
c1351	90.5	6.7	2526	11	US-09-864-426A-102	Sequence 102, App	1424	88	6.6	2402	17	US-10-369-493-32004	Sequence 32004, A
c1352	90.5	6.7	2526	16	US-10-084-839-102	Sequence 102, App	1425	88	6.6	2487	17	US-10-282-122A-32996	Sequence 32996, A
c1353	90.5	6.7	2526	16	US-10-084-839-2700	Sequence 2700, Ap	1426	88	6.6	2517	10	US-09-864-636A-127	Sequence 127, App
1354	90.5	6.7	2538	18	US-10-425-115-174346	Sequence 174346, A	1427	88	6.6	2517	10	US-09-758-282-235	Sequence 235, App
1355	90.5	6.7	135638	16	US-10-314-657-1	Sequence 1, Appl	1428	88	6.6	2517	11	US-09-864-426A-127	Sequence 127, App
1356	90.5	6.7	3309400	9	US-09-738-626-1	Sequence 875, App	1429	88	6.6	2517	16	US-10-084-839-127	Sequence 127, App
c1357	90	6.7	662	18	US-10-437-963-875	Sequence 875, App	1430	88	6.6	2528	18	US-10-437-963-81418	Sequence 81418, A
1358	90	6.7	1195	18	US-10-425-115-26858	Sequence 26858, A	1431	88	6.6	2565	15	US-10-156-761-3914	Sequence 3914, Ap
1359	90	6.7	1338	17	US-10-369-493-45528	Sequence 45528, A	1432	88	6.6	3426	15	US-10-156-761-5493	Sequence 5493, Ap
1360	90	6.7	1443	15	US-10-156-761-559	Sequence 559, App	1433	88	6.6	3730	9	US-09-917-800A-476	Sequence 476, App
c1361	90	6.7	2160	17	US-10-221-596B-23	Sequence 23, Appl	1434	88	6.6	3885	13	US-10-087-192-2021	Sequence 2021, Ap
1362	90	6.7	3084	18	US-10-437-963-1495	Sequence 1495, Ap	1435	88	6.6	4750	18	US-10-723-860-2101	Sequence 2101, Ap
c1363	90	6.7	45814	13	US-10-087-192-256	Sequence 256, App	1436	88	6.6	4874	18	US-10-331-053-65	Sequence 65, Appl
1364	89.5	6.7	849	15	US-10-156-761-925	Sequence 925, App	1437	88	6.6	5130	18	US-10-437-963-59667	Sequence 59667, A
c1365	89.5	6.7	1026	17	US-10-425-114-28163	Sequence 28163, A	1438	88	6.6	11007	17	US-10-402-842-5	Sequence 5, Appl
1366	89.5	6.7	1052	18	US-10-716-803-10	Sequence 10, Appl	1439	88	6.6	47988	17	US-10-402-842-1	Sequence 1, Appl
1367	89.5	6.7	1084	17	US-10-425-114-27197	Sequence 27197, A	1440	87.5	6.5	933	17	US-10-389-647-328	Sequence 328, App
1368	89.5	6.7	1084	18	US-10-425-115-118656	Sequence 118656, A	1441	87.5	6.5	954	15	US-10-437-963-48358	Sequence 48358, A
1369	89.5	6.7	1710	18	US-10-437-963-24299	Sequence 24299, A	1442	87.5	6.5	1053	15	US-10-181-319-5	Sequence 5, Appl
1370	89.5	6.7	2418	17	US-10-369-493-40581	Sequence 40581, A	1443	87.5	6.5	1104	18	US-10-437-963-24858	Sequence 24858, A
c1371	89.5	6.7	10846	17	US-10-074-024-577	Sequence 577, App	1444	87.5	6.5	1287	15	US-10-156-761-3398	Sequence 3398, Ap
c1372	89	6.6	789	18	US-10-437-963-10093	Sequence 10093, A	1445	87.5	6.5	1317	15	US-10-156-761-6949	Sequence 6949, Ap
1373	89	6.6	1254	16	US-10-214-446-51	Sequence 51, Appl	1446	87.5	6.5	1377	17	US-10-389-647-136	Sequence 136, App
c1374	89	6.6	1291	18	US-10-437-963-73204	Sequence 73204, A	1447	87.5	6.5	1402	9	US-09-814-777A-102	Sequence 102, App
1375	89	6.6	1374	17	US-10-282-122A-25943	Sequence 25943, A	1448	87.5	6.5	1803	17	US-10-369-493-26552	Sequence 26552, A
c1376	89	6.6	1428	18	US-10-739-930-2348	Sequence 2348, Ap	1449	87.5	6.5	1823	18	US-10-437-963-48275	Sequence 48275, A
c1377	89	6.6	1791	18	US-10-437-963-78134	Sequence 78134, A	1450	87.5	6.5	1879	17	US-10-425-114-21499	Sequence 21499, A
c1378	89	6.6	5343	17	US-10-062-674-1951	Sequence 1951, Ap	1451	87.5	6.5	2082	17	US-10-104-047-1306	Sequence 1306, Ap
c1379	89	6.6	5619	18	US-10-437-963-9510	Sequence 9510, Ap	1452	87.5	6.5	2169	18	US-10-437-963-72109	Sequence 72109, A
1380	89	6.6	9369	16	US-10-200-562-190	Sequence 190, App	1453	87.5	6.5	2508	11	US-09-864-636A-435	Sequence 435, App
1381	89	6.6	9369	16	US-10-237-551-190	Sequence 190, Appl	1454	87.5	6.5	2508	11	US-09-864-426A-435	Sequence 435, App
c1382	89	6.6	9369	16	US-10-237-551-247	Sequence 247, App	1455	87.5	6.5	2508	16	US-10-084-839-435	Sequence 435, App
c1383	88.5	6.6	447	18	US-10-437-963-40463	Sequence 40463, A	1456	87.5	6.5	2508	16	US-10-084-839-2759	Sequence 2759, App
c1384	88.5	6.6	735	15	US-10-156-761-6746	Sequence 6746, Ap	1457	87.5	6.5	2526	10	US-09-864-636A-101	Sequence 101, App
1385	88.5	6.6	874	18	US-10-425-115-111423	Sequence 111423, A	1458	87.5	6.5	2526	10	US-09-758-282-156	Sequence 156, App
1386	88.5	6.6	939	18	US-10-425-115-103403	Sequence 103403, A	1459	87.5	6.5	2526	11	US-09-864-426A-101	Sequence 101, App
c1387	88.5	6.6	1014	9	US-09-815-242-7828	Sequence 7828, Ap	1460	87.5	6.5	2526	16	US-10-084-839-101	Sequence 101, App
1388	88.5	6.6	1053	15	US-10-282-122A-30311	Sequence 30311, A	1461	87.5	6.5	2526	15	US-10-084-839-2699	Sequence 2699, App
c1389	88.5	6.6	1133	17	US-10-156-761-4486	Sequence 4486, Ap	1462	87.5	6.5	2556	15	US-10-156-761-181	Sequence 181, App
1390	88.5	6.6	1145	18	US-10-425-115-98620	Sequence 98620, A	1463	87.5	6.5	4071	13	US-10-098-841-203	Sequence 203, App
c1391	88.5	6.6	1161	18	US-10-437-963-91630	Sequence 91630, A	1464	87.5	6.5	9745	9	US-09-764-869-2259	Sequence 2259, Ap
c1392	88.5	6.6	1263	17	US-10-282-122A-11556	Sequence 11556, A	1465	87.5	6.5	9745	14	US-10-091-504-2259	Sequence 2259, Ap
c1393	88.5	6.6	1263	17	US-10-282-122A-11556	Sequence 11556, A	1466	87.5	6.5	9745	17	US-10-237-577-2259	Sequence 2259, Ap



c1467	87.5	6.5	12149	9	US-09-764-869-2258	Sequence 2258, Ap
c1468	87.5	6.5	12149	14	US-10-091-504-2258	Sequence 2258, Ap
c1469	87.5	6.5	12149	17	US-10-227-577-2258	Sequence 2258, Ap
c1470	87.5	6.5	25801	15	US-10-181-319-13	Sequence 13, Appl
c1471	87.5	6.5	98546	13	US-10-087-192-1414	Sequence 1414, Ap
c1472	87.5	6.5	1691139	14	US-10-067-514-1	Sequence 1, Appli
c1473	87.5	6.5	1691139	17	US-10-419-723-1	Sequence 1, Appli
c1474	87	6.5	660	17	US-10-369-493-37236	Sequence 37236, A
c1475	87	6.5	1027	17	US-10-282-122A-24068	Sequence 24068, A
c1476	87	6.5	1170	15	US-10-156-761-6478	Sequence 6478, Ap
c1477	87	6.5	1274	18	US-10-739-930-2284	Sequence 2284, Ap
c1478	87	6.5	1625	17	US-10-302-172-594	Sequence 594, App
c1479	87	6.5	2053	18	US-10-437-963-18438	Sequence 18438, A
c1480	87	6.5	2198	17	US-10-094-749-260	Sequence 260, App
c1481	87	6.5	2198	18	US-10-775-920-105	Sequence 105, App
c1482	87	6.5	2745	18	US-10-425-115-82692	Sequence 82692, A
c1483	87	6.5	3297	9	US-09-712-363-144	Sequence 144, App
c1484	87	6.5	6131	17	US-10-435-696-6	Sequence 6, Appli
c1485	87	6.5	7802	17	US-10-282-122A-14528	Sequence 14528, A
c1486	87	6.5	366710	18	US-10-719-993-6792	Sequence 6792, Ap
c1487	86.5	6.4	673	18	US-10-425-115-82571	Sequence 82571, A
c1488	86.5	6.4	855	17	US-10-282-122A-26928	Sequence 26928, A
c1489	86.5	6.4	886	18	US-10-437-963-97467	Sequence 97467, A
c1490	86.5	6.4	921	9	US-09-738-626-179	Sequence 179, App
c1491	86.5	6.4	1428	17	US-10-389-566-296	Sequence 296, App
c1492	86.5	6.4	1581	18	US-10-437-963-66801	Sequence 66801, A
c1493	86.5	6.4	1660	17	US-10-425-114-32132	Sequence 32132, A
c1494	86.5	6.4	1666	15	US-10-128-714-1248	Sequence 1248, Ap
c1495	86.5	6.4	1749	18	US-10-425-115-92673	Sequence 92673, A
c1496	86.5	6.4	1990	18	US-10-723-860-5846	Sequence 5846, Ap
c1497	86.5	6.4	2005	17	US-10-310-154-139	Sequence 139, App
c1498	86.5	6.4	2165	17	US-10-104-047-418	Sequence 418, App
c1499	86.5	6.4	2406	9	US-09-907-495-3	Sequence 3, Appli
c1500	86.5	6.4	2406	18	US-10-860-777-19	Sequence 19, Appl

Search completed: April 19, 2005, 22:42:46  
Job time : 671 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 19, 2005, 22:26:00 ; Search time 466 Seconds  
(without alignments)  
919.967 Million cell updates/sec

Title: US-10-017-407a-306

Perfect score: 1343

Sequence: 1 MTQPVRLSPVRAALGSA.....VRVYISLLPLDGLTLAPKI 262

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DRV=xlh  
-Q=/cgn2\_1/USPTO.spool/US10017407/runat.19042005.142534.29480/app.query.fasta\_1.455  
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LCOPEL=0  
-LOOPEXT=0 -UNITS=Bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi  
-LIST=1500 -DOCAUTIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10017407 @CGN 1.1 177 @runat.19042005.142534.29480 -NCPU=6 -ICPU=3  
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:\*\*  
1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PTCS.COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	429	31.9	846	4	US-09-252-991A-3196
2	405.5	30.2	980	3	US-09-452-239-21
3	401	29.9	891	3	US-09-452-239-1
4	396	29.5	1058	3	US-09-452-239-11
5	394	29.3	1078	3	US-09-452-239-41
6	392.5	29.2	962	3	US-09-452-239-23
7	392.5	29.2	1023	3	US-09-452-239-25
8	389	29.0	997	3	US-09-452-239-13
9	387	28.8	953	3	US-09-452-239-45
10	386.5	28.8	967	3	US-09-452-239-5
11	386	28.7	1012	3	US-09-615-192A-94
12	386	28.7	1012	4	US-09-169-789-94

Sequence 6, Appli  
Sequence 6, Appli  
Sequence 6, Appli  
Sequence 6, Appli  
Sequence 6, Appli  
Sequence 37, Appli  
Sequence 3, Appli  
Sequence 17, Appli  
Sequence 5, Appli  
Sequence 19, Appli  
Sequence 43, Appli  
Sequence 4, Appli  
Sequence 7, Appli  
Sequence 2, Appli  
Sequence 3, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 35, Appli  
Sequence 27, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 9027, Ap  
Sequence 964, App  
Sequence 31, Appli  
Sequence 1, Appli  
Sequence 2, Appli  
Sequence 55, Appli  
Sequence 55, Appli  
Sequence 55, Appli  
Sequence 54, Appli  
Sequence 54, Appli  
Sequence 54, Appli  
Sequence 54, Appli  
Sequence 6750, Ap  
Sequence 25, Appli  
Sequence 25, Appli  
Sequence 25, Appli  
Sequence 45, Appli  
Sequence 27, Appli  
Sequence 33, Appli  
Sequence 2, Appli  
Sequence 1, Appli  
Sequence 194, App  
Sequence 2293, Ap  
Sequence 655, App  
Sequence 105, App  
Sequence 105, App  
Sequence 29, Appli  
Sequence 23, Appli  
Sequence 23, Appli  
Sequence 23, Appli  
Sequence 9, Appli  
Sequence 39, Appli  
Sequence 195, App  
Sequence 53, Appli  
Sequence 53, Appli  
Sequence 53, Appli  
Sequence 2, Appli  
Sequence 1, Appli  
Sequence 193, App  
Sequence 2663, Ap  
Sequence 135, App  
Sequence 51, Appli  
Sequence 15, Appli  
Sequence 2610, Ap  
Sequence 812, App  
Sequence 3788, Ap  
Sequence 258, App  
Sequence 809, App  
Sequence 108, App  
Sequence 3039, App  
Sequence 195, App  
Sequence 195, App  
Sequence 24, Appli  
Sequence 175, App

86	110	8-2	236	4	US-09-169-789-175	Sequence 175, App	159	94.5	7.0	7463	4	US-09-902-540-928	Sequence 928, App
C 87	104	7.7	11502	4	US-09-902-540-1064	Sequence 1064, App	160	94.5	7.0	9622	4	US-09-949-016-14643	Sequence 14643, A
C 88	102.5	7.6	2073	4	US-09-902-540-5730	Sequence 5730, App	161	94.5	7.0	9622	4	US-09-949-016-14644	Sequence 14644, A
C 89	102.5	7.6	8793	4	US-09-902-540-1042	Sequence 1042, App	162	94.5	7.0	9623	4	US-09-949-016-14362	Sequence 14362, A
C 90	102	7.6	1813	5	PCT-US94-12883-3	Sequence 3, Appli	163	94.5	7.0	16347	4	US-09-949-016-14645	Sequence 14645, A
C 91	102	7.6	1898	4	US-08-342-411A-1	Sequence 1, Appli	C 164	94.5	7.0	16347	4	US-09-949-016-14646	Sequence 14646, A
C 92	101	7.5	1786	4	US-09-799-451-657	Sequence 657, App	C 165	94.5	7.0	24207	4	US-09-949-016-14364	Sequence 14364, A
C 93	100.5	7.5	1688	2	US-08-649-619B-2	Sequence 2, Appli	C 166	94	7.0	1527	4	US-09-252-991A-12042	Sequence 12042, A
C 94	100.5	7.5	1815	4	US-10-329-668-3	Sequence 3, Appli	C 167	94	7.0	1862	4	US-09-252-991A-231	Sequence 231, App
C 95	100.5	7.5	1979	2	US-08-649-619B-1	Sequence 1, Appli	C 168	94	7.0	2133	4	US-09-252-991A-11939	Sequence 11939, A
C 96	100.5	7.5	1987	4	US-09-976-594-654	Sequence 654, App	169	93.5	7.0	1233	4	US-09-252-991A-9241	Sequence 9241, App
C 97	100	7.4	8460	1	US-08-469-005A-9	Sequence 9, Appli	C 170	93.5	7.0	1980	4	US-09-252-991A-8712	Sequence 8712, App
C 98	99.5	7.4	2469	4	US-09-252-991A-5908	Sequence 5908, App	171	93.5	7.0	2712	4	US-09-902-540-4301	Sequence 4301, App
C 99	99.5	7.4	24791	4	US-09-902-540-1211	Sequence 1211, App	C 172	93.5	7.0	2811	4	US-09-902-540-2406	Sequence 2406, App
100	99	7.4	636	4	US-09-252-991A-9822	Sequence 9822, App	173	93.5	7.0	16782	4	US-09-902-540-1105	Sequence 1105, App
101	99	7.4	1275	4	US-09-252-991A-9915	Sequence 9915, App	174	93.5	7.0	22807	4	US-09-902-540-1214	Sequence 1214, App
C 102	99	7.4	1443	4	US-09-252-991A-10160	Sequence 10160, A	175	93.5	7.0	154746	4	US-09-827-688-8	Sequence 8, Appli
C 103	99	7.4	2030	1	US-08-330-518-1	Sequence 1, Appli	C 176	93	6.9	1152	4	US-09-902-540-8683	Sequence 8683, App
C 104	99	7.4	2030	2	US-08-330-283-1	Sequence 1, Appli	C 177	93	6.9	1701	4	US-09-252-991A-1960	Sequence 1960, App
C 105	99	7.4	2030	2	US-08-646-248-1	Sequence 1, Appli	C 178	93	6.9	1848	4	US-09-252-991A-9071	Sequence 9071, App
C 106	99	7.4	2030	5	PCT-US95-13924-1	Sequence 1, Appli	179	93	6.9	2169	4	US-09-252-991A-1910	Sequence 1910, App
C 107	99	7.4	2030	5	PCT-US95-13931-1	Sequence 1, Appli	180	93	6.9	2193	4	US-09-902-540-7189	Sequence 7189, App
C 108	99	7.4	2505	1	US-07-977-434-7	Sequence 7, Appli	C 181	93	6.9	2946	4	US-09-252-991A-2045	Sequence 2045, App
C 109	99	7.4	2505	1	US-08-458-819-7	Sequence 7, Appli	182	93	6.9	3744	4	US-09-799-451-585	Sequence 585, App
C 110	99	7.4	2505	5	PCT-US91-07035-7	Sequence 7, Appli	C 183	93	6.9	5051	4	US-09-902-540-667	Sequence 667, App
111	99	7.4	7258	4	US-09-949-016-4832	Sequence 4832, App	C 184	93	6.9	7229	4	US-09-902-540-919	Sequence 919, App
112	99	7.4	8519	3	US-09-361-907-1	Sequence 1, Appli	C 185	93	6.9	20757	4	US-09-902-540-1189	Sequence 1189, App
113	98.5	7.3	855	4	US-09-252-991A-9422	Sequence 9422, App	C 186	92.5	6.9	1200	4	US-09-252-991A-250	Sequence 250, App
C 114	98.5	7.3	1101	4	US-09-252-991A-9455	Sequence 9455, App	187	92.5	6.9	1311	4	US-09-252-991A-3649	Sequence 3649, App
C 115	98.5	7.3	3147	3	US-08-887-534A-84	Sequence 84, Appli	C 188	92.5	6.9	2511	4	US-09-684-938-163	Sequence 163, App
C 116	98.5	7.3	3147	4	US-09-527-431-84	Sequence 84, Appli	C 189	92.5	6.9	2511	4	US-09-308-825A-163	Sequence 163, App
C 117	98.5	7.3	3147	4	US-09-446-861-84	Sequence 84, Appli	C 190	92.5	6.9	2511	4	US-09-758-282B-59	Sequence 59, Appli
C 118	98.5	7.3	77536	4	US-09-410-551B-1	Sequence 1, Appli	C 191	92.5	6.9	2511	4	US-09-758-282B-238	Sequence 238, App
C 119	98.5	7.3	77536	4	US-09-940-316B-1	Sequence 1, Appli	C 192	92.5	6.9	2511	4	US-09-940-244-238	Sequence 244, App
C 120	98	7.3	1713	4	US-09-252-991A-109	Sequence 109, App	C 193	92.5	6.9	2511	4	US-09-777-430C-12	Sequence 12, Appli
C 121	97.5	7.3	657	4	US-09-252-991A-9351	Sequence 9351, App	C 194	92.5	6.9	2514	4	US-09-758-282B-260	Sequence 260, App
C 122	97.5	7.3	1632	4	US-09-351-150A-14	Sequence 14, Appli	C 195	92.5	6.9	2514	4	US-09-577-304A-260	Sequence 260, App
C 123	97.5	7.3	2232	4	US-09-252-991A-11756	Sequence 11756, A	C 196	92.5	6.9	2517	4	US-09-758-282B-74	Sequence 74, Appli
C 124	97.5	7.3	2274	4	US-09-252-991A-11609	Sequence 11609, A	C 197	92.5	6.9	2517	4	US-09-758-282B-238	Sequence 238, App
C 125	97.5	7.3	2613	4	US-09-252-991A-11836	Sequence 11836, A	C 198	92.5	6.9	2517	4	US-09-577-304A-74	Sequence 74, Appli
C 126	97.5	7.3	20235	3	US-07-642-734C-3	Sequence 3, Appli	C 199	92.5	6.9	2517	4	US-09-577-304A-238	Sequence 238, App
C 127	97.5	7.3	20235	1	US-08-439-009A-3	Sequence 3, Appli	C 200	92.5	6.9	2520	4	US-09-758-282B-279	Sequence 279, App
C 128	97.5	7.3	24494	4	US-09-351-150A-1	Sequence 1, Appli	C 201	92.5	6.9	2526	4	US-09-758-282B-64	Sequence 64, Appli
C 129	97	7.2	1086	4	US-09-252-991A-10259	Sequence 10259, A	C 202	92.5	6.9	2526	4	US-09-758-282B-70	Sequence 70, Appli
C 130	97	7.2	1101	4	US-09-252-991A-10597	Sequence 10597, A	C 203	92.5	6.9	2526	4	US-09-758-282B-162	Sequence 162, App
C 131	97	7.2	1707	4	US-09-902-540-2606	Sequence 2606, App	C 204	92.5	6.9	2526	4	US-09-758-282B-165	Sequence 165, App
C 132	97	7.2	11502	4	US-09-902-540-1064	Sequence 1064, App	C 205	92.5	6.9	2526	4	US-09-758-282B-211	Sequence 211, App
C 133	97	7.2	16423	4	US-09-902-540-1120	Sequence 1120, App	C 206	92.5	6.9	2526	4	US-09-758-282B-213	Sequence 213, App
C 134	96.5	7.2	783	4	US-09-252-991A-12098	Sequence 12098, A	C 207	92.5	6.9	2526	4	US-09-758-282B-215	Sequence 215, App
C 135	96.5	7.2	984	4	US-09-252-991A-12173	Sequence 12173, A	C 208	92.5	6.9	2526	4	US-09-758-282B-258	Sequence 258, App
C 136	96.5	7.2	1254	4	US-09-252-991A-12420	Sequence 12420, A	C 209	92.5	6.9	2526	4	US-09-577-304A-64	Sequence 64, Appli
C 137	96.5	7.2	6083	4	US-09-902-540-763	Sequence 763, App	C 210	92.5	6.9	2526	4	US-09-577-304A-70	Sequence 70, Appli
C 138	96	7.1	3135	4	US-09-252-991A-5922	Sequence 5922, App	C 211	92.5	6.9	2526	4	US-09-577-304A-162	Sequence 162, App
C 139	96	7.1	9097	4	US-09-902-540-947	Sequence 947, App	C 212	92.5	6.9	2526	4	US-09-577-304A-165	Sequence 165, App
C 140	96	7.1	14541	4	US-09-902-540-1159	Sequence 1159, App	C 213	92.5	6.9	2526	4	US-09-577-304A-211	Sequence 211, App
C 141	96	7.1	22301	4	US-09-902-540-1208	Sequence 1208, App	C 214	92.5	6.9	2526	4	US-09-577-304A-213	Sequence 213, App
C 142	95.5	7.1	852	4	US-09-252-991A-7607	Sequence 7607, App	C 215	92.5	6.9	2526	4	US-09-577-304A-215	Sequence 215, App
C 143	95.5	7.1	1452	4	US-09-252-991A-3933	Sequence 3933, App	C 216	92.5	6.9	2526	4	US-09-577-304A-258	Sequence 258, App
C 144	95.5	7.1	1794	5	PCT-US95-14418-3	Sequence 3, Appli	C 217	92.5	6.9	2526	4	US-09-777-430C-14	Sequence 14, Appli
C 145	95.5	7.1	1794	5	PCT-US95-15327-3	Sequence 3, Appli	C 218	92.5	6.9	2526	4	US-09-777-430C-19	Sequence 19, Appli
C 146	95.5	7.1	1977	4	US-09-902-540-4798	Sequence 4798, App	C 219	92.5	6.9	2526	4	US-09-777-430C-22	Sequence 22, Appli
C 147	95.5	7.1	3048	5	PCT-US95-14418-1	Sequence 1, Appli	C 220	92.5	6.9	2526	4	US-09-777-430C-25	Sequence 25, Appli
C 148	95.5	7.1	3048	5	PCT-US95-15327-1	Sequence 1, Appli	C 221	92	6.9	1407	4	US-09-252-991A-13018	Sequence 13018, A
C 149	95.5	7.1	4284	4	US-09-252-991A-4006	Sequence 4006, App	C 222	92	6.9	2558	4	US-09-902-540-6342	Sequence 6342, App
C 150	95.5	7.1	29103	4	US-09-902-540-1236	Sequence 1236, App	C 223	92	6.9	2560	4	US-09-902-540-400	Sequence 400, App
C 151	95	7.1	3810	4	US-09-902-540-3021	Sequence 3021, App	C 224	92	6.9	6645	4	US-09-902-540-8819	Sequence 8819, App
C 152	95	7.1	3812	4	US-09-902-540-641	Sequence 641, App	C 225	92	6.9	10210	4	US-09-902-540-938	Sequence 938, App
C 153	95	7.1	13579	4	US-09-902-540-1101	Sequence 1101, App	C 226	92	6.9	67156	4	US-09-949-016-12284	Sequence 12284, A
C 154	94.5	7.0	1638	4	US-09-902-540-8744	Sequence 8744, App	C 227	92	6.9	67157	4	US-09-949-016-15558	Sequence 15558, A
C 155	94.5	7.0	2304	1	US-08-464-266-1	Sequence 1, Appli	C 228	91.5	6.8	1197	4	US-09-252-991A-6737	Sequence 6737, App
C 156	94.5	7.0	2304	1	US-08-464-272-1	Sequence 1, Appli	C 229	91.5	6.8	1272	4	US-09-252-991A-6952	Sequence 6952, App
C 157	94.5	7.0	2304	3	US-08-464-514-1	Sequence 1, Appli	C 230	91.5	6.8	2346	4	US-09-252-991A-6782	Sequence 6782, App
C 158	94.5	7.0	2304	3	US-08-486-403-1	Sequence 1, Appli	C 231	91.5	6.8	2499	4	US-09-758-282B-94	Sequence 94, Appli

C 232	91.5	6.8	2499	4	US-09-577-304A-94	Sequence 94, Appl	C 305	88.5	6.6	1455	4	US-09-252-991A-158	Sequence 158, App
C 233	91.5	6.8	2505	1	US-07-977-434-9	Sequence 9, Appl1	306	88.5	6.6	1566	4	US-09-902-540-7706	Sequence 7706, Ap
C 234	91.5	6.8	2505	1	US-08-458-819-9	Sequence 9, Appl1	307	88.5	6.6	1696	4	US-09-774-528-151	Sequence 151, App
C 235	91.5	6.8	2505	4	US-09-684-938-159	Sequence 159, App	308	88.5	6.6	2413	3	US-09-367-206-2	Sequence 2, Appl1
C 236	91.5	6.8	2505	4	US-09-308-825A-159	Sequence 159, App	C 309	88.5	6.6	2507	2	US-08-471-066B-1	Sequence 1, Appl1
C 237	91.5	6.8	2505	4	US-09-758-282B-266	Sequence 266, App	C 310	88.5	6.6	2511	4	US-09-252-991A-9132	Sequence 9132, Ap
C 238	91.5	6.8	2505	4	US-09-577-304A-266	Sequence 266, App	C 311	88.5	6.6	2670	4	US-09-902-540-517	Sequence 517, App
C 239	91.5	6.8	2505	5	PCT-US91-07035-9	Sequence 9, Appl1	C 312	88.5	6.6	3916	4	US-09-902-540-463	Sequence 463, App
C 240	91.5	6.8	2511	4	US-09-684-938-161	Sequence 161, App	C 313	88.5	6.6	6611	4	US-09-902-540-762	Sequence 762, App
C 241	91.5	6.8	2511	4	US-09-308-825A-161	Sequence 161, App	C 314	88.5	6.6	30350	4	US-10-118-328-3	Sequence 3, Appl1
C 242	91.5	6.8	2511	4	US-09-758-282B-3	Sequence 3, Appl1	315	88.5	6.6	35614	4	US-09-902-540-1259	Sequence 1259, Ap
C 243	91.5	6.8	2511	4	US-09-758-282B-3	Sequence 3, Appl1	316	88	6.6	1446	4	US-09-902-540-5188	Sequence 5188, Ap
C 244	91.5	6.8	2511	4	US-09-777-430C-9	Sequence 9, Appl1	317	88	6.6	1530	4	US-09-902-540-8329	Sequence 8329, Ap
C 245	91.5	6.8	2640	1	US-08-384-490-30	Sequence 30, Appl	C 318	88	6.6	2517	4	US-09-758-282B-235	Sequence 235, App
C 246	91.5	6.8	2640	1	US-08-459-383-30	Sequence 30, Appl	C 319	88	6.6	2517	4	US-09-577-304A-235	Sequence 235, App
C 247	91.5	6.8	2943	4	US-09-379-530B-4	Sequence 4, Appl1	320	88	6.6	7518	4	US-09-902-540-870	Sequence 870, App
C 248	91.5	6.8	3006	4	US-09-252-991A-9720	Sequence 9720, Ap	321	88	6.6	8604	4	US-09-902-540-5331	Sequence 5331, Ap
C 249	91.5	6.8	3660	4	US-09-252-991A-12269	Sequence 12269, A	322	88	6.6	29899	4	US-09-902-540-1365	Sequence 1265, Ap
C 250	91.5	6.8	5226	4	US-09-902-540-3953	Sequence 953, App	C 323	88	6.6	34199	4	US-09-902-540-1355	Sequence 1265, Ap
C 251	91.5	6.8	9556	4	US-09-902-540-929	Sequence 929, App	C 324	88	6.6	35399	4	US-09-902-540-1260	Sequence 1260, Ap
C 252	91.5	6.8	22156	4	US-09-902-540-1195	Sequence 1195, Ap	325	88	6.6	36171	4	US-09-902-540-1365	Sequence 1260, Ap
C 253	91	6.8	906	4	US-09-489-039A-3080	Sequence 3080, Ap	326	88	6.6	36274	4	US-09-949-016-13876	Sequence 13876, A
C 254	91	6.8	966	4	US-09-252-991A-13273	Sequence 13273, A	327	87.5	6.5	669	4	US-09-902-540-7715	Sequence 7715, Ap
C 255	91	6.8	1083	4	US-09-252-991A-7327	Sequence 7327, Ap	328	87.5	6.5	849	4	US-09-252-991A-617	Sequence 617, App
C 256	91	6.8	1200	4	US-09-252-991A-14709	Sequence 14709, A	329	87.5	6.5	1062	4	US-09-902-540-3096	Sequence 3096, App
C 257	91	6.8	1290	4	US-09-252-991A-15040	Sequence 15040, A	330	87.5	6.5	1575	4	US-09-252-991A-3100	Sequence 3100, App
C 258	91	6.8	1299	4	US-09-252-991A-14277	Sequence 14277, A	331	87.5	6.5	1866	4	US-09-252-991A-16213	Sequence 16213, A
C 259	91	6.8	1428	4	US-09-252-991A-13126	Sequence 13126, A	332	87.5	6.5	1956	4	US-09-252-991A-3189	Sequence 3189, App
C 260	91	6.8	1449	4	US-09-252-991A-14921	Sequence 14921, A	333	87.5	6.5	2379	4	US-09-252-991A-686	Sequence 686, App
C 261	91	6.8	1515	4	US-09-252-991A-12966	Sequence 12966, A	C 334	87.5	6.5	2499	4	US-09-252-991A-596	Sequence 596, App
C 262	91	6.8	1824	4	US-09-252-991A-13076	Sequence 13076, A	C 335	87.5	6.5	2526	4	US-09-758-282B-156	Sequence 156, App
C 263	90.5	6.7	2496	4	US-09-252-991A-13526	Sequence 13526, A	C 336	87.5	6.5	2526	4	US-09-577-304A-156	Sequence 156, App
C 264	90.5	6.7	2526	4	US-09-758-282B-159	Sequence 159, App	337	87.5	6.5	2655	4	US-09-902-540-6674	Sequence 6674, Ap
C 265	90.5	6.7	2526	4	US-09-577-304A-159	Sequence 159, App	C 338	87.5	6.5	3798	4	US-09-902-540-523	Sequence 523, App
C 266	90.5	6.7	2622	4	US-09-252-991A-13933	Sequence 13933, A	C 339	87.5	6.5	10059	4	US-09-949-016-16323	Sequence 16323, A
C 267	90.5	6.7	3065	3	US-09-171-710-3	Sequence 3, Appl1	C 340	87.5	6.5	14634	4	US-09-949-016-17384	Sequence 17384, A
C 268	90.5	6.7	3198	4	US-09-902-540-966	Sequence 966, App	341	87.5	6.5	15499	4	US-09-902-540-1140	Sequence 1140, Ap
C 269	90.5	6.7	14555	4	US-09-902-540-1096	Sequence 1096, App	342	87.5	6.5	28783	4	US-09-902-540-1242	Sequence 1242, Ap
C 270	90.5	6.7	1069	4	US-09-614-912-203	Sequence 203, App	343	87.5	6.5	34316	4	US-09-902-540-1257	Sequence 1257, App
C 271	90	6.7	1722	4	US-09-902-540-6825	Sequence 6825, Ap	344	87.5	6.5	57267	4	US-09-949-016-11899	Sequence 11899, A
C 272	90	6.7	1701	4	US-09-902-540-5141	Sequence 5141, Ap	345	87.5	6.5	101015	4	US-09-949-016-16981	Sequence 16981, A
C 273	90	6.7	1929	4	US-09-252-991A-7017	Sequence 7017, Ap	C 346	87	6.5	720	4	US-09-902-540-4895	Sequence 4895, Ap
C 274	90	6.7	1947	4	US-09-252-991A-7111	Sequence 7111, Ap	C 347	87	6.5	930	4	US-09-252-991A-6618	Sequence 6618, Ap
C 275	90	6.7	4407	4	US-09-902-540-569	Sequence 569, App	C 348	87	6.5	1074	4	US-09-351-150A-36	Sequence 36, Appl
C 276	90	6.7	6404	4	US-09-902-540-760	Sequence 760, App	349	87	6.5	1158	4	US-09-252-991A-14214	Sequence 14214, A
C 277	90	6.7	11854	4	US-09-902-540-1037	Sequence 1037, Ap	350	87	6.5	1308	4	US-09-252-991A-6649	Sequence 6649, Ap
C 278	90	6.7	19112	4	US-09-902-540-1181	Sequence 1181, Ap	351	87	6.5	1353	4	US-09-902-540-4241	Sequence 4241, Ap
C 279	90	6.7	32666	4	US-09-949-016-16086	Sequence 16086, A	352	87	6.5	1377	4	US-09-351-150A-12	Sequence 12, Appl
C 280	90	6.7	962	3	US-08-765-907A-16	Sequence 16, Appl	353	87	6.5	1535	1	US-08-910-973-10	Sequence 10, Appl
281	89.5	6.7	962	3	US-08-987-614A-16	Sequence 16, Appl	354	87	6.5	1535	3	US-09-499-227-10	Sequence 10, Appl
282	89.5	6.7	1052	2	US-08-403-852D-10	Sequence 10, Appl	355	87	6.5	1625	4	US-09-799-451-594	Sequence 594, App
283	89.5	6.7	1052	3	US-08-510-646B-10	Sequence 10, Appl	C 356	87	6.5	1650	4	US-09-252-991A-10150	Sequence 10150, A
284	89.5	6.7	1052	3	US-09-635-359B-10	Sequence 10, Appl	357	87	6.5	1725	4	US-09-252-991A-9926	Sequence 9926, A
285	89.5	6.7	1052	3	US-09-231-818-10	Sequence 10, Appl	358	87	6.5	2145	4	US-09-252-991A-13235	Sequence 13235, A
286	89.5	6.7	1366	4	US-09-252-991A-13397	Sequence 13397, A	359	87	6.5	3390	4	US-09-489-039A-3029	Sequence 3029, Ap
287	89.5	6.7	1359	4	US-09-252-991A-13492	Sequence 13492, A	C 360	87	6.5	3741	4	US-09-252-991A-6569	Sequence 6569, App
288	89.5	6.7	1605	4	US-09-252-991A-3610	Sequence 3610, Ap	C 361	87	6.5	4431	4	US-09-252-991A-12856	Sequence 12856, A
C 289	89.5	6.7	2019	4	US-09-902-540-9185	Sequence 9185, Ap	362	87	6.5	4455	4	US-09-902-540-7119	Sequence 7119, Ap
C 290	89.5	6.7	3270	4	US-09-252-991A-3763	Sequence 3763, Ap	C 363	87	6.5	4458	4	US-09-902-540-650	Sequence 650, App
C 291	89.5	6.7	9556	4	US-09-902-540-982	Sequence 982, App	C 364	87	6.5	7463	4	US-09-902-540-928	Sequence 928, App
C 292	89.5	6.7	25686	4	US-09-902-540-1246	Sequence 1246, Ap	365	87	6.5	10095	3	US-08-822-586-45	Sequence 45, Appl
C 293	89.5	6.7	5481	4	US-09-902-540-7351	Sequence 7351, Ap	C 366	87	6.5	16448	4	US-09-902-540-9686	Sequence 9686, Ap
C 294	89	6.6	6402	4	US-09-902-540-702	Sequence 702, App	367	87	6.5	16458	4	US-09-902-540-1098	Sequence 1098, Ap
C 295	89	6.6	9369	4	US-10-237-551-190	Sequence 190, App	368	87	6.5	19598	4	US-09-902-540-1143	Sequence 1143, Ap
C 296	89	6.6	9369	4	US-10-237-551-247	Sequence 247, App	369	87	6.5	24494	4	US-09-351-150A-1	Sequence 1, Appl1
C 297	89	6.6	969	4	US-09-252-991A-8841	Sequence 8841, Ap	C 370	87	6.5	28493	4	US-09-902-540-1241	Sequence 1241, Ap
C 298	88.5	6.6	1008	4	US-09-252-991A-8953	Sequence 8953, Ap	371	86.5	6.4	888	4	US-09-540-236-1514	Sequence 1514, Ap
C 299	88.5	6.6	1035	4	US-09-252-991A-185	Sequence 185, App	C 372	86.5	6.4	1043	4	US-09-902-540-2570	Sequence 2570, Ap
C 300	88.5	6.6	1074	4	US-09-252-991A-162	Sequence 162, App	C 373	86.5	6.4	1086	4	US-09-252-991A-11554	Sequence 11554, A
C 301	88.5	6.6	1293	4	US-09-252-991A-12484	Sequence 12484, A	374	86.5	6.4	1251	4	US-09-252-991A-3770	Sequence 3770, Ap
C 302	88.5	6.6	1305	4	US-09-902-540-6655	Sequence 6655, Ap	375	86.5	6.4	1368	4	US-09-902-540-8624	Sequence 8624, Ap
C 303	88.5	6.6	1422	4	US-09-252-991A-12989	Sequence 12989, A	C 376	86.5	6.4	1425	4	US-09-252-991A-6019	Sequence 6019, Ap
C 304	88.5	6.6					C 377	86.5	6.4	1443	4	US-09-902-540-6808	Sequence 6808, Ap

378	86.5	6.4	1707	4	US-09-489-039A-2690	Sequence 2690, Ap	451	84.5	6.3	1524	4	US-09-252-991A-9472	Sequence 9472, Ap
379	86.5	6.4	1989	4	US-09-252-991A-6290	Sequence 6290, Ap	452	84.5	6.3	2406	4	US-09-252-991A-11299	Sequence 11299, A
380	86.5	6.4	2367	4	US-09-252-991A-726	Sequence 726, App	c 453	84.5	6.3	2517	4	US-09-758-282B-80	Sequence 80, Appl
381	86.5	6.4	2625	4	US-09-302-540-8554	Sequence 8554, Ap	c 454	84.5	6.3	2517	4	US-09-577-304A-80	Sequence 80, Appl
382	86.5	6.4	3825	4	US-09-252-991A-3815	Sequence 3815, Ap	c 455	84.5	6.3	2526	4	US-09-758-282B-92	Sequence 92, Appl
383	86.5	6.4	4282	4	US-09-302-540-563	Sequence 563, App	c 456	84.5	6.3	2526	4	US-09-577-304A-92	Sequence 92, Appl
384	86.5	6.4	4506	4	US-09-252-991A-3695	Sequence 3695, Ap	c 457	84.5	6.3	3162	4	US-09-902-540-373	Sequence 373, App
385	86.5	6.4	7001	1	US-08-258-261B-1	Sequence 1, Appl	c 458	84.5	6.3	3358	3	US-09-248-571-2	Sequence 2, Appl
386	86.5	6.4	7001	1	US-08-456-837-1	Sequence 1, Appl	c 459	84.5	6.3	3358	3	US-09-553-736-2	Sequence 2, Appl
387	86.5	6.4	7001	1	US-08-457-342-1	Sequence 1, Appl	c 460	84.5	6.3	8614	4	US-09-502-540-787	Sequence 787, App
388	86.5	6.4	7001	1	US-08-457-646A-1	Sequence 1, Appl	c 461	84.5	6.3	8773	4	US-09-902-540-965	Sequence 965, App
389	86.5	6.4	7001	1	US-08-458-076A-1	Sequence 1, Appl	c 462	84.5	6.3	10178	4	US-09-902-540-977	Sequence 977, App
390	86.5	6.4	7001	1	US-08-457-335A-1	Sequence 1, Appl	c 463	84.5	6.3	19455	4	US-09-902-540-1147	Sequence 1147, Ap
391	86.5	6.4	7001	1	US-08-761-258-6	Sequence 6, Appl	c 464	84.5	6.3	22311	4	US-09-949-016-12344	Sequence 12344, A
392	86.5	6.4	7001	1	US-08-729-214-1	Sequence 1, Appl	c 465	84.5	6.3	22312	4	US-09-949-016-17217	Sequence 17217, A
393	86.5	6.4	7001	2	US-08-977-306-6	Sequence 6, Appl	c 466	84.5	6.3	34446	3	US-09-103-330-35	Sequence 35, Appl
394	86.5	6.4	7001	3	US-09-028-934-1	Sequence 1, Appl	c 467	84.5	6.3	49225	4	US-09-902-540-1269	Sequence 1269, Ap
395	86.5	6.4	7562	4	US-09-902-540-902	Sequence 902, App	c 468	84.5	6.3	146307	4	US-09-949-016-14881	Sequence 14881, A
396	86.5	6.4	7982	4	US-09-902-540-911	Sequence 911, App	c 469	84.5	6.3	146307	4	US-09-949-016-14882	Sequence 14882, A
397	86.5	6.4	8037	4	US-09-774-528-209	Sequence 209, App	c 470	84.5	6.3	146307	4	US-09-949-016-14883	Sequence 14883, A
398	86.5	6.4	13855	4	US-09-902-540-1117	Sequence 1117, Ap	c 471	84.5	6.3	146307	4	US-09-949-016-14884	Sequence 14884, A
399	86.5	6.4	19068	4	US-09-902-540-1123	Sequence 1123, Ap	c 472	84.5	6.3	146307	4	US-09-949-016-14885	Sequence 14885, A
400	86.5	6.4	26840	4	US-09-949-016-17431	Sequence 17431, A	c 473	84.5	6.3	146307	4	US-09-949-016-14886	Sequence 14886, A
401	86.5	6.4	30780	4	US-09-902-540-1243	Sequence 1243, Ap	c 474	84.5	6.3	146307	4	US-09-949-016-14887	Sequence 14887, A
402	86.5	6.4	53500	4	US-09-266-965-76	Sequence 76, Appl	c 475	84.5	6.3	146307	4	US-09-949-016-14888	Sequence 14888, A
403	86.5	6.4	62909	4	US-09-596-002-32	Sequence 32, Appl	c 476	84.5	6.3	148405	4	US-09-949-016-11747	Sequence 11747, A
404	86	6.4	822	4	US-09-252-991A-6178	Sequence 6178, Ap	c 477	84.5	6.3	148405	4	US-09-949-016-12835	Sequence 12835, A
405	86	6.4	1143	4	US-09-902-540-3850	Sequence 3850, Ap	c 478	84.5	6.3	148405	4	US-09-949-016-12836	Sequence 12836, A
406	86	6.4	1221	4	US-09-252-991A-7107	Sequence 7107, Ap	c 479	84.5	6.3	148405	4	US-09-949-016-12837	Sequence 12837, A
407	86	6.4	1488	4	US-09-252-991A-9231	Sequence 9231, Ap	c 480	84	6.3	314	3	US-09-060-756-582	Sequence 582, App
408	86	6.4	2019	4	US-09-252-991A-8818	Sequence 8818, Ap	c 481	84	6.3	314	4	US-09-583-110-637	Sequence 637, App
409	86	6.4	2094	4	US-09-252-991A-7438	Sequence 7438, Ap	c 482	84	6.3	759	4	US-09-583-110-637	Sequence 637, App
410	86	6.4	2517	4	US-09-758-282B-174	Sequence 174, App	c 483	84	6.3	780	4	US-09-902-540-2969	Sequence 2969, Ap
411	86	6.4	2517	4	US-09-577-304A-174	Sequence 174, App	c 484	84	6.3	971	1	US-08-253-155A-11	Sequence 11, Appl
412	86	6.4	2814	4	US-09-252-991A-15765	Sequence 15765, A	c 485	84	6.3	1065	4	US-09-252-991A-16320	Sequence 16320, A
413	86	6.4	2937	4	US-09-902-540-6675	Sequence 6675, Ap	c 486	84	6.3	1332	4	US-09-252-991A-15961	Sequence 15961, A
414	86	6.4	3012	4	US-09-252-991A-7498	Sequence 7498, Ap	c 487	84	6.3	1341	4	US-09-252-991A-16544	Sequence 16544, A
415	86	6.4	3357	4	US-09-252-991A-15868	Sequence 15868, A	c 488	84	6.3	1405	1	US-08-035-558-3	Sequence 3, Appl
416	86	6.4	3550	4	US-09-902-540-524	Sequence 524, App	c 489	84	6.3	1405	2	US-08-682-847-5	Sequence 5, Appl
417	86	6.4	10528	4	US-09-902-540-945	Sequence 945, App	c 490	84	6.3	1405	3	US-09-063-676-1	Sequence 1, Appl
418	86	6.4	20740	4	US-09-902-540-1223	Sequence 1223, Ap	c 491	84	6.3	1407	1	US-09-902-540-4833	Sequence 4833, Ap
419	86	6.4	21964	4	US-09-902-540-1190	Sequence 1190, Ap	c 492	84	6.3	1785	1	US-07-865-662F-4	Sequence 4, Appl
420	86	6.4	47981	4	US-09-679-279-1	Sequence 1, Appl	c 493	84	6.3	1785	3	US-08-374-219B-4	Sequence 4, Appl
421	85.5	6.4	909	4	US-09-252-991A-12929	Sequence 12929, A	c 494	84	6.3	2055	4	US-09-252-991A-1845	Sequence 1845, Ap
422	85.5	6.4	1047	4	US-09-902-540-4239	Sequence 4239, Ap	c 495	84	6.3	2067	4	US-09-252-991A-1398	Sequence 1398, Ap
423	85.5	6.4	1269	4	US-09-252-991A-8698	Sequence 8698, Ap	c 496	84	6.3	2100	4	US-09-252-991A-1209	Sequence 1209, Ap
424	85.5	6.4	1344	4	US-09-252-991A-9081	Sequence 9081, Ap	c 497	84	6.3	2480	4	US-09-064-199-15	Sequence 15, Appl
425	85.5	6.4	17622	4	US-09-902-540-1125	Sequence 1125, Ap	c 498	84	6.3	2595	4	US-09-902-540-3202	Sequence 3202, Ap
426	85.5	6.4	29598	3	US-09-341-587-6	Sequence 6, Appl	c 499	84	6.3	3393	1	US-08-295-502-1	Sequence 1, Appl
427	85.5	6.4	106929	4	US-09-949-016-12060	Sequence 12060, A	c 500	84	6.3	3393	5	PCT-US95-10691-1	Sequence 1, Appl
428	85.5	6.4	106929	4	US-09-949-016-16618	Sequence 16618, A	c 501	84	6.3	4346	4	US-09-064-199-12	Sequence 12, Appl
429	85.5	6.4	152481	4	US-09-949-016-12521	Sequence 12521, A	c 502	84	6.3	4366	4	US-09-064-199-14	Sequence 14, Appl
430	85.5	6.4	152798	4	US-09-949-016-12775	Sequence 12775, A	c 503	84	6.3	4418	4	US-09-064-199-13	Sequence 13, Appl
431	85.5	6.4	152822	4	US-09-949-016-17518	Sequence 17518, A	c 504	84	6.3	4431	4	US-09-064-199-8	Sequence 8, Appl
432	85.5	6.4	152822	4	US-09-949-016-17519	Sequence 17519, A	c 505	84	6.3	4441	3	US-09-641-999-2	Sequence 2, Appl
433	85.5	6.4	157866	4	US-09-949-016-12982	Sequence 12982, A	c 506	84	6.3	4441	4	US-09-064-199-10	Sequence 10, Appl
434	85.5	6.4	157866	4	US-09-949-016-12983	Sequence 12983, A	c 507	84	6.3	4543	2	US-08-519-547A-5	Sequence 5, Appl
435	85.5	6.4	157866	4	US-09-949-016-12984	Sequence 12984, A	c 508	84	6.3	4549	4	US-09-064-199-9	Sequence 9, Appl
436	85	6.3	666	4	US-09-252-991A-7202	Sequence 7202, Ap	c 509	84	6.3	4564	4	US-09-064-199-2	Sequence 2, Appl
437	85	6.3	798	4	US-09-543-681A-2640	Sequence 2640, Ap	c 510	84	6.3	4649	4	US-09-064-199-11	Sequence 11, Appl
438	85	6.3	984	4	US-09-902-540-3562	Sequence 3562, Ap	c 511	84	6.3	4746	4	US-09-064-199-7	Sequence 7, Appl
439	85	6.3	1902	4	US-09-902-540-8758	Sequence 8758, Ap	c 512	84	6.3	5105	4	US-09-064-199-3	Sequence 3, Appl
440	85	6.3	16924	4	US-09-902-540-1178	Sequence 1178, Ap	c 513	84	6.3	5463	4	US-09-064-199-1	Sequence 1, Appl
441	85	6.3	19019	4	US-09-902-540-1171	Sequence 1171, Ap	c 514	84	6.3	7404	4	US-09-902-540-3115	Sequence 3115, Ap
442	85	6.3	21296	4	US-09-949-016-14504	Sequence 14504, A	c 515	84	6.3	7734	4	US-09-949-016-1095	Sequence 1095, Ap
443	85	6.3	21296	4	US-09-949-016-14505	Sequence 14505, A	c 516	84	6.3	8145	4	US-09-949-016-1093	Sequence 1093, Ap
444	85	6.3	21296	4	US-09-949-016-15701	Sequence 15701, A	c 517	84	6.3	8220	4	US-09-949-016-1094	Sequence 1094, Ap
445	85	6.3	21296	4	US-09-949-016-15702	Sequence 15702, A	c 518	84	6.3	8280	4	US-09-949-016-5	Sequence 5, Appl
446	85	6.3	23496	4	US-09-902-540-5645	Sequence 5645, Ap	c 519	84	6.3	8738	4	US-09-902-540-873	Sequence 873, App
447	85	6.3	25254	4	US-09-902-540-1233	Sequence 1233, Ap	c 520	84	6.3	9054	4	US-09-949-016-13588	Sequence 13588, A
448	85	6.3	51354	4	US-09-902-540-1270	Sequence 1270, Ap	c 521	84	6.3	10391	4	US-09-902-540-958	Sequence 958, App
449	85	6.3	536165	4	US-09-214-808-1	Sequence 1, Appl	c 522	84	6.3	15644	4	US-09-902-540-1133	Sequence 1133, Ap
450	84.5	6.3	1260	4	US-09-252-991A-6317	Sequence 6317, Ap	c 523	84	6.3	18809	4	US-09-902-540-1141	Sequence 1141, Ap



524	84	6.3	19455	4	US-09-902-540-1147	Sequence 1147, Ap	597	83	6.2	43380	2	US-08-804-227C-1	Sequence 1, Appl1
525	84	6.3	24741	4	US-09-949-016-15547	Sequence 15547, A	598	83	6.2	77266	4	US-09-949-016-12608	Sequence 12608, A
526	84	6.3	25733	4	US-09-902-540-1215	Sequence 1215, Ap	599	82.5	6.1	651	4	US-09-252-991A-2095	Sequence 2095, Ap
527	84	6.3	26012	4	US-09-902-540-1217	Sequence 1217, Ap	600	82.5	6.1	786	4	US-09-902-540-5164	Sequence 5164, Ap
528	84	6.3	26659	4	US-09-902-540-1232	Sequence 1232, Ap	c 601	82.5	6.1	816	4	US-09-252-991A-507	Sequence 507, App
529	84	6.3	27219	4	US-09-902-540-1244	Sequence 1244, Ap	602	82.5	6.1	930	4	US-09-902-540-8427	Sequence 8427, Ap
530	84	6.3	27579	4	US-09-949-016-13465	Sequence 13465, A	c 603	82.5	6.1	957	4	US-09-252-991A-6278	Sequence 6278, Ap
531	84	6.3	42232	4	US-09-949-016-11917	Sequence 11917, A	c 604	82.5	6.1	1209	4	US-09-252-991A-572	Sequence 572, App
532	84	6.3	42234	4	US-09-949-016-13705	Sequence 13705, A	605	82.5	6.1	1245	4	US-09-252-991A-594	Sequence 594, App
533	84	6.3	46603	4	US-09-949-016-15636	Sequence 15636, A	606	82.5	6.1	1623	4	US-09-613-303-3	Sequence 3, Appl1
534	83.5	6.2	601	4	US-09-949-016-171096	Sequence 171096,	607	82.5	6.1	1623	4	US-10-267-311-3	Sequence 3, Appl1
535	83.5	6.2	601	4	US-09-949-016-171226	Sequence 171226,	608	82.5	6.1	1764	4	US-09-252-991A-6133	Sequence 6133, Ap
536	83.5	6.2	1107	4	US-09-902-540-8772	Sequence 8772, Ap	c 609	82.5	6.1	1785	4	US-09-252-991A-4278	Sequence 4278, Ap
537	83.5	6.2	1251	4	US-09-252-991A-8004	Sequence 8004, Ap	610	82.5	6.1	1879	4	US-09-614-748A-10	Sequence 10, Appl
538	83.5	6.2	1308	4	US-09-252-991A-7182	Sequence 7182, Ap	611	82.5	6.1	1886	1	US-07-980-526-1	Sequence 1, Appl1
539	83.5	6.2	1344	4	US-09-252-991A-6363	Sequence 6363, Ap	612	82.5	6.1	1920	4	US-09-613-303-16	Sequence 16, Appl
540	83.5	6.2	1550	3	US-09-234-332-3	Sequence 3, Appl1	613	82.5	6.1	1920	4	US-10-267-311-16	Sequence 16, Appl
541	83.5	6.2	1671	4	US-09-252-991A-6188	Sequence 6188, Ap	614	82.5	6.1	1947	4	US-09-613-303-28	Sequence 28, Appl
542	83.5	6.2	1767	1	US-08-399-646-1	Sequence 1, Appl1	615	82.5	6.1	1947	4	US-10-267-311-28	Sequence 28, Appl
543	83.5	6.2	1767	1	US-08-607-321-1	Sequence 1, Appl1	c 616	82.5	6.1	1956	4	US-09-252-991A-12032	Sequence 12032, A
544	83.5	6.2	1767	2	US-08-961-240-1	Sequence 1, Appl1	617	82.5	6.1	2017	4	US-09-614-748A-8	Sequence 8, Appl1
545	83.5	6.2	1767	2	US-08-605-501-1	Sequence 1, Appl1	c 618	82.5	6.1	2067	4	US-09-252-991A-527	Sequence 527, App
546	83.5	6.2	1854	4	US-09-902-540-7177	Sequence 7177, Ap	619	82.5	6.1	2499	4	US-09-758-282B-96	Sequence 96, Appl
547	83.5	6.2	2161	1	US-08-399-646-11	Sequence 11, Appl	c 620	82.5	6.1	2499	4	US-09-577-304A-96	Sequence 96, Appl
548	83.5	6.2	2161	1	US-08-607-321-11	Sequence 11, Appl	c 621	82.5	6.1	2517	4	US-09-758-282B-78	Sequence 78, Appl
549	83.5	6.2	2161	2	US-08-961-240-11	Sequence 11, Appl	c 622	82.5	6.1	2517	4	US-09-758-282B-84	Sequence 84, Appl
550	83.5	6.2	2161	2	US-08-605-501-11	Sequence 11, Appl	c 623	82.5	6.1	2517	4	US-09-758-282B-86	Sequence 86, Appl
551	83.5	6.2	2484	4	US-09-252-991A-7462	Sequence 7462, Ap	c 624	82.5	6.1	2517	4	US-09-758-282B-102	Sequence 102, App
552	83.5	6.2	2499	4	US-09-758-282B-98	Sequence 98, Appl	c 625	82.5	6.1	2517	4	US-09-758-282B-105	Sequence 105, App
553	83.5	6.2	2499	4	US-09-577-304A-98	Sequence 98, Appl	c 626	82.5	6.1	2517	4	US-09-758-282B-108	Sequence 108, App
554	83.5	6.2	3251	3	US-09-085-199B-6	Sequence 6, Appl1	c 627	82.5	6.1	2517	4	US-09-758-282B-111	Sequence 111, App
555	83.5	6.2	3876	4	US-09-849-602-4	Sequence 4, Appl1	c 628	82.5	6.1	2517	4	US-09-758-282B-135	Sequence 135, App
556	83.5	6.2	4162	4	US-09-902-540-664	Sequence 664, App	c 629	82.5	6.1	2517	4	US-09-577-304A-78	Sequence 78, Appl
557	83.5	6.2	7515	4	US-09-949-016-583	Sequence 583, App	c 630	82.5	6.1	2517	4	US-09-577-304A-84	Sequence 84, Appl
558	83.5	6.2	9185	4	US-09-902-540-931	Sequence 931, App	c 631	82.5	6.1	2517	4	US-09-577-304A-86	Sequence 86, Appl
559	83.5	6.2	11219	1	US-07-642-734C-1	Sequence 1, Appl1	c 632	82.5	6.1	2517	4	US-09-577-304A-102	Sequence 102, App
560	83.5	6.2	11219	3	US-08-439-009A-1	Sequence 1, Appl1	c 633	82.5	6.1	2517	4	US-09-577-304A-105	Sequence 105, App
561	83.5	6.2	11706	4	US-09-902-540-1038	Sequence 1038, Ap	c 634	82.5	6.1	2517	4	US-09-577-304A-108	Sequence 108, App
562	83.5	6.2	13624	4	US-09-902-540-1053	Sequence 1053, Ap	c 635	82.5	6.1	2517	4	US-09-577-304A-111	Sequence 111, App
563	83.5	6.2	24018	4	US-09-949-016-17114	Sequence 17114, A	c 636	82.5	6.1	2517	4	US-09-577-304A-135	Sequence 135, App
564	83.5	6.2	112507	4	US-09-949-016-11240	Sequence 12420, A	c 637	82.5	6.1	2526	4	US-09-758-282B-90	Sequence 90, Appl
565	83.5	6.2	112507	4	US-09-949-016-12794	Sequence 12794, A	c 638	82.5	6.1	2526	4	US-09-577-304A-90	Sequence 90, Appl
566	83.5	6.2	112508	4	US-09-949-016-16589	Sequence 16589, A	c 639	82.5	6.1	2766	4	US-09-252-991A-3756	Sequence 3756, Ap
567	83.5	6.2	112508	4	US-09-949-016-16590	Sequence 16590, A	640	82.5	6.1	2847	4	US-09-613-303-20	Sequence 20, Appl
568	83	6.2	774	4	US-09-252-991A-13331	Sequence 13331, A	641	82.5	6.1	2847	4	US-10-267-311-20	Sequence 20, Appl
569	83	6.2	924	4	US-09-902-540-3612	Sequence 3612, Ap	642	82.5	6.1	2874	4	US-09-252-991A-3837	Sequence 3837, Ap
570	83	6.2	933	4	US-09-252-991A-10917	Sequence 10917, A	643	82.5	6.1	3390	4	US-09-252-991A-11981	Sequence 11981, A
571	83	6.2	964	4	US-09-513-999C-14934	Sequence 14934, A	644	82.5	6.1	4380	3	US-08-955-565A-3	Sequence 3, Appl1
572	83	6.2	1152	4	US-09-252-991A-5237	Sequence 5237, Ap	645	82.5	6.1	6553	4	US-09-902-540-885	Sequence 885, App
573	83	6.2	1617	3	US-09-265-013-2	Sequence 2, Appl1	646	82.5	6.1	6553	4	US-09-949-016-15370	Sequence 15370, A
574	83	6.2	1660	4	US-09-902-540-378	Sequence 378, App	647	82.5	6.1	15923	4	US-09-902-540-1095	Sequence 1095, Ap
575	83	6.2	1851	4	US-09-252-991A-9067	Sequence 9067, Ap	648	82.5	6.1	18551	4	US-09-902-540-1187	Sequence 1187, Ap
576	83	6.2	2046	4	US-09-252-991A-5266	Sequence 5266, Ap	649	82.5	6.1	28804	2	US-08-592-87A-1	Sequence 1, Appl1
577	83	6.2	2328	4	US-09-252-991A-11890	Sequence 11890, A	c 650	82.5	6.1	28804	3	US-09-096-942-2	Sequence 2, Appl1
578	83	6.2	4443	4	US-09-252-991A-9151	Sequence 9151, Ap	c 651	82.5	6.1	28804	3	US-09-096-942-2	Sequence 2, Appl1
579	83	6.2	4212	4	US-09-252-991A-8929	Sequence 8929, Ap	c 652	82.5	6.1	125672	4	US-09-949-016-16956	Sequence 16956, A
580	83	6.2	4430	3	US-09-302-540-491	Sequence 491, App	653	82	6.1	789	1	US-08-107-433-1646	Sequence 3, Appl1
581	83	6.2	7308	3	US-09-011-745-3	Sequence 3, Appl1	654	82	6.1	789	1	US-08-181-335B-3	Sequence 3, Appl1
582	83	6.2	7308	3	US-09-011-745-4	Sequence 4, Appl1	655	82	6.1	789	1	US-08-181-335B-5	Sequence 5, Appl1
583	83	6.2	7616	3	US-09-011-745-2	Sequence 2, Appl1	656	82	6.1	789	1	US-08-181-335B-6	Sequence 6, Appl1
584	83	6.2	8202	1	US-08-258-420-13	Sequence 13, Appl	657	82	6.1	789	5	PCT-US95-00129-3	Sequence 3, Appl1
585	83	6.2	8332	3	US-08-850-961-1	Sequence 1, Appl1	658	82	6.1	789	5	PCT-US95-00129-5	Sequence 5, Appl1
586	83	6.2	8332	3	US-09-479-776-1	Sequence 1, Appl1	659	82	6.1	789	5	PCT-US95-00129-6	Sequence 6, Appl1
587	83	6.2	8332	3	US-09-309-572-11	Sequence 11, Appl	c 660	82	6.1	852	4	US-09-252-991A-6125	Sequence 6125, Ap
588	83	6.2	8332	3	US-09-315-127-1	Sequence 1, Appl1	c 661	82	6.1	1068	4	US-09-252-991A-6432	Sequence 6432, Ap
589	83	6.2	8332	3	US-09-265-013-1	Sequence 1, Appl1	662	82	6.1	1218	4	US-09-902-540-9113	Sequence 9113, Ap
590	83	6.2	8332	4	US-09-554-572-25	Sequence 25, Appl	663	82	6.1	1237	4	US-09-902-540-2125	Sequence 2125, Ap
591	83	6.2	8332	4	US-09-718-096-11	Sequence 11, Appl	664	82	6.1	1665	4	US-09-902-540-7864	Sequence 7864, Ap
592	83	6.2	8332	4	US-09-001-039B-15	Sequence 15, Appl	665	82	6.1	1737	4	US-09-252-991A-2085	Sequence 2085, Ap
593	83	6.2	18848	4	US-09-902-540-1174	Sequence 1174, Ap	666	82	6.1	1761	4	US-09-902-540-3727	Sequence 3727, Ap
594	83	6.2	26104	4	US-09-949-016-14045	Sequence 14045, A	c 667	82	6.1	2517	4	US-09-758-282B-138	Sequence 138, App
595	83	6.2	35399	4	US-09-902-540-1260	Sequence 1260, Ap	c 668	82	6.1	2517	4	US-09-577-304A-138	Sequence 138, App
596	83	6.2	42450	4	US-09-815-048-3	Sequence 3, Appl1	669	82	6.1	2667	4	US-09-902-540-9380	Sequence 9380, Ap

670	82	6.1	3186	4	US-09-489-039A-5569	Sequence 5569, Ap	c 743	81	6.0	2499	1	US-08-458-819-1	Sequence 1, Appli
671	82	6.1	3376	3	US-08-961-527-222	Sequence 222, App	c 744	81	6.0	2499	3	US-07-602-848E-1	Sequence 1, Appli
672	82	6.1	3378	4	US-09-252-991A-2158	Sequence 2158, Ap	c 745	81	6.0	2499	3	US-09-587-856-1	Sequence 1, Appli
673	82	6.1	3381	4	US-09-902-540-7493	Sequence 7493, Ap	c 746	81	6.0	2499	3	US-09-777-537-1	Sequence 1, Appli
674	82	6.1	3597	4	US-09-902-540-5402	Sequence 5402, Ap	c 747	81	6.0	2499	3	US-09-777-538-1	Sequence 1, Appli
675	82	6.1	4335	4	US-09-902-540-9587	Sequence 9587, Ap	c 748	81	6.0	2499	4	US-08-758-282B-100	Sequence 100, App
c 676	82	6.1	5661	3	US-08-938-105-2	Sequence 2, Appli	c 749	81	6.0	2499	4	US-09-577-304A-100	Sequence 100, Appli
677	82	6.1	6269	4	US-09-902-540-726	Sequence 726, App	c 750	81	6.0	2499	5	PCT-US91-07035-1	Sequence 1, Appli
678	82	6.1	7861	4	US-09-774-528-305	Sequence 305, App	c 751	81	6.0	2505	2	US-08-757-653-167	Sequence 167, Appl
679	82	6.1	8820	4	US-09-902-540-974	Sequence 974, App	c 752	81	6.0	2505	2	US-08-823-516-65	Sequence 65, Appl
680	82	6.1	11566	4	US-09-902-540-1088	Sequence 1088, Ap	c 753	81	6.0	2505	3	US-08-759-038-106	Sequence 106, App
c 681	82	6.1	11566	4	US-09-902-540-1088	Sequence 1088, Ap	c 754	81	6.0	2505	3	US-08-759-038-106	Sequence 106, App
c 682	82	6.1	12707	4	US-09-949-016-14243	Sequence 14243, A	c 755	81	6.0	2505	4	US-09-684-938-106	Sequence 106, App
683	82	6.1	12707	4	US-09-949-016-14244	Sequence 14244, A	c 756	81	6.0	2505	4	US-09-308-828B-106	Sequence 106, App
c 684	82	6.1	13027	4	US-09-902-540-1074	Sequence 1074, Ap	c 757	81	6.0	2505	4	US-09-758-282B-55	Sequence 55, Appl
c 685	82	6.1	34552	4	US-09-902-540-1262	Sequence 1262, Ap	c 758	81	6.0	2505	4	US-09-940-244-65	Sequence 65, Appl
686	82	6.1	11677	4	US-09-949-016-15946	Sequence 15946, A	c 759	81	6.0	2505	4	US-08-577-304A-55	Sequence 55, Appl
c 687	81.5	6.1	744	4	US-09-252-991A-15563	Sequence 15563, A	c 760	81	6.0	2506	1	US-08-073-384C-1	Sequence 1, Appli
c 688	81.5	6.1	837	4	US-09-252-991A-5702	Sequence 5702, A	c 761	81	6.0	2506	1	US-08-254-359A-1	Sequence 1, Appli
689	81.5	6.1	1080	4	US-09-248-766A-4099	Sequence 4099, Ap	c 762	81	6.0	2506	1	US-08-483-043-1	Sequence 1, Appli
c 690	81.5	6.1	1104	4	US-09-902-540-3201	Sequence 3201, Ap	c 763	81	6.0	2506	1	US-08-481-238-1	Sequence 1, Appli
c 691	81.5	6.1	1161	4	US-09-892-198B-1	Sequence 1, Appli	c 764	81	6.0	2506	2	US-08-484-956-1	Sequence 1, Appli
c 692	81.5	6.1	1221	4	US-09-252-991A-7990	Sequence 7990, Ap	c 765	81	6.0	2506	2	US-08-757-653-1	Sequence 1, Appli
693	81.5	6.1	1233	4	US-09-252-991A-8268	Sequence 8268, Ap	c 766	81	6.0	2506	2	US-08-599-491-1	Sequence 1, Appli
694	81.5	6.1	1245	4	US-09-252-991A-5725	Sequence 5725, Ap	c 767	81	6.0	2506	2	US-08-756-386-1	Sequence 1, Appli
695	81.5	6.1	1302	4	US-09-252-991A-8677	Sequence 8677, Ap	c 768	81	6.0	2506	2	US-08-823-516-1	Sequence 1, Appli
696	81.5	6.1	1362	4	US-09-252-991A-8259	Sequence 8259, Ap	c 769	81	6.0	2506	3	US-08-682-853A-1	Sequence 1, Appli
c 697	81.5	6.1	1424	4	US-09-902-540-3125	Sequence 3125, Ap	c 770	81	6.0	2506	3	US-08-759-038-1	Sequence 1, Appli
c 698	81.5	6.1	1428	4	US-09-902-540-7081	Sequence 7081, Ap	c 771	81	6.0	2506	3	US-08-758-314-1	Sequence 1, Appli
c 699	81.5	6.1	1503	4	US-09-252-991A-13684	Sequence 13684, A	c 772	81	6.0	2506	3	US-09-350-309-1	Sequence 1, Appli
700	81.5	6.1	1584	4	US-09-252-991A-625	Sequence 625, App	c 773	81	6.0	2506	3	US-08-520-946-1	Sequence 1, Appli
701	81.5	6.1	1674	4	US-09-252-991A-3990	Sequence 3990, Ap	c 774	81	6.0	2506	4	US-09-684-938-1	Sequence 1, Appli
702	81.5	6.1	1746	4	US-09-252-991A-13461	Sequence 13461, A	c 775	81	6.0	2506	4	US-09-308-825A-1	Sequence 1, Appli
c 703	81.5	6.1	1983	4	US-09-252-991A-15635	Sequence 15635, A	c 776	81	6.0	2506	4	US-09-758-282B-1	Sequence 1, Appli
c 704	81.5	6.1	2190	4	US-09-252-991A-10256	Sequence 10256, A	c 777	81	6.0	2506	4	US-03-655-378A-1	Sequence 1, Appli
705	81.5	6.1	2211	4	US-09-252-991A-15685	Sequence 15685, A	c 778	81	6.0	2506	4	US-09-940-244-1	Sequence 1, Appli
c 706	81.5	6.1	2325	4	US-09-252-991A-8052	Sequence 8052, Ap	c 779	81	6.0	2506	4	US-09-333-145-1	Sequence 1, Appli
c 707	81.5	6.1	2403	4	US-09-252-991A-8064	Sequence 8064, Ap	c 780	81	6.0	2506	4	US-09-577-304A-1	Sequence 1, Appli
c 708	81.5	6.1	3537	4	US-09-902-540-8144	Sequence 8144, Ap	c 781	81	6.0	2514	4	US-09-758-282B-264	Sequence 264, App
c 709	81.5	6.1	4242	4	US-09-252-991A-7056	Sequence 7056, Ap	c 782	81	6.0	2514	4	US-09-577-304A-264	Sequence 264, App
c 710	81.5	6.1	4346	4	US-09-919-039-112	Sequence 112, App	c 783	81	6.0	2517	4	US-09-758-282B-62	Sequence 62, Appl
c 711	81.5	6.1	6410	4	US-09-902-540-835	Sequence 835, App	c 784	81	6.0	2517	4	US-09-758-282B-71	Sequence 71, Appl
c 712	81.5	6.1	9007	4	US-09-902-540-908	Sequence 908, App	c 785	81	6.0	2517	4	US-09-758-282B-82	Sequence 82, Appl
c 713	81.5	6.1	9497	4	US-09-902-540-1054	Sequence 1054, Ap	c 786	81	6.0	2517	4	US-09-758-282B-88	Sequence 88, Appl
714	81.5	6.1	10023	4	US-09-252-991A-6997	Sequence 6997, Ap	c 787	81	6.0	2517	4	US-09-758-282B-114	Sequence 114, App
c 715	81.5	6.1	12268	4	US-09-902-540-1142	Sequence 1142, Ap	c 788	81	6.0	2517	4	US-09-758-282B-117	Sequence 117, App
c 716	81.5	6.1	23796	4	US-09-949-016-17581	Sequence 17581, A	c 789	81	6.0	2517	4	US-09-758-282B-120	Sequence 120, App
c 717	81.5	6.1	23951	4	US-09-902-540-1245	Sequence 1245, Ap	c 790	81	6.0	2517	4	US-09-758-282B-123	Sequence 123, App
718	81.5	6.1	30135	4	US-09-902-540-1249	Sequence 1249, Ap	c 791	81	6.0	2517	4	US-09-758-282B-126	Sequence 126, App
719	81.5	6.1	39920	4	US-09-902-540-1266	Sequence 1266, A	c 792	81	6.0	2517	4	US-09-758-282B-129	Sequence 129, App
c 720	81.5	6.1	41768	4	US-09-902-540-1266	Sequence 1266, Ap	c 793	81	6.0	2517	4	US-09-758-282B-132	Sequence 132, App
721	81.5	6.1	43507	4	US-09-949-016-13297	Sequence 13297, A	c 794	81	6.0	2517	4	US-09-758-282B-141	Sequence 141, App
722	81.5	6.1	186734	4	US-09-949-016-14870	Sequence 14870, A	c 795	81	6.0	2517	4	US-09-758-282B-147	Sequence 147, App
723	81.5	6.1	193689	4	US-09-949-016-12350	Sequence 12350, A	c 796	81	6.0	2517	4	US-09-758-282B-149	Sequence 149, App
724	81.5	6.1	193689	4	US-09-949-016-13088	Sequence 13088, A	c 797	81	6.0	2517	4	US-09-758-282B-152	Sequence 152, App
725	81	6.0	915	4	US-09-489-039A-2253	Sequence 2253, Ap	c 798	81	6.0	2517	4	US-09-758-282B-168	Sequence 168, App
726	81	6.0	999	2	US-08-960-756-3	Sequence 3, Appli	c 799	81	6.0	2517	4	US-09-758-282B-177	Sequence 177, App
c 727	81	6.0	1152	4	US-09-266-965-45	Sequence 45, Appli	c 800	81	6.0	2517	4	US-09-758-282B-180	Sequence 180, App
728	81	6.0	1307	2	US-08-960-022-17	Sequence 17, Appli	c 801	81	6.0	2517	4	US-09-758-282B-183	Sequence 183, App
c 729	81	6.0	1470	4	US-09-252-991A-3389	Sequence 3389, Ap	c 802	81	6.0	2517	4	US-09-758-282B-186	Sequence 186, App
c 730	81	6.0	1584	4	US-09-489-039A-2524	Sequence 2524, Ap	c 803	81	6.0	2517	4	US-09-758-282B-189	Sequence 189, App
c 731	81	6.0	1682	3	US-09-096-399-1	Sequence 1, Appli	c 804	81	6.0	2517	4	US-09-758-282B-199	Sequence 199, App
c 732	81	6.0	1696	3	US-09-096-399-3	Sequence 3, Appli	c 805	81	6.0	2517	4	US-09-758-282B-201	Sequence 201, App
733	81	6.0	1722	4	US-09-902-540-3668	Sequence 3668, Ap	c 806	81	6.0	2517	4	US-09-758-282B-203	Sequence 203, App
c 734	81	6.0	1854	4	US-09-902-540-340	Sequence 340, App	c 807	81	6.0	2517	4	US-09-758-282B-205	Sequence 205, App
c 735	81	6.0	1899	4	US-09-640-958-3	Sequence 3, Appli	c 808	81	6.0	2517	4	US-09-758-282B-217	Sequence 217, App
c 736	81	6.0	1904	4	US-09-640-958-9	Sequence 9, Appli	c 809	81	6.0	2517	4	US-09-758-282B-220	Sequence 220, App
c 737	81	6.0	1944	4	US-09-252-991A-16245	Sequence 16245, A	c 810	81	6.0	2517	4	US-09-758-282B-225	Sequence 225, App
c 738	81	6.0	1965	4	US-09-640-958-11	Sequence 11, Appli	c 811	81	6.0	2517	4	US-09-758-282B-227	Sequence 227, App
c 739	81	6.0	2004	4	US-09-902-540-5312	Sequence 5312, Ap	c 812	81	6.0	2517	4	US-09-758-282B-229	Sequence 229, App
c 740	81	6.0	2208	4	US-09-902-540-6293	Sequence 6293, Ap	c 813	81	6.0	2517	4	US-09-758-282B-231	Sequence 231, App
741	81	6.0	2291	4	US-09-902-540-376	Sequence 376, App	c 814	81	6.0	2517	4	US-09-758-282B-233	Sequence 233, App
742	81	6.0	2499	1	US-07-977-434-1	Sequence 1, Appli	c 815	81	6.0	2517	4	US-09-577-304A-62	Sequence 62, Appli

C 816	81	6.0	2517	4	US-09-577-304A-71	Sequence 71, Appl	C 889	80.5	6.0	672	4	US-09-252-991A-9638	Sequence 9638, Ap
C 817	81	6.0	2517	4	US-09-577-304A-82	Sequence 82, Appl	890	80.5	6.0	807	4	US-09-489-039A-139	Sequence 139, App
C 818	81	6.0	2517	4	US-09-577-304A-88	Sequence 88, Appl	891	80.5	6.0	885	4	US-09-902-540-8054	Sequence 8054, Ap
C 819	81	6.0	2517	4	US-09-577-304A-114	Sequence 114, App	892	80.5	6.0	936	4	US-09-489-039A-2270	Sequence 2270, Ap
C 820	81	6.0	2517	4	US-09-577-304A-117	Sequence 117, App	893	80.5	6.0	957	4	US-09-252-991A-3959	Sequence 3959, Ap
C 821	81	6.0	2517	4	US-09-577-304A-120	Sequence 120, App	C 894	80.5	6.0	1005	4	US-09-902-540-5305	Sequence 5305, Ap
C 822	81	6.0	2517	4	US-09-577-304A-123	Sequence 123, App	895	80.5	6.0	1095	4	US-09-902-540-7866	Sequence 7866, Ap
C 823	81	6.0	2517	4	US-09-577-304A-126	Sequence 126, App	C 896	80.5	6.0	1362	4	US-09-252-991A-3943	Sequence 3943, Ap
C 824	81	6.0	2517	4	US-09-577-304A-132	Sequence 132, App	897	80.5	6.0	1449	4	US-09-252-991A-1976	Sequence 1976, Ap
C 825	81	6.0	2517	4	US-09-577-304A-133	Sequence 133, App	C 898	80.5	6.0	1524	4	US-09-807-897-3	Sequence 3, Appli
C 826	81	6.0	2517	4	US-09-577-304A-141	Sequence 141, App	899	80.5	6.0	1596	4	US-09-252-991A-10119	Sequence 10119, A
C 827	81	6.0	2517	4	US-09-577-304A-147	Sequence 147, App	C 900	80.5	6.0	1605	4	US-09-252-991A-10729	Sequence 10729, A
C 828	81	6.0	2517	4	US-09-577-304A-149	Sequence 149, App	C 901	80.5	6.0	1866	2	US-08-648-657-14	Sequence 14, Appl
C 829	81	6.0	2517	4	US-09-577-304A-152	Sequence 152, App	902	80.5	6.0	1818	4	US-09-902-540-4685	Sequence 4685, Ap
C 830	81	6.0	2517	4	US-09-577-304A-168	Sequence 168, App	903	80.5	6.0	1854	4	US-09-902-540-5512	Sequence 5512, Ap
C 831	81	6.0	2517	4	US-09-577-304A-177	Sequence 177, App	904	80.5	6.0	2155	4	US-09-620-312D-65	Sequence 65, Appl
C 832	81	6.0	2517	4	US-09-577-304A-180	Sequence 180, App	C 905	80.5	6.0	2220	2	US-08-864-224-1	Sequence 1, Appli
C 833	81	6.0	2517	4	US-09-577-304A-183	Sequence 183, App	906	80.5	6.0	2220	4	US-09-122-384-1	Sequence 1, Appli
C 834	81	6.0	2517	4	US-09-577-304A-186	Sequence 186, App	C 907	80.5	6.0	2325	4	US-09-252-991A-218	Sequence 218, App
C 835	81	6.0	2517	4	US-09-577-304A-189	Sequence 189, App	908	80.5	6.0	2493	4	US-09-252-991A-5433	Sequence 5433, Ap
C 836	81	6.0	2517	4	US-09-577-304A-199	Sequence 199, App	C 909	80.5	6.0	2505	4	US-09-334-818A-1	Sequence 1, Appli
C 837	81	6.0	2517	4	US-09-577-304A-201	Sequence 201, App	910	80.5	6.0	2538	4	US-09-252-991A-1285	Sequence 1285, Ap
C 838	81	6.0	2517	4	US-09-577-304A-203	Sequence 203, App	C 911	80.5	6.0	2571	4	US-09-252-991A-1279	Sequence 1279, Ap
C 839	81	6.0	2517	4	US-09-577-304A-205	Sequence 205, App	C 912	80.5	6.0	2571	4	US-09-252-991A-8489	Sequence 8489, Ap
C 840	81	6.0	2517	4	US-09-577-304A-217	Sequence 217, App	C 913	80.5	6.0	2784	4	US-09-252-991A-1394	Sequence 1394, App
C 841	81	6.0	2517	4	US-09-577-304A-220	Sequence 220, App	914	80.5	6.0	2946	4	US-09-252-991A-227	Sequence 227, App
C 842	81	6.0	2517	4	US-09-577-304A-225	Sequence 225, App	C 915	80.5	6.0	4284	4	US-09-252-991A-10434	Sequence 10434, A
C 843	81	6.0	2517	4	US-09-577-304A-227	Sequence 227, App	C 916	80.5	6.0	4563	4	US-09-252-991A-4765	Sequence 4765, Ap
C 844	81	6.0	2517	4	US-09-577-304A-229	Sequence 229, App	C 917	80.5	6.0	4631	4	US-09-902-540-720	Sequence 720, App
C 845	81	6.0	2517	4	US-09-577-304A-231	Sequence 231, App	918	80.5	6.0	6794	4	US-09-902-540-736	Sequence 736, App
C 846	81	6.0	2517	4	US-09-577-304A-233	Sequence 233, App	919	80.5	6.0	7160	4	US-09-902-540-821	Sequence 821, App
C 847	81	6.0	2526	4	US-09-758-282B-76	Sequence 76, Appl	C 920	80.5	6.0	7266	3	US-08-713-118-1	Sequence 1, Appli
C 848	81	6.0	2526	4	US-09-758-282B-240	Sequence 240, App	C 921	80.5	6.0	7266	3	US-09-452-007-1	Sequence 1, Appli
C 849	81	6.0	2526	4	US-09-758-282B-262	Sequence 262, App	C 922	80.5	6.0	8614	4	US-09-902-540-787	Sequence 787, App
C 850	81	6.0	2526	4	US-09-577-304A-76	Sequence 76, Appl	C 923	80.5	6.0	11254	4	US-09-902-540-1040	Sequence 1040, Ap
C 851	81	6.0	2526	4	US-09-577-304A-240	Sequence 240, App	C 924	80.5	6.0	11613	1	US-08-484-044-10	Sequence 10, Appl
C 852	81	6.0	2526	4	US-09-577-304A-262	Sequence 262, App	C 925	80.5	6.0	12849	4	US-09-902-540-963	Sequence 963, App
C 853	81	6.0	2626	1	US-08-156-020-1	Sequence 1, Appli	C 926	80.5	6.0	19598	4	US-09-902-540-1143	Sequence 1143, Ap
C 854	81	6.0	2626	1	US-08-156-020-3	Sequence 3, Appli	C 927	80.5	6.0	24754	4	US-09-902-540-1230	Sequence 1230, Ap
C 855	81	6.0	2626	1	US-08-156-020-5	Sequence 5, Appli	C 928	80.5	6.0	25497	4	US-09-902-540-1324	Sequence 1224, Ap
C 856	81	6.0	2626	1	US-08-156-020-7	Sequence 7, Appli	C 929	80.5	6.0	49377	1	US-08-764-233A-1	Sequence 1, Appli
C 857	81	6.0	2626	1	US-08-156-020-9	Sequence 9, Appli	C 930	80.5	6.0	50341	1	US-08-247-901C-1	Sequence 1, Appli
C 858	81	6.0	2626	3	US-08-978-806-1	Sequence 1, Appli	931	80.5	6.0	50341	2	US-09-075-904-1	Sequence 1, Appli
C 859	81	6.0	2727	4	US-09-623-326-3	Sequence 3, Appli	932	80.5	6.0	52297	3	US-09-426-436-1	Sequence 1, Appli
C 860	81	6.0	2727	4	US-09-623-326-4	Sequence 4, Appli	933	80.5	6.0	52297	3	US-08-705-557-1	Sequence 1, Appli
C 861	81	6.0	2733	4	US-09-623-326-1	Sequence 1, Appli	934	80.5	6.0	767577	4	US-09-949-016-12147	Sequence 12147, A
C 862	81	6.0	2733	4	US-09-623-326-2	Sequence 2, Appli	935	80.5	6.0	767577	4	US-09-949-016-17361	Sequence 17361, A
C 863	81	6.0	2763	4	US-09-623-326-5	Sequence 5, Appli	C 936	80.5	6.0	618	4	US-09-489-039A-1035	Sequence 1035, Ap
C 864	81	6.0	2850	4	US-09-623-326-6	Sequence 6, Appli	C 937	80.5	6.0	855	4	US-09-252-991A-9422	Sequence 9422, Ap
C 865	81	6.0	2949	4	US-09-623-326-6	Sequence 6, Appli	C 938	80.5	6.0	969	4	US-09-902-540-9029	Sequence 9029, Ap
C 866	81	6.0	3114	4	US-09-252-991A-225	Sequence 225, App	C 939	80.5	6.0	1008	1	US-08-347-826A-3	Sequence 3, Appli
C 867	81	6.0	3261	4	US-09-252-991A-8480	Sequence 8480, Ap	C 940	80.5	6.0	1101	4	US-09-252-991A-9455	Sequence 9455, Ap
C 868	81	6.0	3345	4	US-09-252-991A-8394	Sequence 8394, Ap	C 941	80.5	6.0	1122	4	US-09-252-991A-8798	Sequence 8798, Ap
C 869	81	6.0	3402	4	US-09-252-991A-1374	Sequence 1374, App	C 942	80.5	6.0	1221	4	US-09-902-540-5071	Sequence 5071, Ap
C 870	81	6.0	3687	4	US-09-252-991A-1193	Sequence 1193, Ap	943	80.5	6.0	1353	4	US-09-902-540-9159	Sequence 9159, Ap
C 871	81	6.0	3864	4	US-09-252-991A-13035	Sequence 13035, A	944	80.5	6.0	1417	4	US-09-904-615-31	Sequence 31, Appl
C 872	81	6.0	3876	4	US-09-252-991A-2933	Sequence 2933, Ap	945	80.5	6.0	1524	4	US-09-489-039A-3444	Sequence 3444, Ap
C 873	81	6.0	4266	4	US-09-252-991A-1234	Sequence 1234, Ap	946	80.5	6.0	1791	4	US-09-252-991A-9892	Sequence 9892, Ap
C 874	81	6.0	5337	4	US-09-902-540-810	Sequence 810, App	947	80.5	6.0	2037	4	US-09-489-039A-4049	Sequence 4049, Ap
C 875	81	6.0	5849	3	US-09-134-246-6	Sequence 6, Appli	948	80.5	6.0	2083	4	US-09-774-528-344	Sequence 344, App
C 876	81	6.0	5849	4	US-09-664-186-6	Sequence 6, Appli	C 949	80.5	6.0	2346	4	US-09-949-016-1979	Sequence 1979, Ap
C 877	81	6.0	6714	1	US-08-021-623C-5	Sequence 5, Appli	C 950	80.5	6.0	2350	4	US-09-949-016-342	Sequence 342, App
C 878	81	6.0	6732	4	US-09-976-594-99	Sequence 99, Appl	C 951	80.5	6.0	2379	4	US-09-252-991A-9252	Sequence 9252, Ap
C 879	81	6.0	8321	4	US-09-902-540-979	Sequence 979, App	C 952	80.5	6.0	3033	4	US-09-724-797-81	Sequence 81, Appl
C 880	81	6.0	10263	4	US-09-902-540-1044	Sequence 1024, App	953	80.5	6.0	3841	4	US-09-902-540-607	Sequence 607, App
C 881	81	6.0	21119	3	US-09-453-702B-111	Sequence 111, App	954	80.5	6.0	3860	4	US-09-902-540-2038	Sequence 2038, App
C 882	81	6.0	30360	4	US-09-949-016-15716	Sequence 15716, A	C 955	80.5	6.0	6401	3	US-09-221-017B-804	Sequence 804, App
C 883	81	6.0	35614	4	US-09-902-540-1259	Sequence 1259, Ap	956	80.5	6.0	9053	4	US-09-902-540-815	Sequence 815, App
C 884	81	6.0	38494	4	US-08-311-731A-24	Sequence 24, Appl	957	80.5	6.0	10280	4	US-09-902-540-980	Sequence 980, App
C 885	81	6.0	38675	4	US-08-311-731A-135	Sequence 135, App	958	80.5	6.0	12865	4	US-09-902-540-1048	Sequence 1048, Ap
C 886	81	6.0	50109	4	US-09-949-016-14112	Sequence 14112, A	C 959	80.5	6.0	17173	4	US-09-902-540-1122	Sequence 1122, Ap
C 887	81	6.0	50937	3	US-09-428-517-1	Sequence 1, Appli	960	80.5	6.0	18324	4	US-09-902-540-1196	Sequence 1196, Ap
C 888	81	6.0	53500	4	US-09-266-965-76	Sequence 76, Appl	C 961	80.5	6.0	26930	4	US-09-902-540-1228	Sequence 1228, Ap

962	80	28194	4	US-09-302-540-1250	Sequence 1250, Ap	1035	79.5	5.9	17245	4	US-09-902-540-1073	Sequence 1073, Ap
963	80	35630	4	US-09-949-016-13832	Sequence 13832, A	1036	79.5	5.9	23233	4	US-09-902-540-1184	Sequence 1184, Ap
964	79.5	786	4	US-09-902-540-5264	Sequence 5264, Ap	1037	79.5	5.9	28762	4	US-09-902-540-1232	Sequence 1232, Ap
965	79.5	828	4	US-09-252-991A-11099	Sequence 11099, A	1038	79.5	5.9	30783	4	US-09-902-540-1358	Sequence 1258, Ap
966	79.5	850	1	US-08-114-461-2	Sequence 2, Appl	c1039	79.5	5.9	34662	4	US-09-902-540-1358	Sequence 1261, Ap
967	79.5	850	1	US-08-192-156-2	Sequence 2, Appl	c1040	79.5	5.9	39113	4	US-09-949-016-15634	Sequence 15634, A
968	79.5	852	1	US-08-370-789-2	Sequence 2, Appl	1041	79.5	5.9	41927	4	US-09-902-540-1268	Sequence 1268, Ap
969	79.5	852	1	US-09-252-991A-10276	Sequence 10276, A	1042	79.5	5.9	193303	4	US-09-497-855A-37	Sequence 37, Appl
970	79.5	882	4	US-09-252-991A-16022	Sequence 16022, A	1043	79.5	5.9	193303	4	US-09-497-855A-44	Sequence 44, Appl
971	79.5	1065	4	US-09-370-767-12332	Sequence 12332, A	c1044	79	5.9	939	4	US-09-252-991A-734	Sequence 734, Appl
972	79.5	1191	4	US-09-302-540-4712	Sequence 4712, Ap	c1045	79	5.9	1122	4	US-09-252-991A-3305	Sequence 3305, Ap
973	79.5	1317	4	US-09-252-991A-10989	Sequence 10989, A	c1046	79	5.9	1161	4	US-09-252-991A-11607	Sequence 11607, A
974	79.5	1359	4	US-09-252-991A-2528	Sequence 2528, Ap	c1047	79	5.9	1174	5	PCT-US95-07554-3	Sequence 3, Appl
975	79.5	1377	4	US-09-489-039A-6783	Sequence 6783, Ap	1048	79	5.9	1194	4	US-09-252-991A-7454	Sequence 7454, Ap
976	79.5	1458	4	US-09-302-540-3540	Sequence 3540, Ap	1049	79	5.9	1209	4	US-09-902-540-6604	Sequence 6604, Ap
977	79.5	1473	4	US-09-252-991A-2391	Sequence 2391, Ap	1050	79	5.9	1221	4	US-09-902-540-7412	Sequence 7412, Ap
978	79.5	1715	1	US-07-847-743B-24	Sequence 24, Appl	1051	79	5.9	1229	4	US-09-252-991A-7020	Sequence 7020, Ap
979	79.5	1715	1	US-08-456-201-24	Sequence 24, Appl	c1052	79	5.9	1263	4	US-09-949-016-5000	Sequence 5000, Ap
980	79.5	1715	1	US-08-456-201-24	Sequence 24, Appl	c1053	79	5.9	1263	4	US-09-252-991A-7692	Sequence 7692, Ap
981	79.5	1715	1	US-08-456-201-24	Sequence 24, Appl	1054	79	5.9	1305	4	US-09-252-991A-11762	Sequence 11762, A
982	79.5	1715	5	PCT-US92-04295A-24	Sequence 24, Appl	1055	79	5.9	1350	4	US-09-252-991A-1330	Sequence 1330, Ap
983	79.5	1731	4	US-09-252-991A-15928	Sequence 15928, A	1056	79	5.9	1488	4	US-09-252-991A-197	Sequence 197, Ap
984	79.5	1872	4	US-09-252-991A-13815	Sequence 13815, A	1057	79	5.9	1560	4	US-09-252-991A-166	Sequence 166, Appl
985	79.5	1964	4	US-09-774-528-308	Sequence 308, Appl	1058	79	5.9	1650	4	US-09-344-510B-9	Sequence 9, Appl
986	79.5	2077	4	US-09-921-099A-16	Sequence 16, Appl	1059	79	5.9	1692	4	US-09-252-991A-7872	Sequence 7872, Ap
987	79.5	2232	4	US-09-489-039A-3902	Sequence 3902, Ap	1060	79	5.9	1800	4	US-07-865-662F-5	Sequence 679, Ap
988	79.5	2431	1	US-07-847-743B-25	Sequence 25, Appl	1061	79	5.9	1816	1	US-07-865-662F-5	Sequence 5, Appl
989	79.5	2431	1	US-08-456-201-25	Sequence 25, Appl	1062	79	5.9	1816	3	US-08-374-219B-5	Sequence 5, Appl
990	79.5	2431	5	PCT-US92-04295A-25	Sequence 25, Appl	1063	79	5.9	1822	1	US-07-865-662F-6	Sequence 6, Appl
991	79.5	2431	5	US-09-849-338-1	Sequence 25, Appl	1064	79	5.9	1822	3	US-08-374-219B-6	Sequence 6, Appl
992	79.5	2469	4	US-10-274-878-1	Sequence 1, Appl	1065	79	5.9	1938	4	US-09-543-681A-3585	Sequence 3585, Ap
993	79.5	2469	4	US-10-274-878-1	Sequence 1, Appl	1066	79	5.9	1995	4	US-09-902-540-9209	Sequence 9209, Ap
994	79.5	2469	4	US-10-697-266-1	Sequence 1, Appl	c1067	79	5.9	2244	1	US-08-476-519-10	Sequence 10, Appl
995	79.5	2472	3	US-08-743-168B-35	Sequence 35, Appl	c1068	79	5.9	2244	5	PCT-US95-09323-10	Sequence 10, Appl
996	79.5	2472	3	US-08-743-168B-37	Sequence 37, Appl	1069	79	5.9	2328	4	US-09-252-991A-5729	Sequence 5729, Ap
997	79.5	2478	4	US-09-252-991A-592	Sequence 592, Appl	c1070	79	5.9	2334	1	US-08-476-519-1	Sequence 1, Appl
998	79.5	2490	1	US-07-847-743B-23	Sequence 23, Appl	c1071	79	5.9	2334	5	PCT-US95-09323-1	Sequence 1, Appl
999	79.5	2490	1	US-08-456-201-23	Sequence 23, Appl	c1072	79	5.9	2418	4	US-09-252-991A-2294	Sequence 2294, Ap
1000	79.5	2490	2	US-08-456-201-23	Sequence 23, Appl	1073	79	5.9	2418	4	US-09-949-016-1694	Sequence 1694, Ap
1001	79.5	2490	5	PCT-US92-04295A-23	Sequence 23, Appl	c1074	79	5.9	2610	4	US-09-252-991A-175	Sequence 175, Appl
1002	79.5	2502	4	US-09-252-991A-15767	Sequence 15767, A	1075	79	5.9	2817	4	US-09-252-991A-7311	Sequence 7311, Ap
1003	79.5	2517	4	US-09-758-282B-144	Sequence 144, Ap	c1076	79	5.9	2880	4	US-09-252-991A-7187	Sequence 7187, Ap
1004	79.5	2517	4	US-09-577-304A-144	Sequence 144, Ap	c1077	79	5.9	2943	4	US-09-379-530B-3	Sequence 3, Appl
1005	79.5	2742	4	US-09-252-991A-5556	Sequence 5556, Ap	1078	79	5.9	3113	4	US-09-902-540-500	Sequence 500, Appl
1006	79.5	2778	4	US-09-252-991A-10486	Sequence 10486, A	1079	79	5.9	3134	1	US-07-865-662F-7	Sequence 7, Appl
1007	79.5	2825	4	US-09-949-016-1895	Sequence 1895, Ap	1080	79	5.9	3134	3	US-08-374-219B-7	Sequence 7, Appl
1008	79.5	3293	2	US-08-442-809A-75	Sequence 75, Appl	c1081	79	5.9	3373	1	US-08-273-411-2	Sequence 2, Appl
1009	79.5	3321	4	US-09-252-991A-5668	Sequence 5668, Ap	c1082	79	5.9	3374	4	US-09-949-016-5482	Sequence 5482, Ap
1010	79.5	3339	4	US-09-252-991A-10685	Sequence 10685, A	c1083	79	5.9	4230	4	US-09-252-991A-5711	Sequence 5711, Ap
1011	79.5	4824	4	US-09-902-540-2892	Sequence 2892, Ap	1084	79	5.9	4941	4	US-09-252-991A-5741	Sequence 5741, Ap
1012	79.5	5499	4	US-09-902-540-2892	Sequence 2892, Ap	1085	79	5.9	5001	4	US-09-902-540-8618	Sequence 8618, Ap
1013	79.5	6131	4	US-09-949-016-2451	Sequence 2451, Ap	1086	79	5.9	5032	4	US-09-344-510B-8	Sequence 8, Appl
1014	79.5	6250	4	US-09-949-016-13222	Sequence 13222, A	c1087	79	5.9	5464	4	US-09-902-540-717	Sequence 717, Appl
1015	79.5	6575	3	US-08-949-386-3	Sequence 3, Appl	1088	79	5.9	5630	4	US-09-902-540-764	Sequence 764, Appl
1016	79.5	6575	3	US-08-450-562-3	Sequence 3, Appl	1089	79	5.9	5743	4	US-09-949-016-12687	Sequence 12687, A
1017	79.5	6575	3	US-08-984-709A-3	Sequence 3, Appl	1090	79	5.9	5743	4	US-09-949-016-14451	Sequence 14451, A
1018	79.5	6575	3	US-08-450-272-3	Sequence 3, Appl	1091	79	5.9	5825	4	US-09-949-016-4382	Sequence 4382, Ap
1019	79.5	6575	3	US-08-450-273-3	Sequence 3, Appl	1092	79	5.9	5878	4	US-09-949-016-939	Sequence 939, Appl
1020	79.5	6725	3	US-08-949-386-36	Sequence 36, Appl	c1093	79	5.9	6119	4	US-09-902-540-713	Sequence 713, Appl
1021	79.5	6725	3	US-08-450-562-36	Sequence 36, Appl	1094	79	5.9	6975	4	US-09-230-652-1	Sequence 1, Appl
1022	79.5	6725	3	US-08-984-709A-36	Sequence 36, Appl	1095	79	5.9	8091	4	US-09-902-540-2386	Sequence 2386, Ap
1023	79.5	6725	3	US-08-450-272-36	Sequence 36, Appl	c1096	79	5.9	8174	1	US-07-914-281-5	Sequence 5, Appl
1024	79.5	6725	4	US-08-450-273-36	Sequence 36, Appl	c1097	79	5.9	8174	1	US-08-393-246-5	Sequence 5, Appl
1025	78.5	9839	4	US-09-902-540-996	Sequence 996, Appl	c1098	79	5.9	8174	1	US-08-525-058A-5	Sequence 5, Appl
c1026	79.5	11220	4	US-09-949-016-5061	Sequence 5061, Ap	c1099	79	5.9	8174	2	US-08-696-731-5	Sequence 5, Appl
1027	79.5	11706	4	US-09-902-540-1038	Sequence 1038, Ap	c1100	79	5.9	8174	3	US-09-042-531-5	Sequence 5, Appl
1028	79.5	14382	4	US-09-902-540-1145	Sequence 1145, Ap	c1101	79	5.9	8174	5	PCT-US91-00899-3	Sequence 3, Appl
1029	79.5	15872	3	US-09-105-537-1	Sequence 1, Appl	1102	79	5.9	8257	3	US-09-484-970B-65	Sequence 65, Appl
1030	79.5	15872	4	US-09-091-609-1	Sequence 1, Appl	c1103	79	5.9	8580	4	US-09-949-016-17224	Sequence 17224, A
1031	79.5	15872	4	US-09-091-609-3	Sequence 3, Appl	1104	79	5.9	10301	4	US-09-902-540-985	Sequence 985, Appl
c1032	79.5	15923	4	US-09-902-540-1095	Sequence 1095, Ap	1105	79	5.9	11101	4	US-09-902-540-1005	Sequence 1005, Ap
1033	79.5	16187	4	US-09-902-540-1093	Sequence 1093, Ap	c1106	79	5.9	11276	4	US-09-902-540-1036	Sequence 1034, Ap
1034	79.5	17228	4	US-09-902-540-1170	Sequence 1170, Ap	c1107	79	5.9	12183	4	US-09-902-540-1066	Sequence 1066, Ap

1108	79	5.9	13332	4	US-09-902-540-1047	Sequence 1047, Ap	1181	78.5	5.8	11873	2	US-08-970-269A-32	Sequence 32, Appl
1109	79	5.9	14158	4	US-09-902-540-1069	Sequence 1069, Ap	1182	78.5	5.8	11873	3	US-09-407-562-32	Sequence 32, Appl
1110	79	5.9	14570	4	US-09-902-540-1012	Sequence 1012, Ap	1183	78.5	5.8	11878	2	US-08-970-269A-31	Sequence 31, Appl
1111	79	5.9	15840	4	US-09-902-540-1134	Sequence 1134, Ap	1184	78.5	5.8	11878	3	US-09-407-562-31	Sequence 31, Appl
1112	79	5.9	16080	4	US-09-724-566A-48	Sequence 48, Appl	1185	78.5	5.8	12898	4	US-09-902-540-1000	Sequence 1000, Ap
1113	79	5.9	16080	4	US-09-471-669A-48	Sequence 48, Appl	1186	78.5	5.8	14823	4	US-09-902-540-1087	Sequence 1087, Ap
1114	79	5.9	17315	4	US-09-902-540-1103	Sequence 1103, Ap	1187	78.5	5.8	15447	4	US-09-902-540-1100	Sequence 1100, Ap
1115	79	5.9	19222	4	US-09-902-540-1192	Sequence 1192, Ap	1188	78.5	5.8	15482	4	US-09-902-540-1067	Sequence 1067, Ap
1116	79	5.9	20113	4	US-09-902-540-1173	Sequence 1173, Ap	1189	78.5	5.8	15666	4	US-09-949-016-15929	Sequence 15929, A
1117	79	5.9	29103	4	US-09-902-540-1236	Sequence 1236, Ap	1190	78.5	5.8	33230	4	US-09-949-016-16732	Sequence 16732, A
1118	79	5.9	29977	4	US-09-949-016-17452	Sequence 17452, A	1191	78.5	5.8	34001	4	US-09-596-002-18	Sequence 18, Appl
1119	79	5.9	34446	3	US-09-103-330-35	Sequence 35, Appl	1192	78.5	5.8	152582	4	US-09-949-016-12086	Sequence 12086, A
1120	79	5.9	34741	4	US-09-949-016-12475	Sequence 12475, A	1193	78.5	5.8	152583	4	US-09-949-016-17390	Sequence 17390, A
1121	79	5.9	34745	4	US-09-949-016-16024	Sequence 16024, A	1194	78.5	5.8	152583	4	US-09-949-016-17391	Sequence 17391, A
1122	79	5.9	45314	4	US-09-949-016-14927	Sequence 14927, A	1195	78.5	5.8	202111	4	US-09-949-016-13877	Sequence 13877, A
1123	79	5.9	60990	4	US-09-949-016-14080	Sequence 14080, A	1196	78	5.8	434	4	US-09-513-999C-2126	Sequence 2126, Ap
1124	79	5.9	69701	4	US-09-949-016-14187	Sequence 14187, A	1197	78	5.8	477	4	US-09-621-976-18886	Sequence 18886, A
1125	79	5.9	73308	4	US-09-949-016-16326	Sequence 16326, A	1198	78	5.8	601	4	US-09-949-016-17924	Sequence 17924, A
1126	79	5.9	106315	4	US-09-949-016-16613	Sequence 16613, A	1199	78	5.8	601	4	US-09-949-016-17678	Sequence 17678, A
1127	79	5.9	137000	4	US-10-172-911-11	Sequence 11, Appl	1200	78	5.8	651	4	US-09-251-991A-11549	Sequence 11549, A
1128	79	5.9	1830121	4	US-09-557-884-1	Sequence 1, Appl	1201	78	5.8	732	4	US-09-252-991A-9444	Sequence 9444, Ap
1129	79	5.9	1830121	4	US-09-643-990A-1	Sequence 1, Appl	1202	78	5.8	735	4	US-09-328-352-1496	Sequence 1496, Ap
1130	78.5	5.8	601	4	US-09-949-016-148878	Sequence 148878, A	1203	78	5.8	735	4	US-09-328-352-1496	Sequence 1496, Ap
1131	78.5	5.8	618	4	US-09-902-540-4243	Sequence 4243, Ap	1204	78	5.8	756	4	US-09-252-991A-216	Sequence 216, Ap
1132	78.5	5.8	681	4	US-09-252-991A-3852	Sequence 3852, Ap	1205	78	5.8	768	4	US-09-902-540-5226	Sequence 5226, Ap
1133	78.5	5.8	791	3	US-08-858-207A-219	Sequence 219, Ap	1206	78	5.8	915	4	US-09-252-991A-3133	Sequence 3133, Ap
1134	78.5	5.8	801	4	US-09-489-039A-5911	Sequence 5911, Ap	1207	78	5.8	933	4	US-09-252-991A-12792	Sequence 12792, A
1135	78.5	5.8	831	4	US-09-252-991A-5052	Sequence 5052, Ap	1208	78	5.8	963	4	US-09-902-540-3236	Sequence 3236, Ap
1136	78.5	5.8	933	4	US-09-252-991A-3415	Sequence 3415, Ap	1209	78	5.8	981	4	US-09-252-991A-431	Sequence 431, Ap
1137	78.5	5.8	1014	4	US-09-252-991A-195	Sequence 195, Ap	1210	78	5.8	993	4	US-09-252-991A-8950	Sequence 8950, Ap
1138	78.5	5.8	1245	4	US-09-252-991A-5535	Sequence 5535, Ap	1211	78	5.8	1077	4	US-09-902-540-8685	Sequence 8685, Ap
1139	78.5	5.8	1488	4	US-09-023-655-880	Sequence 880, Ap	1212	78	5.8	1115	4	US-09-943-016-539	Sequence 539, Ap
1140	78.5	5.8	1527	4	US-09-244-111-7	Sequence 7, Appl	1213	78	5.8	1188	4	US-09-902-540-5270	Sequence 5270, Ap
1141	78.5	5.8	1546	3	US-09-383-318A-1	Sequence 1, Appl	1214	78	5.8	1199	1	US-08-395-800A-5	Sequence 5, Appl1
1142	78.5	5.8	1557	4	US-09-902-540-8222	Sequence 8222, Ap	1215	78	5.8	1305	4	US-09-252-991A-9360	Sequence 9360, Ap
1143	78.5	5.8	1563	4	US-09-902-540-4269	Sequence 4269, Ap	1216	78	5.8	1308	4	US-09-902-540-8199	Sequence 8199, Ap
1144	78.5	5.8	1626	4	US-09-902-540-200	Sequence 200, Ap	1217	78	5.8	1335	4	US-09-252-991A-1685	Sequence 1685, Ap
1145	78.5	5.8	1650	4	US-09-252-991A-3338	Sequence 3338, Ap	1218	78	5.8	1407	4	US-09-252-991A-15866	Sequence 15866, A
1146	78.5	5.8	1695	4	US-09-252-991A-1686	Sequence 1686, Ap	1219	78	5.8	1461	4	US-09-398-522-113	Sequence 113, Ap
1147	78.5	5.8	1740	4	US-09-252-991A-1492	Sequence 1492, Ap	1220	78	5.8	1638	4	US-09-902-540-8744	Sequence 8744, Ap
1148	78.5	5.8	1743	4	US-09-949-016-945	Sequence 945, Ap	1221	78	5.8	1644	4	US-09-252-991A-6563	Sequence 6563, Ap
1149	78.5	5.8	1743	4	US-09-949-016-2709	Sequence 2709, Ap	1222	78	5.8	1708	4	US-09-902-540-5058	Sequence 5058, Ap
1150	78.5	5.8	1831	4	US-09-799-451-646	Sequence 646, Ap	1223	78	5.8	1710	4	US-09-252-991A-10677	Sequence 10677, A
1151	78.5	5.8	1869	4	US-09-252-991A-3231	Sequence 3231, Ap	1224	78	5.8	1731	4	US-09-252-991A-15928	Sequence 15928, A
1152	78.5	5.8	1901	4	US-09-902-540-6375	Sequence 6375, Ap	1225	78	5.8	1791	4	US-09-252-991A-6662	Sequence 6662, Ap
1153	78.5	5.8	1986	4	US-09-252-991A-1654	Sequence 1654, Ap	1226	78	5.8	2163	4	US-09-252-991A-3010	Sequence 3010, Ap
1154	78.5	5.8	2054	4	US-09-902-540-418	Sequence 418, Ap	1227	78	5.8	2226	4	US-09-252-991A-10491	Sequence 10491, A
1155	78.5	5.8	2166	2	US-08-408-095-30	Sequence 30, Appl	1228	78	5.8	2230	4	US-09-902-540-6807	Sequence 6807, Ap
1156	78.5	5.8	2283	4	US-09-252-991A-3298	Sequence 3298, Ap	1229	78	5.8	2290	4	US-09-907-794A-72	Sequence 72, Appl
1157	78.5	5.8	2341	4	US-09-902-540-395	Sequence 395, Ap	1230	78	5.8	2290	4	US-09-905-125A-72	Sequence 72, Appl
1158	78.5	5.8	2499	4	US-09-758-282B-51	Sequence 51, Appl	1231	78	5.8	2290	4	US-09-902-775A-72	Sequence 72, Appl
1159	78.5	5.8	2499	4	US-09-758-282B-250	Sequence 250, Ap	1232	78	5.8	2290	4	US-09-906-700-72	Sequence 72, Appl
1160	78.5	5.8	2499	4	US-09-577-304A-51	Sequence 51, Appl	1233	78	5.8	2290	4	US-09-903-603A-72	Sequence 72, Appl
1161	78.5	5.8	2499	4	US-09-577-304A-250	Sequence 250, Ap	1234	78	5.8	2290	4	US-09-904-920A-72	Sequence 72, Appl
1162	78.5	5.8	2511	4	US-09-252-991A-9494	Sequence 9494, Ap	1235	78	5.8	2290	4	US-09-909-064-72	Sequence 72, Appl
1163	78.5	5.8	2514	4	US-09-758-282B-260	Sequence 260, Ap	1236	78	5.8	2290	4	US-09-905-381A-72	Sequence 72, Appl
1164	78.5	5.8	2514	4	US-09-758-282B-264	Sequence 264, Ap	1237	78	5.8	2348	4	US-09-618-72	Sequence 42, Appl
1165	78.5	5.8	2514	4	US-09-577-304A-260	Sequence 260, Ap	1238	78	5.8	2348	4	US-09-724-566A-44	Sequence 44, Appl
1166	78.5	5.8	2514	4	US-09-577-304A-264	Sequence 264, Ap	1239	78	5.8	2348	4	US-09-471-669A-42	Sequence 42, Appl
1167	78.5	5.8	2583	4	US-09-252-991A-9541	Sequence 9541, Ap	1240	78	5.8	2348	4	US-09-471-669A-44	Sequence 44, Appl
1168	78.5	5.8	2911	3	US-09-171-710-1	Sequence 1, Appl	1241	78	5.8	2502	4	US-09-252-991A-15767	Sequence 15767, A
1169	78.5	5.8	3024	1	US-07-923-976-7	Sequence 7, Appl	1242	78	5.8	2505	2	US-08-757-653-187	Sequence 187, Ap
1170	78.5	5.8	3264	4	US-09-252-991A-12013	Sequence 12013, A	1243	78	5.8	2505	2	US-08-757-653-189	Sequence 189, Ap
1171	78.5	5.8	3279	4	US-09-252-991A-11905	Sequence 11905, A	1244	78	5.8	2505	2	US-08-823-516-68	Sequence 68, Appl
1172	78.5	5.8	3279	4	US-09-902-540-7318	Sequence 7318, Ap	1245	78	5.8	2505	2	US-08-823-516-70	Sequence 70, Appl
1173	78.5	5.8	3625	4	US-09-023-655-1180	Sequence 1180, Ap	1246	78	5.8	2505	3	US-08-759-038-139	Sequence 129, Ap
1174	78.5	5.8	3702	4	US-09-252-991A-6666	Sequence 6666, Ap	1247	78	5.8	2505	3	US-08-759-038-131	Sequence 131, Ap
1175	78.5	5.8	3771	4	US-09-902-540-559	Sequence 559, Ap	1248	78	5.8	2505	3	US-08-758-314-139	Sequence 129, Ap
1176	78.5	5.8	4632	4	US-09-902-540-8368	Sequence 8368, Ap	1249	78	5.8	2505	3	US-08-758-314-131	Sequence 131, Ap
1177	78.5	5.8	4704	4	US-09-252-991A-3906	Sequence 3906, Ap	1250	78	5.8	2505	4	US-09-684-938-129	Sequence 129, Ap
1178	78.5	5.8	5318	4	US-09-902-540-849	Sequence 849, Ap	1251	78	5.8	2505	4	US-09-684-938-131	Sequence 131, Ap
1179	78.5	5.8	5656	4	US-09-902-540-694	Sequence 694, Ap	1252	78	5.8	2505	4	US-09-308-825A-129	Sequence 129, Ap
1180	78.5	5.8	5868	4	US-09-949-016-16884	Sequence 16884, A	1253	78	5.8	2505	4	US-09-308-825A-131	Sequence 131, Ap

c1254	78	5.8	2505	4	US-09-940-244-68	Sequence 68, Appl	c1327	77.5	5.8	2013	4	US-09-903-540-5920	Sequence 5920, Ap
c1255	78	5.8	2505	4	US-09-940-244-70	Sequence 70, Appl	1328	77.5	5.8	2039	4	US-09-903-540-1179	Sequence 179, App
c1256	78	5.8	2517	4	US-09-758-282B-171	Sequence 171, Appl	1329	77.5	5.8	2153	2	US-08-577-492-31	Sequence 31, Appl
c1257	78	5.8	2517	4	US-09-577-304A-171	Sequence 171, Appl	1330	77.5	5.8	2153	3	US-09-070-630-31	Sequence 31, Appl
c1258	78	5.8	2781	4	US-08-765-907A-1	Sequence 15980, A	c1331	77.5	5.8	2377	4	US-09-920-668-3	Sequence 3, Appl
c1259	78	5.8	2888	3	US-08-765-907A-1	Sequence 1, Appl	1332	77.5	5.8	2658	4	US-09-252-991A-9558	Sequence 9558, Ap
c1260	78	5.8	2888	4	US-09-987-614A-1	Sequence 1, Appl	c1333	77.5	5.8	2676	4	US-09-252-991A-14053	Sequence 14053, A
c1261	78	5.8	2952	4	US-09-252-991A-16297	Sequence 16297, A	c1334	77.5	5.8	2703	4	US-09-903-540-8634	Sequence 8634, Ap
c1262	78	5.8	3294	4	US-09-252-991A-6008	Sequence 6008, Ap	c1335	77.5	5.8	2733	4	US-09-902-540-3104	Sequence 3104, Ap
c1263	78	5.8	3486	4	US-09-252-991A-6301	Sequence 6301, Ap	1336	77.5	5.8	2799	4	US-09-252-991A-9604	Sequence 9604, Ap
c1264	78	5.8	3648	4	US-09-902-540-624	Sequence 624, Appl	c1337	77.5	5.8	2822	4	US-09-949-016-1184	Sequence 1184, Ap
c1265	78	5.8	4239	4	US-09-815-048-1	Sequence 1, Appl	1338	77.5	5.8	2853	4	US-09-949-016-4282	Sequence 4282, Ap
c1266	78	5.8	4493	4	US-09-949-016-14034	Sequence 14034, A	c1339	77.5	5.8	2874	4	US-09-252-991A-14101	Sequence 14101, A
c1267	78	5.8	4800	4	US-09-902-540-562	Sequence 562, Appl	1340	77.5	5.8	3331	4	US-09-976-594-131	Sequence 131, App
c1268	78	5.8	4835	3	US-08-976-259-58	Sequence 58, Appl	c1341	77.5	5.8	3402	4	US-09-252-991A-15560	Sequence 15560, A
c1269	78	5.8	4835	4	US-09-956-004-58	Sequence 58, Appl	c1342	77.5	5.8	3606	4	US-09-252-991A-15688	Sequence 15688, A
c1270	78	5.8	6625	4	US-09-949-016-13534	Sequence 13534, A	1343	77.5	5.8	3846	4	US-09-903-540-2520	Sequence 2520, Ap
c1271	78	5.8	7419	4	US-09-252-991A-481	Sequence 481, Appl	c1344	77.5	5.8	4084	4	US-09-903-540-697	Sequence 697, App
c1272	78	5.8	7449	4	US-09-252-991A-396	Sequence 396, Appl	1345	77.5	5.8	4530	4	US-09-799-451-881	Sequence 881, App
c1273	78	5.8	7760	4	US-09-902-540-845	Sequence 845, Appl	c1346	77.5	5.8	6063	4	US-09-902-540-807	Sequence 807, App
c1274	78	5.8	12950	4	US-09-902-540-1036	Sequence 1036, Appl	c1347	77.5	5.8	6599	4	US-09-902-540-724	Sequence 724, App
c1275	78	5.8	14431	4	US-09-902-540-1149	Sequence 1149, Appl	1348	77.5	5.8	8320	4	US-09-902-540-913	Sequence 913, App
c1276	78	5.8	16265	4	US-09-902-540-1126	Sequence 1126, Appl	1349	77.5	5.8	8931	3	US-09-028-934-28	Sequence 28, Appl
c1277	78	5.8	16427	4	US-09-902-540-1160	Sequence 1160, Appl	c1350	77.5	5.8	9335	4	US-09-902-540-940	Sequence 940, App
c1278	78	5.8	17348	4	US-09-949-016-17403	Sequence 17403, A	1351	77.5	5.8	11382	4	US-09-902-540-904	Sequence 904, App
c1279	78	5.8	17592	4	US-09-902-540-1138	Sequence 1138, Appl	c1352	77.5	5.8	14464	4	US-09-902-540-1135	Sequence 1135, App
c1280	78	5.8	17612	3	US-08-911-853-29	Sequence 29, Appl	c1353	77.5	5.8	15499	4	US-09-902-540-1140	Sequence 1140, App
c1281	78	5.8	17612	3	US-09-479-409-29	Sequence 29, Appl	c1354	77.5	5.8	17503	4	US-09-902-540-1114	Sequence 1114, App
c1282	78	5.8	17612	3	US-09-479-453-29	Sequence 29, Appl	1355	77.5	5.8	23677	4	US-09-902-540-1218	Sequence 1218, App
c1283	78	5.8	18609	3	US-08-943-731-1	Sequence 1, Appl	c1356	77.5	5.8	26289	4	US-09-902-540-1210	Sequence 1210, App
c1284	78	5.8	19726	4	US-09-902-540-1164	Sequence 1164, Appl	c1357	77.5	5.8	36470	4	US-08-311-731A-123	Sequence 123, App
c1285	78	5.8	24741	4	US-09-949-016-15547	Sequence 15547, A	1358	77.5	5.8	64518	4	US-09-949-016-17289	Sequence 17289, A
c1286	78	5.8	27490	4	US-09-902-540-1227	Sequence 1227, Appl	1359	77.5	5.8	119981	4	US-09-949-016-11844	Sequence 11844, A
c1287	78	5.8	28257	4	US-09-949-016-13076	Sequence 13076, A	1360	77.5	5.8	119982	4	US-09-949-016-13606	Sequence 13606, A
c1288	78	5.8	30783	4	US-09-902-540-1258	Sequence 1258, Appl	c1361	77	5.7	601	4	US-09-949-016-91732	Sequence 91732, A
c1289	78	5.8	37861	4	US-09-949-016-15872	Sequence 16872, A	c1362	77	5.7	601	4	US-09-949-016-109219	Sequence 109219, A
c1290	78	5.8	41106	4	US-09-949-016-15796	Sequence 15796, A	c1363	77	5.7	601	4	US-09-949-016-109220	Sequence 109220, A
c1291	78	5.8	43717	4	US-09-949-016-16821	Sequence 16821, A	c1364	77	5.7	601	4	US-09-949-016-194673	Sequence 194673, A
c1292	78	5.8	50725	4	US-09-902-540-1271	Sequence 1271, Appl	c1365	77	5.7	645	4	US-09-252-991A-7665	Sequence 7665, Ap
c1293	78	5.8	197336	4	US-09-949-016-12881	Sequence 12881, A	c1366	77	5.7	669	4	US-09-252-991A-5618	Sequence 5618, Ap
c1294	78	5.8	197337	4	US-09-949-016-14376	Sequence 14376, A	1367	77	5.7	810	4	US-09-540-236-319	Sequence 319, App
c1295	78	5.8	203475	4	US-09-949-016-14516	Sequence 14516, A	c1368	77	5.7	810	4	US-09-902-540-3599	Sequence 3599, Ap
c1296	78	5.8	203475	4	US-09-949-016-14517	Sequence 14517, A	1369	77	5.7	990	4	US-09-902-540-4759	Sequence 4759, Ap
c1297	78	5.8	203475	4	US-09-949-016-14518	Sequence 14518, A	c1370	77	5.7	1005	4	US-09-902-540-5305	Sequence 5305, Ap
c1298	78	5.8	203475	4	US-09-949-016-14519	Sequence 14519, A	c1371	77	5.7	1032	4	US-09-252-991A-748	Sequence 748, App
c1299	78	5.8	203475	4	US-09-949-016-17226	Sequence 17226, A	c1372	77	5.7	1128	4	US-09-252-991A-9049	Sequence 9049, Ap
c1300	78	5.8	203475	4	US-09-949-016-17227	Sequence 17227, A	c1373	77	5.7	1152	4	US-09-252-991A-8964	Sequence 8964, Ap
c1301	78	5.8	203475	4	US-09-949-016-17228	Sequence 17228, A	c1374	77	5.7	1257	4	US-09-252-991A-15524	Sequence 15524, A
c1302	78	5.8	203475	4	US-09-949-016-17229	Sequence 17229, A	1375	77	5.7	1461	4	US-09-902-540-7265	Sequence 7265, Ap
c1303	78	5.8	234288	4	US-09-949-016-17272	Sequence 17272, A	1376	77	5.7	1582	3	US-09-180-109A-32	Sequence 32, Appl
c1304	77.5	5.8	429	4	US-09-252-991A-12815	Sequence 12815, A	1377	77	5.7	1585	4	US-09-949-016-617	Sequence 617, App
c1305	77.5	5.8	477	4	US-09-902-540-4517	Sequence 4517, Appl	1378	77	5.7	1587	4	US-09-023-655-1192	Sequence 1192, App
c1306	77.5	5.8	654	4	US-09-489-039A-618	Sequence 618, Appl	c1379	77	5.7	1686	2	US-08-648-657-1	Sequence 1, Appl
c1307	77.5	5.8	894	4	US-09-252-991A-6276	Sequence 6276, Appl	c1380	77	5.7	1689	2	US-08-648-657-2	Sequence 2, Appl
c1308	77.5	5.8	1041	4	US-09-252-991A-4916	Sequence 4916, Appl	1381	77	5.7	1776	4	US-09-902-540-7046	Sequence 7046, Ap
c1309	77.5	5.8	1101	4	US-09-902-540-4233	Sequence 4233, Appl	1382	77	5.7	1836	4	US-09-252-991A-1026	Sequence 1026, Ap
c1310	77.5	5.8	1155	1	US-08-434-151-1	Sequence 1, Appl	c1383	77	5.7	1848	1	US-08-635-137-1	Sequence 1, Appl
c1311	77.5	5.8	1155	1	US-08-208-889A-1	Sequence 1, Appl	c1384	77	5.7	1848	3	US-09-136-981-1	Sequence 1, Appl
c1312	77.5	5.8	1155	2	US-08-433-271-1	Sequence 1, Appl	c1385	77	5.7	1965	4	US-09-252-991A-8852	Sequence 8852, Ap
c1313	77.5	5.8	1155	2	US-08-715-259-1	Sequence 1, Appl	1386	77	5.7	2070	4	US-09-902-540-9138	Sequence 9138, Ap
c1314	77.5	5.8	1200	4	US-09-252-991A-5386	Sequence 5386, Appl	c1387	77	5.7	2157	4	US-09-252-991A-9125	Sequence 9125, Ap
c1315	77.5	5.8	1227	4	US-09-489-039A-5352	Sequence 5352, Appl	1388	77	5.7	2197	4	US-09-252-991A-8738	Sequence 8738, Ap
c1316	77.5	5.8	1266	4	US-09-252-991A-15755	Sequence 15755, A	c1389	77	5.7	2415	4	US-09-252-991A-7480	Sequence 7480, Ap
c1317	77.5	5.8	1451	4	US-09-902-540-7976	Sequence 7976, Appl	1390	77	5.7	2588	2	US-08-796-414B-6	Sequence 6, Appl
c1318	77.5	5.8	1491	4	US-09-252-991A-14743	Sequence 14743, A	1391	77	5.7	2667	4	US-09-252-991A-7216	Sequence 7216, Ap
c1319	77.5	5.8	1500	4	US-09-252-991A-4920	Sequence 4920, Appl	1392	77	5.7	2689	1	US-08-465-795-2	Sequence 2, Appl
c1320	77.5	5.8	1536	4	US-09-902-540-8768	Sequence 8768, Appl	c1393	77	5.7	2865	4	US-09-252-991A-4675	Sequence 4675, Ap
c1321	77.5	5.8	1539	4	US-09-252-991A-14886	Sequence 14886, Appl	1394	77	5.7	2872	3	US-09-327-487A-2	Sequence 2, Appl
c1322	77.5	5.8	1599	4	US-09-252-991A-5850	Sequence 5850, Appl	1395	77	5.7	3195	4	US-09-252-991A-937	Sequence 937, App
c1323	77.5	5.8	1614	4	US-09-252-991A-15010	Sequence 15010, A	c1396	77	5.7	3739	4	US-09-902-540-477	Sequence 477, App
c1324	77.5	5.8	1620	4	US-09-252-991A-4922	Sequence 4922, Appl	1397	77	5.7	3837	4	US-09-902-540-9503	Sequence 9503, Ap
c1325	77.5	5.8	1863	4	US-09-252-991A-5819	Sequence 5819, Appl	1398	77	5.7	4324	4	US-09-902-540-684	Sequence 684, App
c1326	77.5	5.8	1992	4	US-09-252-991A-5693	Sequence 5693, Appl	c1399	77	5.7	4497	4	US-09-252-991A-14663	Sequence 14663, A





```
Db 244 CTGGCGGAAACCCCGTGTATGATCCCGCTGCGGAGGAAACCGGAAAGCTGCCAACGCA 303
Qy 83 AspSerMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeuLeuGln 102
Db 304 CGCTGGCAGATCGCCCGGAGCAGGCGCCAGTTTCATCGCCTTGCTGTACCTGATCGGC 363
Qy 103 AlaLysLysAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeuAlaLeu 122
Db 364 GCGCGCGCGGCTGAGGTGGCAGCTTCACCGGCTACAGCGCTGTGCATGGCTACC 423
Qy 123 AlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnProGluLeu 142
Db 424 GCCCTGGCGAGCAGGCGGTCTTACCTGTGGACCTGCCCGGAGCTACCACTGACT 483
Qy 143 GlyArgProLeuTrpArgGlnAlaGluAlaGluHisLysLysLeuAspLeuArgLeuLysPro 162
Db 484 GCGCGCGCTACTTGGCGGCGAAGCGCTGTGAGGAGCGCATCGAGCTACGCTCGGGGCC 543
Qy 163 AlaLeuGluThrLeuAspGluLeuLeuAlaAlaGlyGluAlaGlyThrPheAspValAla 182
Db 544 GCGCTGGAAACCTGGCTGCTGTCTGACGAGGCTGCGCGGAGTTCCACCTGGCC 603
Qy 183 ValValAspAlaAspLysGluAsnCysSerAlaTyrGluArgCysLeuGlnLeuLeu 202
Db 604 TTCATCGACGCGCAGACAGGCCAACTACCCCGAATACCTGGAGCGCGCTGGCGCTGGTG 663
Qy 203 ArgProGlyGlyLeuLeuAlaValLeuArgValLeuTrpArgGlyLysValLeu----- 220
Db 664 CGCCACGGTGGCTGTGCTTTTCGACAACTGCTGTGGAGCGCGGCTGCTCGAAGCG 723
Qy 221 GlnProProLysGlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArg 240
Db 724 CAGCCGAGAGTGGGATACCGCGGC-----ATCCACAGCTCAACTCGCGCTGAAG 777
Qy 241 ArgAspValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPhe 260
Db 778 AACGACGCGCGGTGGACTACTCGTGTGCTGCGGATCGGCGAGCGGCTGAGCTGTCTGCG 837
Qy 261 Lys 261
Db 838 AAG 840
```

## RESULT 2

```
US-09-452-239-21
; Sequence 21, Application US/09452239
; Patent No. 6465229
; GENERAL INFORMATION:
; APPLICANT: Rafaleki, Antoni J.
; APPLICANT: Fader, Gary M.
; APPLICANT: Cahoon, Rebecca E.
; TITLE OF INVENTION: Plant Caffeoyl-CoA O-Methyltransferase
; FILE REFERENCE: BBI284 US NA
; CURRENT APPLICATION NUMBER: US/09/452,239
; EARLIER FILING DATE: 1999-12-01
; EARLIER FILING DATE: 1998-December-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 21
; LENGTH: 980
; TYPE: DNA
; ORGANISM: Glycine max
US-09-452-239-21
```

```
Alignment Scores:
Pred. No.: 7,63e-37 Length: 980
Score: 405.50 Matches: 92
Percent Similarity: 57.2% Conservative: 45
Best Local Similarity: 38.1% Mismatches: 93
Query Match: 30.1% Indels: 10
DB: 3 Gaps: 3
```

```
US-10-017-407A-306 (1-262) x US-09-452-239-21 (1-980)
Qy 32 GlyArgCysProTrpArgGlyArgGluGlnCysLeuLeuProGluAs 51
Db 48 GGAAACAGAAACACCACTTTCGGCATCAAGATCTCGTCAACAAGCTCTCTTCAGAG 107
Qy 51 pSerArgLeuTrpGlnTyrLeuLeuSerArgSerMet-----ArgGluHisProAlaLe 69
Db 108 TGATGCATCTATCATATATATCTTGAAACCACTGTCTTCAAGAGAGCAGAGTGCTT 167
Qy 69 uArgSerLeuArgLeuLeuThrLeuGluGlnProGlnGlyAspSerMetThrCysGln 89
Db 168 GAAAGAGATACCAAGATGACTGCAAAACACCCACTGAACATCATCGCAACACCAAGCAG 227
Qy 89 uGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeuLeuGlnAlaLysLysAlaLeuAspLe 109
Db 228 CCAAGGACAACCTTCGAGCATGCTTTGTAAGCTCAGCAATTCAAAGAACGCTTGAATA 287
Qy 109 uGlyThrPheThrGlyTyrSerAlaLeuAlaLeuAlaLeuAlaLeuProAlaAspGlyAr 129
Db 288 TGGTGTATTCACTGCTTACTCTCTCTCCACTGCCCTGGCTCTTCCCTCGATGATAA 347
Qy 129 gValValThrCysGluValAspAlaGlnProProGluLeuGlyArgProLeuTrpArgGln 149
Db 348 GATCTTGGCTTGGATGTGAATCGCAATCTATGAGTTAGGATGCCAATAATTCAAAA 407
Qy 149 nAlaGluAlaGluHisLysLysLeuAspLeuArgLeuLysProAlaLeuGluThrLeuAspGln 169
Db 408 AGCTGGATGGCTCAAGATTTGATTTCAGAGAGGAGCTGCTCTTCGTTTCTTGACGA 467
Qy 169 uLeuLeuAlaAlaGlyGluAlaGlyThrPheAspValAlaValAlaValAlaAspLys 188
Db 468 GATGCTTAAAGATGAAATAAAAGGGTCTGTGATTTCTGTTTCTGGATGCTGATAA 527
Qy 188 sGluAsnCysSerAlaTyrGluArgCysLeuGlnLeuLeuArgProGlyGlyLeuLe 208
Db 528 GGACAATTACTTGAACCTACCAAGAGGCTACTAGAGCTTGTGAAGATTGGAGGAGCTGAT 587
Qy 208 uAlaValLeuArgValLeuTrpArgGlyLysValLeuGlnProProLysGlyAspValAl 228
Db 588 CGGATACGATAACACCTTATGGGCTGTGCTGCTGCACCCCGATGACCAATTGAT 647
Qy 228 aAlaGluCys-----ValArgAsnLeuAsnGluArgGlyLeuArgAs 242
Db 648 GGATTACATTAAAGCTCTTCGCGGCCATGTGATGGAGCTCAACAAGTATCTGGCTCAAGA 707
Qy 242 pValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPheLysL 262
Db 708 TTCGAGGATCGAGATTTCGCAGCTCCCGTGGTGTATGGGATTACCTGTGCGCGCGCAT 767
Qy 262 e 262
Db 768 C 768
```

RESULT 3  
US-09-452-239-1  
; Sequence 1, Application US/09452239  
; Patent No. 6465229  
; GENERAL INFORMATION:  
; APPLICANT: Rafaleki, Antoni J.  
; APPLICANT: Fader, Gary M.  
; APPLICANT: Cahoon, Rebecca E.  
; TITLE OF INVENTION: Plant Caffeoyl-CoA O-Methyltransferase  
; FILE REFERENCE: BBI284 US NA  
; CURRENT APPLICATION NUMBER: US/09/452,239  
; EARLIER FILING DATE: 1999-12-01  
; EARLIER FILING DATE: 1998-December-02  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 1  
; LENGTH: 891  
; TYPE: DNA

```
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (806)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (810)
US-09-452-239-1

Alignment Scores:
Pred. No.: 2,17e-36 Length: 891
Score: 401.00 Matches: 100
Percent Similarity: 56.03% Conservative: 44
Best Local Similarity: 38.91% Mismatches: 88
Query Match: 29.86% Indels: 25
DB: 3 Gaps: 6

US-10-017-407A-306 (1-262) x US-09-452-239-1 (1-891)

QY 17 GlySerAlaLeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgArg----- 34
DB 107 GCGCGGCGCGCGCGAGAGAGCA-----GCGCAACGCAACG 145
QY 35 -----CysProProTrpArgGlyArgGluGlnCysLeuLeuProGluAsp 51
DB 146 CGAGCAGAGACCGCGGACTCCGAGGTGCGCCACAAGAG-----CCTGCTCAAGAG 196
QY 52 SerArg-LeuTrpGlnTrpLeuLeuSerArgSerMet-----ArgGluHisProAlaLe 69
DB 197 CGAGGAGCTTACCACTATCTCGACACGAGCGTGATCCCGCGGGAGCGGAGGACAT 256
QY 69 uArgSerLeuArgLeuLeuThrLeuGluGlnProGlnGlyAspSerMetThrCysG 89
DB 257 GAAGGAGCTCCGCGAGATCACCGCAAGCACCATGGAACCTGATGACGACCTCCGCGCA 316
QY 89 uGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeuIleGlnAlaIleValAlaLeuAspLe 109
DB 317 CGAGGGCGAGTTCCTGAACATGCTCAAGCTCATCGCGCGCCCAAGAACCATGAGAT 376
QY 109 uGlyThrPheThrGlyTyrSerAlaLeuAlaLeuAlaLeuLeuProAlaAspGlyAr 129
DB 377 CGCGGTCTACACCGGTACTCGTCTCGCCACCGCGTCTCGACTCCCGGAGAGCGGCAC 436
QY 129 gValValThrCysGluValAspAlaGlnProGluLeuGlyArgProLeuTrpArg 149
DB 437 GATCTTGCGCATGGACATCAACCGCGAGAACTACGAGTAGGCTTCCCTGCATCAACAA 496
QY 149 nAlaGluAlaGluHisIleAspLeuArgLeuLysProAlaLeuGluThrLeuAspG 169
DB 497 GCGCGCGGTGGGCGCAAGATCGACTTCGCGGAGGCGCGCGCTCCCGCTCTCGGACGA 556
QY 169 uLeuLeuAlaAlaGlyGluAla---GlyThrPheAspValAlaValAlaAspAlaAsp 188
DB 557 CTTCTGGGCGGACAGGACGACGCGGTCTCGACTTCGCTTCGTTGGACGCGCGACAA 616
QY 188 sGluAsnCysSerAlaTyrTrpGluArgCysLeuGlnLeuLeuArgProGlyGlyIle 208
DB 617 CGACAACTACCTCAGCTACACGAGCGGTCTGAAGTGGTGGAGCGCGCGGCTCAT 676
QY 208 uAlaValLeuArgValLeuTrpArgGlyValLeuGlnProProIleAspValAl 228
DB 677 CGGCTACGACACACGCTGTGGAACCGCTCCGCTCGTCCCGGAGCGCGCCATGGG 736
QY 228 a-----AlaGluCysValArgAsnLeuAsnGluArgIleArgAs 242
DB 737 CAAGTACATCCGGTCTTACCGGCACTTCGCTCCGCCCTCAACAGCGCGGTCTCCGCCGGA 796
QY 242 pValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeu 258
DB 797 CGACCGCGGTNAGANTCTGCCAGTCTCCCGTTCGCGGAGCGGCTCACGCTC 845

RESULT 4
US-09-452-239-11
```

```
; Sequence 11, Application US/09452239
; Patent No. 6465229
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni J.
; APPLICANT: Fader, Gary M.
; APPLICANT: Cahoon, Rebecca E.
; TITLE OF INVENTION: Plant Caffeoyle-CoA O-Methyltransferase
; FILE REFERENCE: BB1284 US NA
; CURRENT APPLICATION NUMBER: US/09/452,239
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 60/110,594
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 11
; LENGTH: 1058
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-452-239-11

Alignment Scores:
Pred. No.: 1,06e-35 Length: 1058
Score: 396.00 Matches: 97
Percent Similarity: 55.86% Conservative: 46
Best Local Similarity: 37.89% Mismatches: 93
Query Match: 29.49% Indels: 20
DB: 3 Gaps: 5

US-10-017-407A-306 (1-262) x US-09-452-239-11 (1-1058)

QY 18 SerAlaLeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgArgCysProPro 37
DB 120 AGCAGCGCAATGGGAGCAGCGCGCGGAGC-----AGAAAGA----- 155
QY 38 TrpArgGlyArgGluGlnCysLeuLeuProGluAspSerArg-LeuTrpGln 57
DB 156 ---CGCGGACTCGGAGTCCGCGCCCAAGAGCTCTCAAGAGCGGAGTCTCTACAGT 212
QY 57 TrpLeuLeuSerArgSerMet-----ArgGluHisProAlaLeuArgSerLeuArgLeu 75
DB 213 ACATCTGGAGACGAGCGGTACCCGCGGAGCAGCAGCATGAAGAGTCCGCGAGG 272
QY 75 euThrLeuGluGlnProGlnGlyAspSerMetThrCysGluGlnAlaGlnLeuLeu 95
DB 273 TCACCGCCCAACCAACCATGGAACCTGATGACGACGTCGCGCGGAGGCGGCAATTCTGA 332
QY 95 laAsnLeuAlaArgLeuIleGlnAlaIleValAlaLeuAspLeuGlyThrPheThrGly 115
DB 333 ACCTGCTGTGAGCTCATCGCGCCCAAGAACCATGGAGATCGGCGGTCTACCGGCT 392
QY 115 TrpSerAlaLeuAlaLeuAlaLeuProAlaAspGlyArgValValThrCysGlu 135
DB 393 ACTCCCTCTCGCCACCGCTCCCATCCCGACGACGACGATCTTGGCGATGGACA 452
QY 135 alAspAlaGlnProGluLeuGlyArgProLeuTrpArgGlnAlaGluAlaGluHis 155
DB 453 TCAACCGGAGAGACTACGAGCTGGGCTCCCGTCGATCGAGAGGCGGAGTGGCGCAC 512
QY 155 ValLeuAspLeuArgLeuLysProAlaLeuGluThrLeuAspGluLeuLeu---AlaAla 174
DB 513 AGATGACATTCGCGGAGGAGGACCGCGCTCCCGTGTGGACCCAGCTGGTGGAGAGAGG 572
QY 174 lYgluAlaGlyThrPheAspValAlaValAlaAspAlaAspLysGluAsnCysSerAla 194
DB 573 GCAACCATCGGTCTCGACTTCGTGTTCTGTCGACCGCGCAGCAGGACAACTACTCAACT 632
QY 194 TrpGluArgCysLeuGlnLeuLeuArgProGlyGlyIleLeuAlaValLeuArgVal 214
DB 633 ACCACGAGCGGTGATGAAGTGGTCAAGGTGGCGGCTCGTCTCGCTACGACACACGC 692
QY 214 euTrpArgGlyValLeuGlnProProIleAspValAla----- 228
DB 693 TCTGGAACCGGCTCCGCTCGTCCCGCGGACGCGCCCATATGCGCAAGTACATCCGCTACT 752
```

```
QY 229 --AlaGluCysValArgAsnLeuAsnGluArgIleArgArgAspValArgValTyrIles 248
Db 753 ACCGGAGCTTGGTCTGAGCTCAACAGCCCTCGCCGCGACACCCGCGTGGAGATCT 812
QY 248 exLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPheLysIle 262
Db 813 GCCAGCTCCCGTCCGCGCGGCGCATCACCTCTCTGCCGCGCGTC 856

RESULT 5
US-09-452-239-41
; Sequence 41, Application US/09452239
; Patent No. 6465229
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni J.
; APPLICANT: Fader, Gary M.
; APPLICANT: Cahoon, Rebecca E.
; TITLE OF INVENTION: Plant Caffeoyle-CoA O-Methyltransferase
; FILE REFERENCE: BB1284 US NA
; CURRENT APPLICATION NUMBER: US/09/452,239
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 60/110,594
; EARLIER FILING DATE: 1998-December-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 41
; LENGTH: 1078
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-09-452-239-41

Alignment Scores:
Pred. No.: 1,85e-35 Length: 1078
Score: 394.00 Matches: 102
Percent Similarity: 54.14% Conservative: 42
Best Local Similarity: 38.35% Mismatches: 100
Query Match: 29.34% Indels: 23
DB: 6 Gaps: 6

US-10-017-407A-306 (1-262) x US-09-452-239-41 (1-1078)
QY 6 ProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAlaLeuGlyAlaAla--- 24
Db 97 CCAGCAATGGCCACACCGCGAGCGCGCCAC-GGCGCGGGCGCCCAAGGACCGCCGCG 155
QY 25 -----PheAlaThrGlyLeuPheLeuGlyArgCysProProTrpArgGlyArgArg 42
Db 156 CAACGGTTCCGAGCAGGT-----CACGCGCCCACTCCGAGGTCGGCCA 197
QY 43 GluGlnCysLeuLeuProGluAspSerArg-LeuTrpGlnTyrLeuLeuSerArgSe 62
Db 198 CAAGAG-----CCTGCTCAGAGCGAGCGCCCTTACAGATACATCTCGAGACGAG 248
QY 62 rMet-----ArgGluHisProAlaLeuArgSerLeuArgLeuLeuThrLeuGluGlnPr 80
Db 249 CGTGATACCGCGGAGCAGCAGTGATGAGGAGGCTCCGCGAGATCACCGCCCAACCC 308
QY 80 oGlnGlyAspSerMetMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLe 100
Db 309 ATGGAACTGTATGATGACGACGCTCGCGCGAGCGCCAGTTCTCTCAACATGCTGCTCAAGT 368
QY 100 uIleGlnAlaIleLysLeuAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLe 120
Db 369 CATCGGCGCAAGAGACCATCGAGATCGCGTGTACACCGGCTACTCTCTCGCCAC 428
QY 120 uAlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnProPr 140
Db 429 CGGCTCGCCATCCCGAGCGGACCATCTTGGCCATGGACATCAACCGCGAGACTA 488
QY 140 oGlnLeuGlyArgProLeuTrpArgGlnAlaGluAlaGluHisLysIleAspLeuArgLe 160
Db 489 CGAGCTGGGGCTCGCGTGTATGATGATGAGAGCGCGGTGGCGCAAGATCGACTCTCCGCA 548
```

```
QY 160 uLysProAlaLeuGluThrLeuAspGlyLeuLeuAla-----AlaGlyGluAlaGlyThrPh 179
Db 549 GGGCCCGCGCTGCGGTGCTGGAGCGCTGCTGGAGGAGCGGCCAACACCGGACCTT 608
QY 179 eAspValAlaValValAspAlaAspLysGluAsnCysSerAlaTyrTyrGluArgCysLe 199
Db 609 CGACTTCTGTTCTGCTGGAGCGCGCAAGGACAACTACTCTCAACTACCGAGCGCTCAT 668
QY 199 uGlnLeuLeuArgProGlyGlyIleLeuAlaValLeuArgValLeuTrpArgGlyLysVa 219
Db 669 GAAGCTCGTCAAGCTCGCGCGCTCTCTGGCTACGACACACGCTCTGGAACGGCTCCGT 728
QY 219 lLeuGlnProLysGlyAspValAla-----AlaGluCysValAr 233
Db 729 CGTGTCTCCCGCGAGCGCCCATCGCAAGTACATCGCTACTACCGGACTTCGTCTCT 788
QY 233 gAsnLeuAsnGluArgIleArgArgAspValArgValTyrIleSerLeuLeuProLeuGl 253
Db 789 CGACCTCAACAGGCGCTCGCGCGGACCGAGCGCGTGGAGATCTGCCAGCTCCCGTCCG 848
QY 253 yAspGlyLeuThrLeu 258
Db 849 CGACGCGCATCACCCCTC 864

RESULT 6
US-09-452-239-23
; Sequence 23, Application US/09452239
; Patent No. 6465229
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni J.
; APPLICANT: Fader, Gary M.
; APPLICANT: Cahoon, Rebecca E.
; TITLE OF INVENTION: Plant Caffeoyle-CoA O-Methyltransferase
; FILE REFERENCE: BB1284 US NA
; CURRENT APPLICATION NUMBER: US/09/452,239
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 60/110,594
; EARLIER FILING DATE: 1998-December-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 23
; LENGTH: 962
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (22)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (68)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (866)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (902)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (905)
US-09-452-239-23

Alignment Scores:
Pred. No.: 2.31e-35 Length: 962
Score: 392.50 Matches: 88
Percent Similarity: 58.11% Conservative: 41
Best Local Similarity: 39.64% Mismatches: 84
Query Match: 29.23% Indels: 9
DB: 3 Gaps: 3

US-10-017-407A-306 (1-262) x US-09-452-239-23 (1-962)
QY 50 GluAspSerArgLeuTrpGlnTyrLeuLeuSerArgSerMet-----ArgGluHisPro 67
Db 50 GluAspSerArgLeuTrpGlnTyrLeuLeuSerArgSerMet-----ArgGluHisPro 67
```

```

Db 125 CAGAGCGATGCCTCTATCAGTATATCTTAAACCCAGTGTGTACCCAGAGAGCATGAG 184
Qy 68 AlaLeuArgSerLeuLeuThrLeuGluGlnProGlnGlyAspSerMetMetThr 87
   ::::: ||||| ::::: |||||
Db 185 AGCTTGAAGGAGCTACGAGAGTTGACGGAACACACCTTGGAACTGTGGCTACACCA 244
Qy 88 CysGluGlnAlaGlnLeuLeuAlaLeuAlaArgLeuLeuGlnAlaLysAlaLeu 107
   ::::: ||||| ::::: |||||
Db 245 CCTGACGAAGGACAACTTCTAGGCATGCTCTTAAAGCTTATCAATCCCAAGAACACCATG 304
Qy 108 AspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeuAlaLeuProAlaAsp 127
   ::::: ||||| ::::: |||||
Db 305 GAAATAGGCGTCTTCACTGGTACTCTTCTTCCACTGCTTCCCTCCCTCTCTGAC 364
Qy 128 GlyArgValValThrCysGluValAlaAspAlaGlnProProGluLeuGlyArgProLeuTrp 147
   ::::: ||||| ::::: |||||
Db 365 GGAAGAGCTTAGCTATGATGTTAACCGGAATATTATGAATTGGGTTGCCCGTGATT 424
Qy 148 ArgGlnAlaGluAlaGluHisLysIleAspLeuArgLeuLysProAlaLeuGluThrLeu 167
   ::::: ||||| ::::: |||||
Db 425 GAAAGGCTGGAGTGGCTCACAAGATTGACTTCAGAGAAGGACCCGCTCTTCTCTTCTT 484
Qy 168 AspGluLeuLeuAla---AlaGlyGluAlaGlyThrPheAspValAlaValValAla 186
   ||||| ::::: |||||
Db 485 GACGTTCTCATTAAGACGAAAGAAATAAGGGCTTTTCGATTTCACTATGTGGATGCT 544
Qy 187 AspLysGluAsnCysSerAlaTyrTyrGluArgCysLeuGlnLeuLeuArgProGlyGly 206
   ::::: ||||| ::::: |||||
Db 545 GATAAGGACAATTACTTGAACCTACCAAGAGGGTGATGAGCTTGTGAAGCTTGGGGA 604
Qy 207 IleLeuAlaValLeuArgValLeuTrpArgGlyLysValLeuGlnProProLysGlyAsp 226
   ::::: ||||| ::::: |||||
Db 605 TTGATCGGCTAGCATAACACCTTATGGAATGGTCCGTCGTCGCCACCCGATGCTCCT 664
Qy 227 ValAla-----AlaGluCysValArgAsnLeuAsnGluArgIleArg 240
   ::::: |||||
Db 665 CTCATGGATTGTAAAGTATTATCCGATTATTCGAGCTCAACAGCTCTTGCA 724
Qy 241 ArgAspValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPhe 260
   ::::: ||||| ::::: |||||
Db 725 CTTGATTCAAGGTCGAGATTGCCAGCTTCCCGTTGGTGGATGATGGGATTACCCCTGTCCGC 784
Qy 261 LysIle 262
   ::::: |||||
Db 785 CGCATC 790

RESULT 7
US-09-452-239-25
; Sequence 25, Application US/09452239
; Patent No. 6465229
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni J.
; APPLICANT: Cahoon, Rebecca E.
; TITLE OF INVENTION: Plant Caffeoyle-CoA O-Methyltransferase
; FILE REFERENCE: BB1284 US NA
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: US/09/452,239
; EARLIER FILING DATE: 1998-December-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 25
; LENGTH: 1023
; TYPE: DNA
; ORGANISM: Glycine max
US-09-452-239-25
Alignment Scores:
Pred. No.: 2 54e-35 Length: 1023
Score: 32.50 Matches: 88
Percent Similarity: 58.11% Conservatives: 41
Best Local Similarity: 39.64% Mismatches: 84

```

```

Query Match: 29.23% Indels: 9
DB: 3 Gaps: 3
US-10-017-407A-306 (1-262) x US-09-452-239-25 (1-1023)
Qy 50 GluAspSerArgLeuTrpGlnTyrLeuLeuSerArgSerMet-----ArgGluHisPro 67
   ::::: ||||| ::::: |||||
Db 132 CAGAGCGATGCCTCTATCAGTATATCTTAAACCCAGTGTGTACCCAGAGAGCATGAG 191
Qy 68 AlaLeuArgSerLeuLeuThrLeuGluGlnProGlnGlyAspSerMetMetThr 87
   ::::: ||||| ::::: |||||
Db 192 AGCTTGAAGGAGCTACGAGAGTTGACGGAACACACCTTGGAACTGTGGCTACACCA 251
Qy 88 CysGluGlnAlaGlnLeuLeuAlaLeuAlaArgLeuLeuGlnAlaLysAlaLeu 107
   ::::: ||||| ::::: |||||
Db 252 CCTGACGAAGGACAACTTCTAGGCATGCTCTTAAAGCTTATCAATCCCAAGAACACCATG 311
Qy 108 AspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeuAlaLeuProAlaAsp 127
   ::::: ||||| ::::: |||||
Db 312 GAAATAGGCGTCTTCACTGGTACTCTTCCACTGCTTCCCTCCCTCTCTGAC 371
Qy 128 GlyArgValValThrCysGluValAlaAspAlaGlnProProGluLeuGlyArgProLeuTrp 147
   ::::: ||||| ::::: |||||
Db 372 GGAAGAGCTTAGCTATGATGTTAACCGGAATATTATGAATTGGGTTGCCCGTGATT 431
Qy 148 ArgGlnAlaGluAlaGluHisLysIleAspLeuArgLeuLysProAlaLeuGluThrLeu 167
   ::::: ||||| ::::: |||||
Db 432 GAAAGGCTGGAGTGGCTCACAAGATTGACTTCAGAGAAGGACCCGCTCTTCTCTTCTT 491
Qy 168 AspGluLeuLeuAla---AlaGlyGluAlaGlyThrPheAspValAlaValValAla 186
   ||||| ::::: |||||
Db 492 GACGTTCTCATTAAGACGAAAGAAATAAGGGCTTTTCGATTTCACTATGTGGATGCT 551
Qy 187 AspLysGluAsnCysSerAlaTyrTyrGluArgCysLeuGlnLeuLeuArgProGlyGly 206
   ::::: ||||| ::::: |||||
Db 552 GATAAGGACAATTACTTGAACCTACCAAGAGGGTGATGAGCTTGTGAAGCTTGGGGA 611
Qy 207 IleLeuAlaValLeuArgValLeuTrpArgGlyLysValLeuGlnProProLysGlyAsp 226
   ::::: ||||| ::::: |||||
Db 612 TTGATCGGCTAGCATAACACCTTATGGAATGGTCCGTCGTCGCCACCCGATGCTCCT 671
Qy 227 ValAla-----AlaGluCysValArgAsnLeuAsnGluArgIleArg 240
   ::::: |||||
Db 672 CTCATGGATTGTAAAGTATTATCCGATTATTCGAGCTCAACAGCTCTTGCA 731
Qy 241 ArgAspValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPhe 260
   ::::: ||||| ::::: |||||
Db 732 CTTGATTCAAGGTCGAGATTGCCAGCTTCCCGTTGGTGGATGATGGGATTACCCCTGTCCGC 791
Qy 261 LysIle 262
   ::::: |||||
Db 792 CGCATC 797

RESULT 8
US-09-452-239-13
; Sequence 13, Application US/09452239
; Patent No. 6465229
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni J.
; APPLICANT: Cahoon, Rebecca E.
; TITLE OF INVENTION: Plant Caffeoyle-CoA O-Methyltransferase
; FILE REFERENCE: BB1284 US NA
; CURRENT FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: US/09/452,239
; EARLIER FILING DATE: 1998-December-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 997
; TYPE: DNA
; ORGANISM: Oryza sativa

```

;  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (483)  
US-09-452-239-13

Alignment Scores: 6.17e-35 Length: 997  
Pred. No.: 389.00 Matches: 87  
Score: 389.00 Matches: 87  
Percent Similarity: 57.47% Conservative: 40  
Best Local Similarity: 39.37% Mismatches: 82  
Query Match: 28.97% Indels: 12  
DB: 3 Gaps: 3

US-10-017-407A-306 (1-262) x US-09-452-239-13 (1-997)

```
QY 54 LeuTrpGlnTyrLeuLeuSerArgSerMet-----ArgGluHisProAlaLeuArgSer 71
DB 151 CTGTCAAGTATGCTCTGGACACGACGAGTGTGCTGCCACGGGAGCGGAGTGCATGGCGCAT 210
QY 72 LeuArgLeuLeuThrLeuGlnProGlnGlyArgSerMetMetThrCysGluGlnAla 91
DB 211 CTGGGCTCATCAGGACAGACAGCAGTGGGGGTTTCATGAGTGTGCGGGGATGAGGGC 270
QY 92 GlnLeuLeuAlaAsnLeuAlaArgLeuLeuGlnAlaLysLeuAlaLeuAspLeuGlyThr 111
DB 271 CAGCTGCTGGGATGCTGTGAAGATGTCGCGGAGCGAAGAGCAATCGAGTGGGTGTC 330
QY 112 PheThrGlyTyrSerAlaLeuAlaLeuAlaLeuProAlaAspGlyArgValVal 131
DB 331 TTCACGGCTACTCGCTGTGTCGACGCGGCTGCGGCTGCCGAGACGGGAAGTGTGTG 390
QY 132 ThrCysGluValAspAlaGlnProGlnLeuGlyArgProLeuTrpArgGlnAlaGlu 151
DB 391 GCGATCGACCGGACAGGAGAGCTACGAGATCGGGCGCGCTTCTTGGAGAAAGCCGGG 450
QY 152 AlaGluHisLysLeuAspLeuArgLeuLysProAlaLeuGluThrLeuAspGluLeu 171
DB 451 GTGGCGCACAAAGTGGACTTCCCAAGGGGAAANGGCTGGAGAAGCTGGACGAGTGCTC 510
QY 172 -----AlaAlaGlyGluAlaGlyThrPheAspValAlaValAspAlaAsp 187
DB 511 GCGAGGAGCGCGCGCGGCGCGGCGGCTTCGACTTCGCGTTCGTGGACGCGGAC 570
QY 188 LysGluAsnCysSerAlaTyrTyrGluArgCysLeuGlnLeuLeuArgProGlyGlyTle 207
DB 571 AAGCCCAACTACGTCAAGTACACAGAGACGTGTCACGTGTCGCGCTCGCGCGGAC 630
QY 208 LeuAlaValLeuArgValLeuTrpArgGlyLysValLeuGlnProLysGlyAspVal 227
DB 631 ATCGGTGTACGACACACACGCTGTGGGCGGACCGGTGGCGCTGCCGCGACACGCGCTG 690
QY 228 Ala-----AlaGluCysValArgAsnLeuAsnGluArgileArg 241
DB 691 TCGGACCTGGACCGGAGTTCCTCGTCGCATCAGGGACCTCAACTCCAGGCTCCCGCGC 750
QY 242 AspValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPheLys 261
DB 751 GACCCGCGCATCGCTGTGCCAACTCGCCATCGCGGACGGATCACCATCTGCCGCGCGC 810
QY 262 Ile 262
DB 811 CTC 813
```

## RESULT 9

US-09-452-239-45  
; Sequence 45, Application US/09452239  
; Patent No. 6465229  
; GENERAL INFORMATION:  
; APPLICANT: Rafaleki, Antoni J.  
; APPLICANT: Fader, Gary W.  
; APPLICANT: Cahoon, Rebecca E.  
; TITLE OF INVENTION: Plant Caffeoyl-CoA O-Methyltransferase  
; FILE REFERENCE: BB1284 US NA

;  
; CURRENT APPLICATION NUMBER: US/09/452,239  
; CURRENT FILING DATE: 1999-12-01  
; EARLIER APPLICATION NUMBER: 60/110,594  
; EARLIER FILING DATE: 1998-December-02  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 45  
; LENGTH: 953  
; TYPE: DNA  
; ORGANISM: Triticum aestivum  
US-09-452-239-45

## Alignment Scores:

Pred. No.: 9.77e-35 Length: 953  
Score: 387.00 Matches: 105  
Percent Similarity: 55.51% Conservative: 46  
Best Local Similarity: 38.60% Mismatches: 104  
Query Match: 28.82% Indels: 18  
DB: 3 Gaps: 8

US-10-017-407A-306 (1-262) x US-09-452-239-45 (1-953)

```
QY 3 GlnProValPro-----ArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla 20
DB 6 CAACCCATTCTCTCTACTACTCTCGGCACAAACAGCCCAACAGAACTAGCGAGCAGGCC 65
QY 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgArgCysProProTrpArgGly 40
DB 66 AT-GGCGCC-----CAACGGAGACAAACCGTGTGCCAACGT-----CCACAGCGGCAT 112
QY 41 ArgArgGluGln-CysLeuLeuProProGluAspSerArgLeuTrpGlnTyrLeuLeuSe 60
DB 113 CGACAGACCAACACAGACGCTGCTCAAGAGCGAGCC---CTCTACACTTACTCTCGA 169
QY 60 rArgSerMet-----ArgGluHisProAlaLeuArgSerLeuArgLeuLeuGlu 78
DB 170 CACCACCGCTGTCCCGCGGACGACGAGTGTGCGGACCTGCGCCTCATCCAGCAAA 229
QY 78 uGlnProGlnGlyAspSerMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAl 98
DB 230 GCACCCATGGGGTTACATGTCAGTGTCTCGACAGGCGGAGCTGTGGGATGCTGAT 289
QY 98 aArgLeuIleGlnAlaLysLysAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaIle 118
DB 290 CAAGATGCGCGGCGCCAAAGAGACGATCGAGTGGCGGTTCACGGGCTACTCTCGTGT 349
QY 118 uAlaLeuAlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaG 138
DB 350 GGCACCGCGCTGGCGCTCCCGGAGGACGGAAGGTGGTGGCCATCGACACCGCGCA 409
QY 138 nProGluLeuGlyArgProLeuTrpArgGlnAlaGluAlaGluHisLysIleAspLe 158
DB 410 GTGTTACAGGTGGTGTCCCGCTTCATCGAAGGCGCGGATGGCGGCAAGTGAGCTT 469
QY 158 uArgLeuLysProAlaLeuGluThrLeuAspGluLeuLeuAlaAlaGlyGlu---AlaG 177
DB 470 CGCGAGGCGCACCGCGCTGGCGCGCTCGACGAGCTCTCTCGTCGAGGACGAGCGCGC 529
QY 177 yThrPheAspValAlaValValAspAlaAspLysGluAsnCysSerAlaTyrTyrGluAr 197
DB 530 GAGCTACGACTTCGCGTTCGTGGAGCGGACAAAGCCCAACTACGTGCGCTACACGAGCA 589
QY 197 gCysLeuGlnLeuLeuArgProGlyLysLeuAlaValLeuArgValLeuTrpArgG 217
DB 590 GCTGCTGAAGTGTGTTCGCGGCGGCACTATCATCTACGACAAACACGCTCTGGGGCGG 649
QY 217 yLysValLeuGlnPro-----ProLysGlyAspVal-----AlaAlaGluCy 231
DB 650 CACGCTGGCGCTGCGCGGCGGACCCCTCATGTCGCGCTCGACACCCGCTTCTCGCGCG 709
QY 231 sValArgAsnLeuAsnGluArgIleArgArgAspValArgValTyrIleSerLeuLeuPr 251
DB 710 CCTCAGGACCTCAACGCAAGCTCGCGCGGACCCGCGGATCGAGGTCGCGCAGCTCGC 769
```



Qy	Db	Sequence	Length	Score	Percent Similarity	Best Local Similarity	Query Match	DB
251	oLeuGlyAspGlyLeuThrLeuAlaPheLysile 262	ATCAGGAAATACGTAAGGTACTATATAGGACCTTCGATTGGAACTTACCAAGCTTTTGGCA 672	114e-34	386.50	57.56%	36.13%	28.74%	1012
770	CATCGCGGAGGAGTCCCATCTGCGCGGCATC 803	ATCAGGAAATACGTAAGGTACTATATAGGACCTTCGATTGGAACTTACCAAGCTTTTGGCA 672	386.50	57.56%	36.13%	28.74%	1012	86
241	ArgAspValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPhe 260	ATCAGGAAATACGTAAGGTACTATATAGGACCTTCGATTGGAACTTACCAAGCTTTTGGCA 672	386.50	57.56%	36.13%	28.74%	1012	51
673	GCTGATCCCAAGAAATTGAGATTTCATGCTTCCCGTGTGTGATGAATTAACCTCTGCGCG 732	ATCAGGAAATACGTAAGGTACTATATAGGACCTTCGATTGGAACTTACCAAGCTTTTGGCA 672	386.50	57.56%	36.13%	28.74%	1012	88
261	Lysile 262	ATCAGGAAATACGTAAGGTACTATATAGGACCTTCGATTGGAACTTACCAAGCTTTTGGCA 672	386.50	57.56%	36.13%	28.74%	1012	13
733	CGCATC 738	ATCAGGAAATACGTAAGGTACTATATAGGACCTTCGATTGGAACTTACCAAGCTTTTGGCA 672	386.50	57.56%	36.13%	28.74%	1012	4
<p>RESULT 11</p> <p>US-09-453-323-5</p> <p>Sequence 5, Application US/09453323</p> <p>Patent No. 6441272</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Ye, Zheng-Hua</p> <p>TITLE OF INVENTION: MODIFICATION OF LIGNIN CONTENT AND COMPOSITION IN PLANTS</p> <p>FILE REFERENCE: 235,0090101</p> <p>CURRENT APPLICATION NUMBER: US/09/453,323</p> <p>CURRENT FILING DATE: 1999-12-02</p> <p>PRIOR APPLICATION NUMBER: 60/110,676</p> <p>PRIOR FILING DATE: 1998-12-02</p> <p>NUMBER OF SEQ ID NOS: 13</p> <p>SOFTWARE: PatentIn Ver. 2.0</p> <p>SEQ ID NO 5</p> <p>LENGTH: 967</p> <p>TYPE: DNA</p> <p>ORGANISM: Nicotiana tabacum</p> <p>US-09-453-323-5</p>								
<p>Alignment Scores:</p> <p>Pred. No.: 1,14e-34 Length: 967</p> <p>Score: 386.50 Matches: 82</p> <p>Percent Similarity: 58.56% Conservative: 48</p> <p>Best Local Similarity: 36.94% Mismatches: 83</p> <p>Query Match: 28.78% Indels: 9</p> <p>DB: 3 Gaps: 3</p>								
<p>US-10-017-407A-306 (1-262) x US-09-453-323-5 (1-967)</p>								
Qy	50	GlusAspSerArgLeuThrGlnTyrLeuLeuSerArgSerMet-----ArgGluHisPro 67	114e-34	386.50	57.56%	36.13%	28.74%	1012
Db	73	CAAGTGATGCTCTTTACCATGATACATCTTGAGACCGGTATACCCCAAGAGAGAGAGAA 132	386.50	57.56%	36.13%	28.74%	1012	86
Qy	68	AlaLeuArgSerLeuArgLeuThrLeuLeuGlnProGlnGlyAspSerMetThr 87	386.50	57.56%	36.13%	28.74%	1012	51
Db	133	CCCATGAAAGAGCTCAGAGAAATGACTGTCAAGCATCCATGGAATCTAATGACAACTTCG 192	386.50	57.56%	36.13%	28.74%	1012	88
Qy	88	CysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeuLeuGlnAlaLysLeuAlaLeu 107	386.50	57.56%	36.13%	28.74%	1012	13
Db	193	GCGGATGAGGACAAATCTTGAGCATGCTATTGAAGCATGATCAATGCTTAAATAATACAAAT 252	386.50	57.56%	36.13%	28.74%	1012	4
Qy	108	AspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeuAlaLeuAlaLeuProAlaAsp 127	386.50	57.56%	36.13%	28.74%	1012	86
Db	253	GAAATTTGGTGTTPACACTGGCTACTCCCTTCTTTGCAACTGCTCTTGTCTCTTCTGATGAT 312	386.50	57.56%	36.13%	28.74%	1012	51
Qy	128	GlyArgValValThrCysGluValAspAlaGlnProGlnGlyAspSerMetThr 147	386.50	57.56%	36.13%	28.74%	1012	88
Db	313	GGAAGATATTGCAATGATATTACAGAGAAATATACGAACTCGGTTCCCGGTAATC 372	386.50	57.56%	36.13%	28.74%	1012	13
Qy	148	ArgGlnAlaGluAlaGluHisLysLeuLeuAspLeuLeuLeuProAlaLeuGluThrLeu 167	386.50	57.56%	36.13%	28.74%	1012	4
Db	373	CAAAAGCTGGCTGGCTCATAAATTTGATTTTAGAGAGAGGCTCTGCTTTGCTGTTCTT 432	386.50	57.56%	36.13%	28.74%	1012	86
Qy	168	AspGluLeuLeuAla---AlaGlyGluAlaGlyThrPheAspValAlaValAspAla 186	386.50	57.56%	36.13%	28.74%	1012	51
Db	433	GATTTAATGATGAAGATAAATAATATCATGCGACATATGATTTTCATTTTCGTGGATGCT 492	386.50	57.56%	36.13%	28.74%	1012	88
Qy	187	AspGlyGluAsnCysSerAlaTyrTyrGluArgCysLeuGlnLeuLeuArgProGlyGly 206	386.50	57.56%	36.13%	28.74%	1012	13
Db	493	GACAAGGACAAATATACATCACTACCAAGAGAAATAATAGATTAATGAAAGTTGGTGGT 552	386.50	57.56%	36.13%	28.74%	1012	86
Qy	207	IleLeuAlaValLeuArgValLeuThrArgGlyLysValLeuGlnProProLysGlyAsp 226	386.50	57.56%	36.13%	28.74%	1012	51
Db	553	GTGATTTGGCTACGACAAACCCCTTGAATGTTCTGTGGCTCTGCTACCTGCTGCTCCA 612	386.50	57.56%	36.13%	28.74%	1012	88
Qy	227	ValAla-----AlaGlyCysValArgAsnLeuAsnGluArgLys 240	386.50	57.56%	36.13%	28.74%	1012	13

Db 486 TGCCACAGATTGACTTCAGAGAGGGCCCTGCTCTGCCAGTTCTGGACGAACCTGCTTAA 545  
Qy 172 aalaGlyGluAa---GlyThrPheaspValalavalAlaaspAlaaspLysGluasnCy 191  
Db 546 GAATGAGGACATGCATGGATCGTTGATTTGTTGCGTGGATGCGGACAAAGACAACTA 605  
Qy 191 sSerAlaTyTyGluArgCysLeuGlnLeuLeuArgProGlyGlyLeuAlaValle 211  
Db 606 TCTAACTACACAGCGTCTGATCGATCTGTTGAGGTTGAGGTTGATTCATATGA 665  
Qy 211 uArgValLeuTrpArgGlyLysValLeuGlnProProLysGlyAspValAla----- 228  
Db 666 CAACACCCCTGTGGAACGGATCTGTGCTGCTCCACCGATGCTCCCTCTGCGAAATATGT 725  
Qy 229 -----AlaGluCysValArgAsnLeuGluArgGlyLeuAlaPheLysle 785  
Db 726 GAGATATTACAGAGATTTCGTGATGAGCTAACAAGGCCCTTGTGTCGATCCCGCAT 785  
Qy 245 lTyrlleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPheLysle 262  
Db 786 TGAGATCAGCCAAATCCAGTGGTGACGGCGTCCACCTTTTCAGGCGGTGTC 837

RESULT 12  
US-09-169-789-94  
; Sequence 94, Application US/09169789  
; Patent No. 6653528  
; GENERAL INFORMATION:  
; APPLICANT: Bloksberg, Leonard N.  
; APPLICANT: Havukkala, Ilkka  
; TITLE OF INVENTION: Materials and Methods for the  
; FILE REFERENCE: 11000.1003c2  
; CURRENT APPLICATION NUMBER: US/09/169,789  
; CURRENT FILING DATE: 1998-10-09  
; EARLIER APPLICATION NUMBER: US 08/975,316  
; EARLIER FILING DATE: 1997-11-21  
; EARLIER APPLICATION NUMBER: US 08/713,000  
; EARLIER FILING DATE: 1996-09-11  
; NUMBER OF SEQ ID NOS: 185  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 94  
; LENGTH: 1012  
; TYPE: DNA  
; ORGANISM: Pinus radiata  
US-09-169-789-94

Alignment Scores:  
Pred. No.: 1.4e-34 Length: 1012  
Score: 386.00 Matches: 86  
Percent Similarity: 57.56% Conservative: 51  
Best Local Similarity: 36.13% Mismatches: 88  
Query Match: 28.74% Indels: 13  
DB: 4 Gaps: 4

US-10-017-407a-306 (1-262) x US-09-169-789-94 (1-1012)

Qy 35 CysProTrpTrpArgGlyArgGluGln-CysLeuLeuProProGluAspSerArgle 54  
Db 135 TGTCCGCCATCAAGAGTGGGACACAAAAGTCTTTTG-----CAGCGCATGCCCT 185  
Qy 54 uTrpGlnTyTyLeuSerArgSerMet-----ArgGluHisProAlaLeuArgSerle 72  
Db 186 CTATCAGTATATTGGAAACAGAGGTGTACCTCTGTAGCCCGAGCCCATGAAGAGCT 245  
Qy 72 uArgLeuLeuThrLeuGluGlnProGlnGlyAspSerMetMetCysGluGlnAlaGl 92  
Db 246 CGCGCAAGTGAAGTCCCAAGCATCCCTGGAACTCATGACTACTTCTGCCGATGAGGTC 305  
Qy 92 nLeuLeuAlaLeuAlaArgLeuGlnAlaLysLysAlaLeuAspLeuGlyThrPh 112  
Db 306 ATTTCTGGCCCTCTCTGCTGAAGCTCATTAAACCCCAAGACACACATGGAGATTGGGTGTA 365  
Qy 112 eThrGlyTyTySerAlaLeuAlaLeuAlaLeuProAlaAspGlyArgValValTh 132

Db 366 CACTGGTTACTCGTCTCTCAGCACAGCCCTTGCATTTGCCCGATGATGGAAGATTTCTAGC 425  
Qy 132 rCysGluValaspAlaGlnProProGluLeuLeuGlyArgProLeuTrpArgGluAlaGlual 152  
Db 426 CATGACATCAACAGAGAACTATGATATCGATTGCTTATTTATGAGAAAAGCAGGAGT 485  
Qy 152 aGluHisLysleAspLeuArgLeuLysProAlaLeuGluThrLeuAspGluLeuAl 172  
Db 486 TCCCCACAGATTGACTTCAGAGAGGGCCCTGCTCTGCCAGTTCTGGACGAACCTGCTTAA 545  
Qy 172 aalaGlyGluAa---GlyThrPheaspValalavalAlaaspAlaaspLysGluasnCy 191  
Db 546 GAATGAGGACATGCATGGATCGTTGATTTGTTGCTGATGCGGACAAAGACAACTA 605  
Qy 191 sSerAlaTyTyGluArgCysLeuGlnLeuLeuArgProGlyGlyLeuAlaValle 211  
Db 606 TCTAACTACACAGCGTCTGATCGATCTGTGAGGTTGAGGTTGATTCATATGA 665  
Qy 211 uArgValLeuTrpArgGlyLysValLeuGlnProProLysGlyAspValAla----- 228  
Db 666 CAACACCCCTGTGGAACGGATCTGTGCTCCACCGATGCTCCCTCTGAGGAATATGT 725  
Qy 229 -----AlaGluCysValArgAsnLeuGluArgGlyLeuAlaPheLysle 785  
Db 726 GAGATATTACAGAGATTTCGTGATGAGCTAACAAGGCCCTTGTGTCGATCCCGCAT 785  
Qy 245 lTyrlleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPheLysle 262  
Db 786 TGAGATCAGCCAAATCCAGTGGTGACGGCGTCCACCTTTTCAGGCGGTGTC 837

RESULT 13  
US-08-713-000-6  
; Sequence 6, Application US/08713000  
; Patent No. 5850020  
; GENERAL INFORMATION:  
; APPLICANT: Bloksberg, Leonard N.  
; APPLICANT: Havukkala, Ilkka  
; APPLICANT: Grierson, Alastair  
; TITLE OF INVENTION: MATERIALS AND METHODS FOR THE  
; TITLE OF INVENTION: MODIFICATION OF PLANT LIGNIN CONTENT  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Speckman Picard PLLC  
; STREET: 2601 Elliott Avenue, Suite 4185  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98121  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/713,000  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sleath, Janet  
; REGISTRATION NUMBER: 37,007  
; REFERENCE/DOCKET NUMBER: 11000.1003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 206-269-0565  
; TELEFAX: 206-269-0563  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1026 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-713-000-6

## Alignment Scores:

Pred. No.: 1.42e-34 Length: 1026  
 Score: 386.00 Matches: 86  
 Percent Similarity: 57.56% Conservative: 51  
 Best Local Similarity: 36.13% Mismatches: 88  
 Query Match: 28.74% Indels: 13  
 DB: 2 Gaps: 4

US-10-017-407A-306 (1-262) x US-08-713-000-6 (1-1026)

```

QY 35 CysProTyrArgGlyArgGluGln-CysLeuLeuProGluAspSerArgLe 54
DB 149 TGTCCGCCATCAAGAGTGGACAAAAGTCTTTG-----CAGAGCATCCCT 199
QY 54 uTrpGlnTyrLeuLeuSerArgSerMet-----ArgGluHisProAlaLeuArgSerLe 72
DB 200 CTATCAGTATATATTGGAACGAGCGTGTACCCCTGTGAGCCGAGCCCAATGAAGGAGCT 259
QY 72 uArgLeuLeuThrLeuGluGlnProGlnGlyAspSerMetMetThrCysGluGlnAlaGl 92
DB 260 CCGCGAAGTGAAGTCCCAAGCATCCTCGAACCTCATGACTACTTCTCGCGATGAGGGTCA 319
QY 92 nLeuLeuAlaAsnLeuAlaArgLeuileGlnAlaLysLysAlaLeuAspLeuGlyThrPh 112
DB 320 ATTCTGGGCCCTCTCTGAGCTCATTAACGCCAAGAACACCATGGAGATTGGGGTGTA 379
QY 112 eThrGlyTyrSerAlaLeuAlaLeuAlaLeuAlaLeuProAlaAspGlyArgValValTh 132
DB 380 CACTGGTACTCGCTCTCAGCACAGCCCTTGCAATGCCGATGATGGAAGATTCCTAGC 439
QY 132 rCysGluValAspAlaGlnProGluLeuGlyArgProLeuTrpArgGlnAlaGlual 152
DB 440 CATGGACATCAACAGAGAACTATGATATCGGATTCCTATTATTGAGAAAGCAGGAGT 499
QY 152 aGluHisLysIleAspLeuArgLeuLysProAlaLeuGluThrLeuAspGluLeuAl 172
DB 500 TGCCCAACAAGATTGACTTCAGAGAGGCCCTCTGCTGCCAGATTCTCGAGCAACTGCTTAA 559
QY 172 aAlaGlyGluAla---GlyThrPheAspValAlaValAlaValAlaAspLysGluAsnCy 191
DB 560 GAATGAGGACATCGATGGATCGTTTCGATTTTGTGTCGTGGATGCGGACAAAGCAACTA 619
QY 191 sSerAlaTyrTyrGluArgCysLeuGlnLeuLeuArgProGlyGlyIleLeuAlaVal 211
DB 620 TCTAAACTACCAACAGCGTCTGATCATCTGTGTAAGGTGGAGGTCTGATTCATATCA 679
QY 211 uArgValLeuTrpArgGlyLysValLeuGlnProProLysGlyAspValAla----- 228
DB 680 CAACACCCCTGTGGAACGAGTCTGTGGTGTCTCCACCCGATGCTCCCTCAGGAAATATGT 739
QY 229 -----AlaGluCysValArgAsnLeuAsnGluArgIleArgAspValArgVa 245
DB 740 GAGATATTACAGAGATTCTGTGATGAGCTTAACAGAGGCCCTTGTGTGATCCCGCAT 799
QY 245 lTyrIleSerLeuLeuProGluGlyAspGlyLeuThrLeuAlaPheLysIle 262
DB 800 TGAGATCAGCAAAATCCCATCGTCCGTCAGCGCGTCCACCCCTTTCAGCGCGTCTC 851

```

## RESULT 14

US-08-975-316-6  
 Sequence 6, Application US/08975316  
 Patent No. 5952486  
 GENERAL INFORMATION:  
 APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, Ilkka  
 APPLICANT: and GRIERSON, Alastair W.  
 TITLE OF INVENTION: MATERIALS AND METHODS FOR  
 TITLE OF INVENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT  
 NUMBER OF SEQUENCES: 88  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Law Offices of Ann W. Speckman  
 STREET: 2601 Elliott Avenue, Suite 4185  
 CITY: Seattle  
 STATE: WA

COUNTRY: USA  
 ZIP: 98121  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/975,316  
 FILING DATE:  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/713,000  
 FILING DATE: September 11, 1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: SLEATH, Janet  
 REGISTRATION NUMBER: 37,007  
 REFERENCE/DOCKET NUMBER: 11000/1003C1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 206-269-0565  
 TELEFAX: 206-269-0563  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1026 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-975-316-6

Alignment Scores:  
 Pred. No.: 1.42e-34 Length: 1026  
 Score: 386.00 Matches: 86  
 Percent Similarity: 57.56% Conservative: 51  
 Best Local Similarity: 36.13% Mismatches: 88  
 Query Match: 28.74% Indels: 13  
 DB: 2 Gaps: 4

US-10-017-407A-306 (1-262) x US-08-975-316-6 (1-1026)

```

QY 35 CysProTyrArgGlyArgGluGln-CysLeuLeuProGluAspSerArgLe 54
DB 149 TGTCCGCCATCAAGAGTGGGACAAAAGTCTTTG-----CAGAGCATCCCT 199
QY 54 uTrpGlnTyrLeuLeuSerArgSerMet-----ArgGluHisProAlaLeuArgSerLe 72
DB 200 CTATCAGTATATATTGGAACGAGCGTGTACCCCTGTGAGCCGAGCCCAATGAAGGAGCT 259
QY 72 uArgLeuLeuThrLeuGluGlnProGlnGlyAspSerMetMetThrCysGluGlnAlaGl 92
DB 260 CCGCGAAGTGAAGTCCCAAGCATCCTCGAACCTCATGACTACTTCTCGCGATGAGGGTCA 319
QY 92 nLeuLeuAlaAsnLeuAlaArgLeuileGlnAlaLysLysAlaLeuAspLeuGlyThrPh 112
DB 320 ATTCTGGGCCCTCTCTGAGCTCATTAACGCCAAGAACACCATGGAGATTGGGGTGTA 379
QY 112 eThrGlyTyrSerAlaLeuAlaLeuAlaLeuAlaLeuProAlaAspGlyArgValValTh 132
DB 380 CACTGGTACTCGCTCTCAGCACAGCCCTTGCAATGCCGATGATGGAAGATTCCTAGC 439
QY 132 rCysGluValAspAlaGlnProGluLeuGlyArgProLeuTrpArgGlnAlaGlual 152
DB 440 CATGGACATCAACAGAGAACTATGATATCGGATTCCTATTATTGAGAAAGCAGGAGT 499
QY 152 aGluHisLysIleAspLeuArgLeuLysProAlaLeuGluThrLeuAspGluLeuAl 172
DB 500 TGCCCAACAAGATTGACTTCAGAGAGGCCCTCTCTGCCAGATTCTGCGAGCAACTGCTTAA 559
QY 172 aAlaGlyGluAla---GlyThrPheAspValAlaValAlaValAlaAspLysGluAsnCy 191
DB 560 GAATGAGGACATCGATGGATCGTTTCGATTTTGTGTCGTGGATGCGGACAAAGCAACTA 619
QY 191 sSerAlaTyrTyrGluArgCysLeuGlnLeuLeuArgProGlyGlyIleLeuAlaVal 211

```

```
Db 620 TCTAAACTACCAACAGCGTCTGATCGATCTGTGTAAGGTTGGAGGTCTGATTCATATGA 679
QY 211 uargValLeuTTPArgGlyLysValLeuGlnProPolysGlyAspValala----- 228
Db 680 CAACACCCCTGTGGAACGGATCTGTGTGGCTCCACCCGATGTCCTCCCTGAGGAATATGT 739
QY 229 -----AlaGluCysValArgAsnLeuAsnGluArgIleArgAspValArgVa 245
Db 740 GAGATATTACAGAGATTCTGTGATGAGCTAAACAAGGCCCTTGTGTGATCCCGCAT 799
QY 245 lTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPheLysIle 262
Db 800 TGAGATCAGCAAAATCCAGTCGGTGACGCGCTCACCTTTGACGCGGTGC 851
```

## RESULT 15

```
US-09-211-710-6
; Sequence 6, Application US/09211710A
; Patent No. 6204434
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N.
; APPLICANT: Havukkala, Ilkka
; APPLICANT: Grierson, Alastair
; TITLE OF INVENTION: Materials and Methods for the
; FILE OF INVENTION: Modification of Plant Lignin Content
; FILE REFERENCE: 11000.1003C3
; CURRENT APPLICATION NUMBER: US/09/211,710A
; CURRENT FILING DATE: 1998-12-14
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-211-710-6
```

## Alignment Scores:

```
Pred. No.: 1,42e-34 Length: 1026
Score: 386.00 Matches: 86
Percent Similarity: 57.56% Conservative: 51
Best Local Similarity: 36.13% Mismatches: 88
Query Match: 28.74% Indels: 13
DB: 3 Gaps: 4
```

US-10-017-407A-306 (1-262) x US-09-211-710-6 (1-1026)

```
QY 35 CysProTrpArgGlyArgGluGln-CysLeuLeuProGluAspSerArgIle 54
Db 149 TGTCCGCCATCAAGAGTGGGACACAAAAGTCTTTTG-----CAGAGCGATGCCCT 199
QY 54 uTrpGlnTyrLeuSerArgSerMet-----ArgGluHisProAlaLeuArgSerIle 72
Db 200 CTATCAGTATATTTGGAACAGCGGTGTACCCTCTGTAGCCCGAGCCCAATGAAGAGCT 259
QY 72 uArgLeuLeuThrLeuGluGlnProGlnGlyAspSerMetThrCysGluGlnAlaG1 92
Db 260 CGCGAAGTGAAGTGCACAGCATCCCTGGAACTCATGACTACTTCTGCCGATGAGGTC 319
QY 92 nLeuLeuAlaAsnLeuAlaArgLeuIleGlnAlaLysIleAlaLeuAspLeuGlyThrPh 112
Db 320 ATTTCTGGGCCCTCTGCTGAAGCTATTAAACCGCAAGAACACCATGGAGATTGGGGTGA 379
QY 112 eThrGlyTyrSerAlaLeuAlaLeuAlaLeuAlaLeuProAlaAspGlyArgValTh 132
Db 380 CACTGGTACTCGCTTCTCAGCAGACCCCTTGATGATGATGATGATGATGATGATGATG 439
QY 132 rCysGluValAlaGlnProProGluLeuGlyArgProLeuTrpArgGlnAlaGluAl 152
Db 440 CATGCACATCAACAGAGAACTATGATATCGGATTCCTATTATTGAGAAAGCAGGAGT 499
QY 152 aGluHisIleAspLeuArgLeuLysProAlaLeuThrLeuAspGluLeuAl 172
Db 500 TGCCCAACAGATTGCTTTCAGAGAGGCCCTCTCTGCGAGTTCTGGACGAACCTGCTTAA 559
```

Search completed: April 20, 2005, 02:30:48  
Job time : 489 secs

```
QY 172 aAlaGlyGluAla---GlyThrPheAspValAlaValValAspAlaAspLysGluAsnCy 191
Db 560 GAATGAGGACATGCATGATCGTTCGATTTTGTGTTGATGCGGACAAAGCAACTA 619
QY 191 sSerAlaTyrTyrGluArgCysLeuGlnLeuLeuArgProGlyGlyIleLeuAlaValle 211
Db 620 TCTAAACTACCAACAGCGTCTGATCGATCTGTGAAGGTTGGAGGTCTGATTCATATGA 679
QY 211 uArgValLeuTTPArgGlyLysValLeuGlnProPolysGlyAspValAla----- 228
Db 680 CAACACCCCTGTGGAACGGATCTGTGTGGCTCCACCCGATGTCCTCCCTGAGGAATATGT 739
QY 229 -----AlaGluCysValArgAsnLeuAsnGluArgIleArgAspValArgVa 245
Db 740 GAGATATTACAGAGATTCTGTGATGAGCTAAACAAGGCCCTTGTGTGATCCCGCAT 799
QY 245 lTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPheLysIle 262
Db 800 TGAGATCAGCAAAATCCAGTCGGTGACGCGCTCACCTTTGACGCGGTGC 851
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.  
OM protein - nucleic search, using frame\_plus\_p2n model  
Run on: April 19, 2005, 22:32:16 ; Search time 586 Seconds  
(without alignments)  
2646.710 Million cell updates/sec

US-10-017-407a-306  
Title: 1343  
Perfect score: 1343  
Sequence: BLOSUM62  
Scoring table: 1 MTOPVRLSPVPAALALGSA.....VRVYISLLPLGDLGLTAFKI 262

US-10-017-407a-306  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues  
Total number of hits satisfying chosen parameters: 8780412  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=xlh  
-O=/cgn2\_1/USPTO.spool/US10017407/runat\_19042005\_142607\_29831/app\_query.fasta\_1.455  
-DB=N Geneseq\_16Dec04 -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOPCL=0  
-LOPEXT=0 -UNITS=bits -START=1 -ENDs=1 -MATRIX=biosum62 -TRANS=human40.cdi  
-LIST=1500 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=1500  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10017407 @CGN 1 1 644 @runat\_19042005\_142607\_29831 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG -SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq\_16Dec04:  
1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002as:\*  
7: Geneseqn2002bs:\*  
8: Geneseqn2003as:\*  
9: Geneseqn2003bs:\*  
10: Geneseqn2003cs:\*  
11: Geneseqn2003ds:\*  
12: Geneseqn2004as:\*  
13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match Length	DB ID	Description
RESULT 1				
ID	ABA05420	standard; cDNA; 789 BP.		
DE	Human O-methyltransferase family member 25692	coding sequence.		
PN	WO200183719-A2.			
PA	(MILL-) MILLENNIUM PHARM INC.			
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 2				
ID	ADQ87466	standard; cDNA; 927 BP.		
DE	Human tumour-associated antigenic target (TAT) cDNA	sequence #4343.		
PN	WO2004060270-A2.			
PA	(GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 3				
ID	AZ98166	standard; cDNA; 985 BP.		
DE	Human NOVX polynucleotide #61.			
PN	US2004058338-A1.			
PA	(AGEE) AGEE M L.			
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 4				
ID	ADQ42272	standard; cDNA; 988 BP.		
DE	Human NOVX polynucleotide #61.			
PN	US2004058338-A1.			
PA	(AGEE) AGEE M L.			
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 5				
ID	AAA37107	standard; cDNA; 989 BP.		
DE	Human PRO1558 (UNQ766) cDNA	sequence SEQ ID NO:305.		
PN	WO200012708-A2.			
PA	(GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 6				
ID	AAF54419	standard; DNA; 989 BP.		
DE	DNA encoding protein of the invention #84.			
PN	WO200078961-A1.			
PA	(GETH) GENENTECH INC.			
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
RESULT 7				
ID	AZ98166	standard; cDNA; 985 BP.		
DE	Human NOVX polynucleotide #61.			
PN	US2004058338-A1.			
PA	(AGEE) AGEE M L.			
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	

```
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
RESULT 7
ID ABK40264 standard; cDNA; 989 BP.
DE cDNA encoding human PRO1558 polypeptide.
PN WO200153486-A1.
PD 26-JUL-2001.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
RESULT 8
ID ACD68458 standard; cDNA; 989 BP.
DE Novel human secreted and transmembrane protein PRO1558 cDNA.
PN US20030731130-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
RESULT 9
ID ACHO4560 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003044841-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
RESULT 10
ID ACD68104 standard; cDNA; 989 BP.
DE Novel human secreted and transmembrane protein PRO1558 cDNA.
PN US20030731129-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
RESULT 11
ID ADC18174 standard; cDNA; 989 BP.
DE Human PRO polynucleotide #86.
PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
RESULT 12
ID ADD70820 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003099625-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
RESULT 13
ID ADD39897 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
RESULT 14
ID ADD70343 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
RESULT 15
ID ADD38464 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
RESULT 16
ID ADD39420 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
RESULT 17
ID ADD38943 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
RESULT 18
ID ADD40374 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
RESULT 19
ID ADE50595 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003069179-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
RESULT 20
ID ADE20207 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003092883-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
RESULT 21
ID ADE50118 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003082626-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
RESULT 22
ID ADE21676 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003082628-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
```



```

RESULT 23
ID ADF30101 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003204053-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 100.00%
RESULT 24
ID ADF55994 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003204054-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 100.00%
RESULT 25
ID ADH9498 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003065142-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 100.00%
RESULT 26
ID ADJ37302 standard; cDNA; 989 BP.
DE Human tumour therapy associated PRO1558 cDNA.
PN US2003211096-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 100.00%
RESULT 27
ID ADE96678 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003195347-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 100.00%
RESULT 28
ID ADF25989 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003199675-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 100.00%
RESULT 29
ID ADF24888 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003198993-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 100.00%
RESULT 30
ID ADF29624 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003203401-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 100.00%
RESULT 31

```

```

ID ADE97155 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003195334-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 100.00%
RESULT 32
ID ADH03193 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003216562-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 100.00%
RESULT 33
ID ADH04147 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003220471-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 100.00%
RESULT 34
ID ADH03670 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003224478-A1.
PD 04-DEC-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 100.00%
RESULT 35
ID ADG68226 standard; cDNA; 989 BP.
DE Human PRO polypeptide cDNA #11.
PN US2003170228-A1.
PD 11-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 100.00%
RESULT 36
ID ADH04624 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2004005626-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 100.00%
RESULT 37
ID ADH61625 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2004014130-A1.
PD 22-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 100.00%
RESULT 38
ID ADL94824 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2004073015-A1.
PD 15-APR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 100.00%
RESULT 39
ID ADO42276 standard; cDNA; 989 BP.

```

```

DE Human NOVX polynucleotide #63.
PN US2004058338-A1.
PD 25-MAR-2004.
PA (AGEE//) AGEE M L.
PA (ALSO//) ALSOBROOK J P.
PA (ANDE//) ANDERSON D W.
PA (BERG//) BERGHS C.
PA (BOLD//) BOLDOG F L.
PA (BURG//) BURGESS C E.
PA (CATT//) CATTERTON E.
PA (DIPI//) DIPIPO V A.
PA (EDIN//) EDINGER S R.
PA (EISE//) EISEN A.
PA (ELLE//) ELLERMAN K.
PA (GANG//) GANGOLLI E A.
PA (GERL//) GERLACH V.
PA (GORM//) GORMAN L.
PA (ROTH//) ROTHBERG B G.
PA (GUOX//) GUO X S.
PA (HERE//) HEREMANN J L.
PA (HALV//) HALVORSEN Y.
PA (JIWW//) JI W.
PA (KEKU//) KEKUDA R.
PA (KHRA//) KHRAMTSOV N V.
PA (LARO//) LAROCHELLE W J.
PA (LEPL//) LEPLY D M.
PA (LILL//) LI L.
PA (MACD//) MACDOUGALL J R.
PA (MILL//) MILLER C E.
PA (ORTT//) ORT T.
PA (PADI//) PADIGARU M.
PA (PATT//) PATTURAJAN M.
PA (PENA//) PENA C E A.
PA (PEYM//) PEYMAN J A.
PA (RIEG//) RIEGER D K.
PA (ROTH//) ROTHENBERG M E.
PA (SHEN//) SHENOY S G.
PA (SMIT//) SMITHSON G.
PA (SPAD//) SPADERNA S K.
PA (SPYT//) SPYTEK K A.
PA (STON//) STONE D J.
PA (TAUP//) TAUPIER R J.
PA (VERN//) VERNET C A M.
PA (VOSS//) VOSS E Z.
PA (ZHON//) ZHONG W.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 40
ID ABA05419 standard; cDNA; 1037 BP.
DE Human O-methyltransferase family member 25692 encoding cDNA.
PN WO200183719-A2.
PD 08-NOV-2001.
PA (MILL//) MILLENNIUM PHARM INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 41
ID ABQ61039 standard; cDNA; 1100 BP.
DE Human PRO1558 protein encoding sequence.
PN WO200231111-A2.
PD 18-APR-2002.
PA (HYSE//) HYSEQ INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 42
ID AAH33455 standard; cDNA; 967 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:511.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA//) HUMAN GENOME SCI INC.
Percent Similarity: 98.85%
Best Local Similarity: 98.85%
Query Match: 98.59%
Indels: 0
Mismatch: 3
Indels: 0
RESULT 43
ID AAC76634 standard; cDNA; 812 BP.
DE Human ORFX RF2189 polynucleotide sequence SEQ ID NO:4377.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA//) CURAGEN CORP.
Percent Similarity: 99.14%
Best Local Similarity: 99.14%
Query Match: 87.79%
Indels: 0
Conservative: 0
Mismatch: 2
Indels: 0
RESULT 44
ID AAD56372 standard; DNA; 876 BP.
DE Human secreted protein-encoding gene 11 cDNA clone HTAQO18, SEQ ID NO:32.
PN WO2003038038-A2.
PD 08-MAY-2003.
PA (HUMA//) HUMAN GENOME SCI INC.
Percent Similarity: 82.51%
Best Local Similarity: 82.51%
Query Match: 76.40%
Indels: 46
Conservative: 0
Mismatch: 1
Indels: 46
RESULT 45
ID AAD56361 standard; DNA; 885 BP.
DE Human secreted protein-encoding gene 11 cDNA clone HTAQO18, SEQ ID NO:21.
PN WO2003038038-A2.
PD 08-MAY-2003.
PA (HUMA//) HUMAN GENOME SCI INC.
Percent Similarity: 82.51%
Best Local Similarity: 82.51%
Query Match: 76.40%
Indels: 46
Conservative: 0
Mismatch: 1
Indels: 46
RESULT 46
ID ADO42274 standard; cDNA; 787 BP.
DE Human NOVX polynucleotide #62.
PN US2004058338-A1.
PD 25-MAR-2004.
PA (AGEE//) AGEE M L.
PA (ALSO//) ALSOBROOK J P.
PA (ANDE//) ANDERSON D W.
PA (BERG//) BERGHS C.
PA (BOLD//) BOLDOG F L.
PA (BURG//) BURGESS C E.
PA (CATT//) CATTERTON E.
PA (DIPI//) DIPIPO V A.
PA (EDIN//) EDINGER S R.
PA (EISE//) EISEN A.
PA (ELLE//) ELLERMAN K.
PA (GANG//) GANGOLLI E A.
PA (GERL//) GERLACH V.
PA (GORM//) GORMAN L.
PA (ROTH//) ROTHBERG B G.
PA (GUOX//) GUO X S.
PA (KHRA//) KHRAMTSOV N V.
PA (LARO//) LAROCHELLE W J.
PA (LEPL//) LEPLY D M.
PA (LILL//) LI L.
PA (MACD//) MACDOUGALL J R.
PA (MILL//) MILLER C E.
PA (ORTT//) ORT T.
PA (PADI//) PADIGARU M.
PA (PATT//) PATTURAJAN M.
PA (PENA//) PENA C E A.
PA (PEYM//) PEYMAN J A.
PA (RIEG//) RIEGER D K.
PA (ROTH//) ROTHENBERG M E.
PA (SHEN//) SHENOY S G.
PA (SMIT//) SMITHSON G.
PA (SPAD//) SPADERNA S K.
PA (SPYT//) SPYTEK K A.
PA (STON//) STONE D J.
PA (TAUP//) TAUPIER R J.
PA (VERN//) VERNET C A M.
PA (VOSS//) VOSS E Z.
PA (ZHON//) ZHONG W.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indels: 0

```

PA (VERN/) VERNET C A M.  
PA (VOSS/) VOSS E Z.  
PA (ZHONG/) ZHONG M.  
Percent Similarity: 70.23%  
Best Local Similarity: 70.23%  
Query Match: 65.82%  
Indels: 78  
RESULT 47  
ID ADD34178 standard; DNA; 770 BP.  
DE Mouse mitochondrial DNA sequence SEQ ID NO:1956.  
PN WO2003020220-A2.  
PD 13-MAR-2003.  
PA (UYEM-) UNIV EMORY.  
Percent Similarity: 92.49%  
Best Local Similarity: 84.97%  
Query Match: 56.22%  
Indels: 0  
RESULT 48  
ID ACH35890 standard; cDNA; 458 BP.  
DE Human endothelial cell cDNA #4023.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Percent Similarity: 99.02%  
Best Local Similarity: 98.04%  
Query Match: 37.90%  
Indels: 0  
RESULT 49  
ID ACH35195 standard; cDNA; 474 BP.  
DE Human endothelial cell cDNA #3328.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Percent Similarity: 99.02%  
Best Local Similarity: 98.04%  
Query Match: 37.90%  
Indels: 0  
RESULT 50  
ID ADM80035 standard; DNA; 11171 BP.  
DE Spiramycin biosynthesis related DNA, SEQ ID 2.  
PN FR2845394-A1.  
PD 09-APR-2004.  
PA (AVET ) AVENTIS PHARMA SA.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Percent Similarity: 50.49%  
Best Local Similarity: 39.09%  
Query Match: 33.73%  
Indels: 56  
RESULT 51  
ID ADN97551 standard; DNA; 11171 BP.  
DE S ambofaciens spiramycin biosynthetic enzyme genomic region #2.  
PN WO2004033689-A2.  
PD 22-APR-2004.  
PA (AVET ) AVENTIS PHARMA SA.  
PA (CNRS ) CNRS.  
Percent Similarity: 50.49%  
Best Local Similarity: 39.09%  
Query Match: 33.73%  
Indels: 56  
RESULT 52  
ID AAA81501 standard; DNA; 48275 BP.  
DE N. meningitidis partial DNA sequence gnm\_48 SEQ ID NO:48.  
PN WO200022430-A2.  
PD 20-APR-2000.  
PA (CHIR ) CHIRON CORP.  
Percent Similarity: 53.45%  
Best Local Similarity: 36.90%  
Query Match: 33.54%  
Indels: 37  
RESULT 53  
ID AAA81489 standard; DNA; 837096 BP.  
DE N. meningitidis partial DNA sequence gnm\_37 SEQ ID NO:37.

PN WO200022430-A2.  
PD 20-APR-2000.  
PA (CHIR ) CHIRON CORP.  
Percent Similarity: 53.45%  
Best Local Similarity: 36.90%  
Query Match: 33.54%  
Indels: 37  
RESULT 54  
ID AAF21610 standard; DNA; 349980 BP.  
DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:111.  
PN WO200066791-A1.  
PD 09-NOV-2000.  
PA (CHIR ) CHIRON CORP.  
PA (GENO-) INST GENOMIC RES.  
Percent Similarity: 53.45%  
Best Local Similarity: 36.90%  
Query Match: 33.54%  
Indels: 37  
RESULT 55  
ID ABZ40101 standard; DNA; 666 BP.  
DE N. gonorrhoeae nucleotide sequence SEQ ID 4791.  
PN WO200279243-A2.  
PD 10-OCT-2002.  
PA (CHIR-) CHIRON SPA.  
Percent Similarity: 62.15%  
Best Local Similarity: 42.52%  
Query Match: 32.69%  
Indels: 10  
RESULT 56  
ID ADM80044 standard; DNA; 675 BP.  
DE Spiramycin biosynthesis orfs\*, SEQ ID 11.  
PN FR2845394-A1.  
PD 09-APR-2004.  
PA (AVET ) AVENTIS PHARMA SA.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Percent Similarity: 60.99%  
Best Local Similarity: 46.19%  
Query Match: 32.61%  
Indels: 8  
RESULT 57  
ID ADN97560 standard; DNA; 675 BP.  
DE S ambofaciens spiramycin biosynthetic gene ORF5\*.  
PN WO2004033689-A2.  
PD 22-APR-2004.  
PA (AVET ) AVENTIS PHARMA SA.  
PA (CNRS ) CNRS.  
Percent Similarity: 60.99%  
Best Local Similarity: 46.19%  
Query Match: 32.61%  
Indels: 8  
RESULT 58  
ID ABD04592 standard; DNA; 846 BP.  
DE Pseudomonas aeruginosa polynucleotide #3196.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 55.19%  
Best Local Similarity: 42.32%  
Query Match: 31.94%  
Indels: 26  
RESULT 59  
ID AAQ44449 standard; DNA; 2381 BP.  
DE 3-acylating enzyme coding sequence.  
PN JP06038750-A.  
PD 15-FEB-1994.  
PA (MEIJ ) MEIJI SEIKA KAISHA.  
Percent Similarity: 54.12%  
Best Local Similarity: 39.61%  
Query Match: 31.68%  
Indels: 24  
RESULT 60  
ID ADM45913 standard; DNA; 84428 BP.  
DE Streptomyces mycarofaciens midcamycin polyketide synthetase DNA.  
PN JP2004049100-A.  
PD 19-FEB-2004.  
PA (MEIJ ) MEIJI SEIKA KAISHA LTD.  
Percent Similarity: 54.12%  
Best Local Similarity: 39.61%  
Query Match: 31.68%  
Indels: 24  
RESULT 61

```

ID AAX25215 standard; cDNA; 1218 BP.
DE Maize caffeoyl-CoA 3-O-methyltransferase cDNA.
PN WO9910498-A2.
PD 04-MAR-1999.
PA (PION-) PIONEER HI-BRED INT INC.
Percent Similarity: 56.59%
Best Local Similarity: 39.15%
Query Match: 30.75%
Indels: 15
Conservative: 45
Mismatch: 97
Indel: 15
RESULT 62
ID AAD05742 standard; cDNA; 1218 BP.
DE Maize caffeoyl-CoA 3-O-methyltransferase (CCoA-OMT) cDNA.
PN WO200134817-A2.
PD 17-MAY-2001.
PA (PION-) PIONEER HI-BRED INT INC.
Percent Similarity: 56.59%
Best Local Similarity: 39.15%
Query Match: 30.75%
Indels: 15
Conservative: 45
Mismatch: 97
Indel: 15
RESULT 63
ID ADI39160 standard; DNA; 86941 BP.
DE Streptomyces hygroscopicus herbimycin gene cluster, SEQ ID NO:2.
PN WO2003106653-A2.
PD 24-DEC-2003.
PA (KOSA-) KOSAN BIOSCIENCES INC.
Percent Similarity: 54.25%
Best Local Similarity: 38.87%
Query Match: 30.60%
Indels: 21
Conservative: 38
Mismatch: 92
Indel: 21
RESULT 64
ID ADI39159 standard; DNA; 85692 BP.
DE Streptomyces hygroscopicus geldanamycin gene cluster, SEQ ID NO:1.
PN WO2003106653-A2.
PD 24-DEC-2003.
PA (KOSA-) KOSAN BIOSCIENCES INC.
Percent Similarity: 59.71%
Best Local Similarity: 42.72%
Query Match: 30.49%
Indels: 3
Conservative: 35
Mismatch: 80
Indel: 3
RESULT 65
ID ABS63417 standard; cDNA; 980 BP.
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).
PN US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAFA/) RAFALSKI J A.
Percent Similarity: 57.26%
Best Local Similarity: 38.17%
Query Match: 30.19%
Indels: 10
Conservative: 46
Mismatch: 93
Indel: 10
RESULT 66
ID ABS63407 standard; cDNA; 891 BP.
DE DNA encoding corn caffeoyl-CoA O-methyltransferase (CCOMT).
PN US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAFA/) RAFALSKI J A.
Percent Similarity: 56.03%
Best Local Similarity: 38.91%
Query Match: 29.86%
Indels: 25
Conservative: 44
Mismatch: 88
Indel: 25
RESULT 67
ID AAD19545 standard; cDNA; 744 BP.
DE Medicago sativa caffeic acid 3-O-methyltransferase (COMT) cDNA.
PN WO200173090-A2.
PD 04-OCT-2001.
PA (ROBE-) ROBERTS NOBLE FOUND INC SAMMUEL.
Percent Similarity: 59.91%
Best Local Similarity: 36.49%
Query Match: 29.67%
Indels: 9
Conservative: 52
Mismatch: 80
Indel: 9
RESULT 68
ID ADI30327 standard; cDNA; 744 BP.
DE Alfalfa harvest inducible cDNA sequence H12.
PN WO2004002216-A2.
PD 08-JAN-2004.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAFA/) RAFALSKI J A.
Percent Similarity: 58.11%
Best Local Similarity: 39.64%
Query Match: 29.23%
Indels: 9
Conservative: 41
Mismatch: 84
Indel: 9
RESULT 69
ID ADI30333 standard; DNA; 1906 BP.
DE Alfalfa harvest inducible H12 gene genomic DNA sequence.
PN WO2004002216-A2.
PD 08-JAN-2004.
PA (UYGU-) UNIV GUELPH.
Percent Similarity: 59.91%
Best Local Similarity: 36.49%
Query Match: 29.67%
Indels: 9
Conservative: 52
Mismatch: 80
Indel: 9
RESULT 70
ID ADA70823 standard; DNA; 783 BP.
DE Rice gene, SEQ ID 4146.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Percent Similarity: 55.86%
Best Local Similarity: 37.89%
Query Match: 29.43%
Indels: 20
Conservative: 46
Mismatch: 93
Indel: 20
RESULT 71
ID ABS63412 standard; cDNA; 1058 BP.
DE DNA encoding rice caffeoyl-CoA O-methyltransferase (CCOMT).
PN US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAFA/) RAFALSKI J A.
Percent Similarity: 55.86%
Best Local Similarity: 37.89%
Query Match: 29.43%
Indels: 20
Conservative: 46
Mismatch: 93
Indel: 20
RESULT 72
ID ABS63427 standard; cDNA; 1078 BP.
DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).
PN US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAFA/) RAFALSKI J A.
Percent Similarity: 54.14%
Best Local Similarity: 38.35%
Query Match: 29.34%
Indels: 23
Conservative: 42
Mismatch: 100
Indel: 23
RESULT 73
ID ADA71076 standard; DNA; 1338 BP.
DE Rice gene, SEQ ID 4399.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Percent Similarity: 57.87%
Best Local Similarity: 40.74%
Query Match: 29.28%
Indels: 12
Conservative: 37
Mismatch: 79
Indel: 12
RESULT 74
ID ABS63418 standard; cDNA; 962 BP.
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).
PN US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAFA/) RAFALSKI J A.
Percent Similarity: 58.11%
Best Local Similarity: 39.64%
Query Match: 29.23%
Indels: 9
Conservative: 41
Mismatch: 84
Indel: 9
RESULT 75
ID ABS63419 standard; cDNA; 1023 BP.
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).
PN US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAFA/) RAFALSKI J A.
Percent Similarity: 58.11%
Best Local Similarity: 39.64%
Query Match: 29.23%
Indels: 9
Conservative: 41
Mismatch: 84
Indel: 9

```

Best Local Similarity: 39.64% Mismatches: 84  
Query Match: 29.23% Indels: 9  
RESULT 76  
ID ADC68436 standard; cDNA; 1051 BP.  
DE Lolium perenne lignin biosynthesis protein cDNA SEQ ID NO:146.  
PN WO2003040306-A2.  
PD 15-MAY-2003.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (WRIG-) WRIGHTSON SEEDS LTD.  
Percent Similarity: 56.43% Conservative: 42  
Best Local Similarity: 39.00% Mismatches: 87  
Query Match: 29.23% Indels: 18  
RESULT 77  
ID ADC68544 standard; cDNA; 1059 BP.  
DE Lolium perenne lignin biosynthesis protein cDNA SEQ ID NO:36.  
PN WO2003040306-A2.  
PD 15-MAY-2003.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (WRIG-) WRIGHTSON SEEDS LTD.  
Percent Similarity: 56.43% Conservative: 42  
Best Local Similarity: 39.00% Mismatches: 87  
Query Match: 29.23% Indels: 18  
RESULT 78  
ID ADN74200 standard; cDNA; 780 BP.  
DE Thale cress cDNA expressed in E2Fa/Dpa expressing plants SeqID 2095.  
PN WO2004035798-A2.  
PD 29-APR-2004.  
PA (CROP-) CROPDESIGN NV.  
Percent Similarity: 58.85% Conservative: 48  
Best Local Similarity: 37.61% Mismatches: 82  
Query Match: 29.15% Indels: 11  
RESULT 79  
ID ADN73162 standard; cDNA; 780 BP.  
DE Thale cress cDNA upregulated in E2Fa/Dpa expressing plants SeqID 1057.  
PN WO2004035798-A2.  
PD 29-APR-2004.  
PA (CROP-) CROPDESIGN NV.  
Percent Similarity: 58.85% Conservative: 48  
Best Local Similarity: 37.61% Mismatches: 82  
Query Match: 29.15% Indels: 11  
RESULT 80  
ID AAC42559 standard; cDNA; 1033 BP.  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 36009.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Percent Similarity: 58.85% Conservative: 48  
Best Local Similarity: 37.61% Mismatches: 82  
Query Match: 29.15% Indels: 11  
RESULT 81  
ID ABN98364 standard; cDNA; 1072 BP.  
DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 132.  
PN US2002023281-A1.  
PD 21-FEB-2002.  
PA (GORL-) GORLACH J.  
PA (ANY/) AN Y.  
PA (HAM/) HAMILTON C M.  
PA (PRIC/) PRICE J L.  
PA (RAIN/) RAINES T M.  
PA (YUY/) YU Y.  
PA (RAME/) RAMEKA J G.  
PA (PAGE/) PAGE A.  
PA (MATH/) MATHAW A V.  
PA (LEDF/) LEDFORD B L.  
PA (WOES/) WOESSNER J P.  
PA (HAAS/) HAAS W D.  
PA (GARC/) GARCIA C A.  
PA (KRICK/) KRICKER M.  
PA (SLAT/) SLATER T.  
PA (DAVI/) DAVIS K R.  
PA (ALLE/) ALLEN K.  
PA (HOFF/) HOFFMAN N.  
PA (HURB/) HURBAN P.  
Percent Similarity: 58.85% Conservative: 48

Best Local Similarity: 37.61% Mismatches: 82  
Query Match: 29.15% Indels: 11  
RESULT 82  
ID AAC44172 standard; cDNA; 1180 BP.  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 41890.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Percent Similarity: 58.85% Conservative: 48  
Best Local Similarity: 37.61% Mismatches: 82  
Query Match: 29.15% Indels: 11  
RESULT 83  
ID AAC45547 standard; cDNA; 1032 BP.  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 46896.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Percent Similarity: 55.14% Conservative: 49  
Best Local Similarity: 34.98% Mismatches: 88  
Query Match: 29.00% Indels: 21  
RESULT 84  
ID ABS63413 standard; cDNA; 997 BP.  
DE DNA encoding rice caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAFALSKI J A.  
Percent Similarity: 57.47% Conservative: 40  
Best Local Similarity: 39.37% Mismatches: 82  
Query Match: 28.97% Indels: 12  
RESULT 85  
ID ABS63429 standard; cDNA; 953 BP.  
DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAFALSKI J A.  
Percent Similarity: 55.51% Conservative: 46  
Best Local Similarity: 38.60% Mismatches: 104  
Query Match: 28.82% Indels: 18  
RESULT 86  
ID ABS54115 standard; cDNA; 967 BP.  
DE Tobacco-caffeoyl CoA O-methyltransferase-9 (CCOAMT-9) cDNA.  
PN US6441272-B1.  
PD 27-AUG-2002.  
PA (UYGE-) UNIV GEORGIA RES FOUND INC.  
Percent Similarity: 58.56% Conservative: 48  
Best Local Similarity: 36.94% Mismatches: 83  
Query Match: 28.78% Indels: 9  
RESULT 87  
ID ADA49212 standard; cDNA; 798 BP.  
DE Maize gene conferring disease resistance in plants.  
PN WO2003000906-A2.  
PD 03-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Percent Similarity: 55.56% Conservative: 48  
Best Local Similarity: 37.16% Mismatches: 91  
Query Match: 28.74% Indels: 25  
RESULT 88  
ID AAA68001 standard; cDNA; 1012 BP.  
DE Pinus radiata OMT nucleotide sequence SEQ ID NO:94.  
PN WO200022099-A1.  
PD 20-APR-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Percent Similarity: 57.56% Conservative: 51  
Best Local Similarity: 36.13% Mismatches: 88  
Query Match: 28.74% Indels: 13  
RESULT 89  
ID ADD41751 standard; cDNA; 1012 BP.  
DE O-methyl transferase DNA #9.  
PN US200313173-A1.  
PD 10-JUL-2003.

PA (BLOK/) BLOKSBERG L N.  
 PA (HAVU/) HAVUKKALA I.  
 Percent Similarity: 57.56%  
 Best Local Similarity: 36.13%  
 Query Match: 28.74%  
 RESULT 90  
 ID AAV23912 standard; DNA; 1026 BP.  
 DE Plant OMT enzyme DNA sequence.  
 PN WO9811205-A2.  
 PD 19-MAR-1998.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Percent Similarity: 57.56%  
 Best Local Similarity: 36.13%  
 Query Match: 28.74%  
 RESULT 91  
 ID AAZ06875 standard; cDNA; 1026 BP.  
 DE Pine O-methyl transferase (OMT) partial cDNA 1.  
 PN US952486-A.  
 PD 14-SEP-1999.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Percent Similarity: 57.56%  
 Best Local Similarity: 36.13%  
 Query Match: 28.74%  
 RESULT 92  
 ID AAA67913 standard; DNA; 1026 BP.  
 DE Pinus radiata OMT nucleotide sequence SEQ ID NO:6.  
 PN WO200022099-A1.  
 PD 20-APR-2000.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Percent Similarity: 57.56%  
 Best Local Similarity: 36.13%  
 Query Match: 28.74%  
 RESULT 93  
 ID ADD41663 standard; DNA; 1026 BP.  
 DE O-methyl transferase DNA #1.  
 PN US200313173-A1.  
 PD 10-JUL-2003.  
 PA (BLOK/) BLOKSBERG L N.  
 PA (HAVU/) HAVUKKALA I.  
 Percent Similarity: 57.56%  
 Best Local Similarity: 36.13%  
 Query Match: 28.74%  
 RESULT 94  
 ID ABS63425 standard; cDNA; 1118 BP.  
 DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Percent Similarity: 55.56%  
 Best Local Similarity: 37.16%  
 Query Match: 28.74%  
 RESULT 95  
 ID ABS63408 standard; cDNA; 1146 BP.  
 DE DNA encoding corn caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Percent Similarity: 55.56%  
 Best Local Similarity: 37.16%  
 Query Match: 28.74%  
 RESULT 96  
 ID AAX25208 standard; cDNA; 1160 BP.  
 DE Maize caffeoyl-CoA 3-O-methyltransferase cDNA.  
 PN WO9910498-A2.  
 PD 04-MAR-1999.  
 PA (PION-) PIONEER HI-BRED INT INC.

Percent Similarity: 55.56%  
 Best Local Similarity: 37.16%  
 Query Match: 28.74%  
 RESULT 97  
 ID ABS63415 standard; cDNA; 931 BP.  
 DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Percent Similarity: 59.46%  
 Best Local Similarity: 36.04%  
 Query Match: 28.70%  
 RESULT 98  
 ID ADC8545 standard; cDNA; 1063 BP.  
 DE S. arundinaceus lignin biosynthesis protein cDNA SEQ ID NO:37.  
 PN WO2003040306-A2.  
 PD 15-MAY-2003.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (WRIG-) WRIGHTSON SEEDS LTD.  
 Percent Similarity: 54.85%  
 Best Local Similarity: 37.69%  
 Query Match: 28.70%  
 RESULT 99  
 ID ADA71075 standard; DNA; 783 BP.  
 DE Rice gene. SEQ ID 4398.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Percent Similarity: 52.73%  
 Best Local Similarity: 38.67%  
 Query Match: 28.59%  
 RESULT 100  
 ID AAX25210 standard; cDNA; 1003 BP.  
 DE Maize caffeoyl-CoA 3-O-methyltransferase cDNA.  
 PN WO9910498-A2.  
 PD 04-MAR-1999.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Percent Similarity: 52.55%  
 Best Local Similarity: 36.50%  
 Query Match: 28.56%  
 RESULT 101  
 ID ABS63409 standard; cDNA; 1057 BP.  
 DE DNA encoding corn caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Percent Similarity: 52.55%  
 Best Local Similarity: 36.50%  
 Query Match: 28.56%  
 RESULT 102  
 ID ABS63416 standard; cDNA; 929 BP.  
 DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Percent Similarity: 56.43%  
 Best Local Similarity: 36.93%  
 Query Match: 28.48%  
 RESULT 103  
 ID ACN60610 standard; cDNA; 617 BP.  
 DE Cotton gynoecium tissue EST Clone ID: LTB3829-025-Q6-K6-F5, SEQ:15391.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.



Percent Similarity:	60.00%	Conservative:	38
Best Local Similarity:	41.00%	Mismatches:	79
Query Match:	28.44%	Indels:	1
RESULT 104			
ID	ABS63428 standard; cDNA; 1049 BP.		
DE	DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).		
PN	US2002081693-A1.		
PD	27-JUN-2002.		
PA	(CAHO)/ CAROON R E.		
PA	(FADE)/ FADER G M.		
PA	(RAFA)/ RAFALSKI J A.		
Percent Similarity:	55.15%	Conservative:	46
Best Local Similarity:	38.24%	Mismatches:	105
Query Match:	28.37%	Indels:	18
RESULT 105			
ID	ABS4114 standard; DNA; 845 BP.		
DE	Tobacco caffeoyl CoA O-methyltransferase-3 (CCOAMT-3) cDNA.		
PN	US6441272-B1.		
PD	27-AUG-2002.		
PA	(UYGE-) UNIV GEORGIA RES FOUND INC.		
Percent Similarity:	57.66%	Conservative:	47
Best Local Similarity:	36.49%	Mismatches:	85
Query Match:	28.26%	Indels:	9
RESULT 106			
ID	ADA49019 standard; DNA; 1112 BP.		
DE	Maize gene conferring disease resistance in plants.		
PN	WO2003000906-A2.		
PD	03-JAN-2003.		
PA	(SYGN ) SYNGENTA PARTICIPATIONS AG.		
Percent Similarity:	53.58%	Conservative:	40
Best Local Similarity:	38.49%	Mismatches:	103
Query Match:	28.22%	Indels:	22
RESULT 107			
ID	AX25209 standard; cDNA; 944 BP.		
DE	Maize caffeoyl-CoA 3-O-methyltransferase cDNA.		
PN	WO9910498-A2.		
PD	04-MAR-1999.		
PA	(PION-) PIONEER HI-BRED INT INC.		
Percent Similarity:	52.42%	Conservative:	42
Best Local Similarity:	36.80%	Mismatches:	114
Query Match:	28.15%	Indels:	15
RESULT 108			
ID	ABN87108 standard; cDNA; 1113 BP.		
DE	Lolium perenne lpCCOAMTa nucleotide sequence SEQ ID NO:1.		
PN	WO200226994-A1.		
PD	04-APR-2002.		
PA	(AGRI-) AGRIC VICTORIA SERVICES PTY LTD.		
PA	(AGRE-) AGRESEARCH LTD.		
Percent Similarity:	56.02%	Conservative:	44
Best Local Similarity:	37.76%	Mismatches:	88
Query Match:	28.11%	Indels:	18
RESULT 109			
ID	ADR65554 standard; cDNA; 1233 BP.		
DE	Cotton cDNA sequence, SEQ ID 6335.		
PN	US2004181830-A1.		
PD	16-SEP-2004.		
PA	(KOVA)/ KOVALIC D K.		
PA	(ZHOU)/ ZHOU Y.		
PA	(CAOY)/ CAO Y.		
Percent Similarity:	56.91%	Conservative:	53
Best Local Similarity:	35.37%	Mismatches:	88
Query Match:	28.07%	Indels:	18
RESULT 110			
ID	ABN87245 standard; cDNA; 1161 BP.		
DE	Lolium perenne CCOAMT1 cDNA sequence SEQ ID NO:168.		
PN	WO200226994-A1.		
PD	04-APR-2002.		
PA	(AGRI-) AGRIC VICTORIA SERVICES PTY LTD.		
PA	(AGRE-) AGRESEARCH LTD.		
Percent Similarity:	56.41%	Conservative:	43
Best Local Similarity:	38.03%	Mismatches:	88
Query Match:	28.03%	Indels:	14
RESULT 111			

ID	AAQ32259 standard; cDNA; 1258 BP.				
DE	Caffeoyl-CoA-3-O-methyltransferase gene (pL2-4).				
PN	DS4117747-A.				
PD	03-DEC-1992.				
PA	(FARB.) BAYER AG.				
Percent Similarity:	57.21%	Conservative:	45		
Best Local Similarity:	36.94%	Mismatches:	86		
Query Match:	28.03%	Indels:	9		
RESULT 112					
ID	ABS63410 standard; cDNA; 923 BP.				
DE	DNA encoding corn caffeoyl-CoA O-methyltransferase (CCOMT).				
PN	US2002081693-A1.				
PD	27-JUN-2002.				
PA	(CAHO)/ CAHOON R E.				
PA	(FADE)/ FADER G M.				
PA	(RAFA)/ RAPALSKI J A.				
Percent Similarity:	53.10%	Conservative:	41		
Best Local Similarity:	37.21%	Mismatches:	109		
Query Match:	28.00%	Indels:	13		
RESULT 113					
ID	ASN87246 standard; cDNA; 1199 BP.				
DE	Lolium perenne CCOAMT2 cDNA sequence SEQ ID NO:170.				
PN	WO200226594-A1.				
PD	04-APR-2002.				
PA	(AGRI-) AGRIC VICTORIA SERVICES PTY LTD.				
PA	(AGRE-) AGRESEARCH LTD.				
Percent Similarity:	56.36%	Conservative:	42		
Best Local Similarity:	38.56%	Mismatches:	85		
Query Match:	27.89%	Indels:	18		
RESULT 114					
ID	ABS54112 standard; DNA; 870 BP.				
DE	Tobacco caffeoyl CoA O-methyltransferase-1 (CCOAMT-1) cDNA.				
PN	US6441272-B1.				
PD	27-AUG-2002.				
PA	(UYGE-) UNIV GEORGIA RES FOUND INC.				
Percent Similarity:	58.11%	Conservative:	50		
Best Local Similarity:	35.59%	Mismatches:	84		
Query Match:	27.81%	Indels:	9		
RESULT 115					
ID	ABS54113 standard; DNA; 811 BP.				
DE	Tobacco caffeoyl CoA O-methyltransferase-2 (CCOAMT-2) cDNA.				
PN	US6441272-B1.				
PD	27-AUG-2002.				
PA	(UYGE-) UNIV GEORGIA RES FOUND INC.				
Percent Similarity:	58.72%	Conservative:	49		
Best Local Similarity:	36.24%	Mismatches:	81		
Query Match:	27.74%	Indels:	9		
RESULT 116					
ID	AAC45004 standard; DNA; 917 BP.				
DE	Arabidopsis thaliana DNA fragment SEQ ID NO: 44938.				
PN	EP1033405-A2.				
PD	06-SEP-2000.				
Percent Similarity:	56.64%	Conservative:	40		
Best Local Similarity:	38.94%	Mismatches:	86		
Query Match:	27.48%	Indels:	12		
RESULT 117					
ID	ADR73686 standard; DNA; 1252 BP.				
DE	Rice promoter putative caffeoyl CoA3O methyltransferase CDS.				
PN	WO2004070039-A2.				
PD	19-AUG-2004.				
PA	(CROP-) CROPDESIGN NV.				
Percent Similarity:	57.47%	Conservative:	40		
Best Local Similarity:	39.37%	Mismatches:	82		
Query Match:	27.48%	Indels:	13		
RESULT 118					
ID	ABS63424 standard; cDNA; 1018 BP.				
DE	DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).				
PN	US2002081693-A1.				
PD	27-JUN-2002.				
PA	(CAHO)/ CAHOON R E.				
PA	(FADE)/ FADER G M.				
PA	(RAFA)/ RAPALSKI J A.				
Percent Similarity:	50.55%	Conservative:	42		

Best Local Similarity: 35.06% Mismatches: 84  
 Query Match: 27.44% Indels: 50  
 RESULT 119  
 ID ADA48371 standard; DNA; 835 BP.  
 DE Rice gene conferring disease resistance in plants.  
 PN WO200300906-A2.  
 PD 03-JAN-2003.  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 Percent Similarity: 56.76% Conservative: 46  
 Best Local Similarity: 39.00% Mismatches: 89  
 Query Match: 27.36% Indels: 24  
 RESULT 120  
 ID ADR62522 standard; cDNA; 995 BP.  
 DE Cotton cDNA sequence, SEQ ID 3303.  
 PN US2004181830-A1.  
 PD 16-SEP-2004.  
 PA (KOVA/) KOVALIC D K.  
 PA (ZHOU/) ZHOU Y.  
 PA (CAOY/) CAO Y.  
 Percent Similarity: 58.30% Conservative: 49  
 Best Local Similarity: 36.32% Mismatches: 83  
 Query Match: 27.29% Indels: 10  
 RESULT 121  
 ID AEN94134 standard; DNA; 326 BP.  
 DE Gene #632 used to diagnose liver cancer.  
 PN WO200223103-A2.  
 PD 11-APR-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 98.65% Conservative: 0  
 Best Local Similarity: 98.65% Mismatches: 0  
 Query Match: 27.25% Indels: 1  
 RESULT 122  
 ID AEN87118 standard; cDNA; 1103 BP.  
 DE Lolium perenne LpCCoMTb nucleotide sequence SEQ ID NO:12.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Percent Similarity: 54.23% Conservative: 50  
 Best Local Similarity: 35.00% Mismatches: 100  
 Query Match: 26.99% Indels: 19  
 RESULT 123  
 ID AB214595 standard; DNA; 729 BP.  
 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2400.  
 PN WO200218655-A2.  
 PD 28-FEB-2002.  
 PA (SCRI ) SCRIPPS RES INST.  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 Percent Similarity: 56.28% Conservative: 37  
 Best Local Similarity: 39.07% Mismatches: 84  
 Query Match: 26.81% Indels: 10  
 RESULT 124  
 ID AAC42096 standard; DNA; 1186 BP.  
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 34272.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 PA (ITFL-) INT FLOWER DEV PTY LTD.  
 Percent Similarity: 60.66% Conservative: 48  
 Best Local Similarity: 37.91% Mismatches: 76  
 Query Match: 26.58% Indels: 7  
 RESULT 125  
 ID ADH02852 standard; cDNA; 1006 BP.  
 DE Toronia TMT5.nt cDNA #SEQ ID 11.  
 PN WO2003062428-A1.  
 PD 31-JUL-2003.  
 PA (ITFL-) INT FLOWER DEV PTY LTD.  
 Percent Similarity: 56.58% Conservative: 46  
 Best Local Similarity: 36.40% Mismatches: 84  
 Query Match: 26.40% Indels: 15  
 RESULT 126  
 ID ABS63420 standard; cDNA; 912 BP.  
 DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.

PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAPALSKI J A.  
 Percent Similarity: 53.71% Conservative: 39  
 Best Local Similarity: 36.68% Mismatches: 96  
 Query Match: 26.36% Indels: 10  
 RESULT 127  
 ID ADK69931 standard; DNA; 1181 BP.  
 DE Maize W64A CCoAOMT2 gene substitution mutant #10.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Percent Similarity: 48.57% Conservative: 45  
 Best Local Similarity: 32.50% Mismatches: 71  
 Query Match: 26.32% Indels: 73  
 RESULT 128  
 ID ADK69906 standard; DNA; 1180 BP.  
 DE Maize F4 CCoAOMT2 gene, seq id 3.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Percent Similarity: 41.83% Conservative: 45  
 Best Local Similarity: 29.36% Mismatches: 98  
 Query Match: 26.28% Indels: 112  
 RESULT 129  
 ID ADK69932 standard; DNA; 1199 BP.  
 DE Maize W64A CCoAOMT2 gene insertion mutant #5.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Percent Similarity: 42.90% Conservative: 45  
 Best Local Similarity: 30.11% Mismatches: 97  
 Query Match: 26.21% Indels: 104  
 RESULT 130  
 ID ADK69927 standard; DNA; 1178 BP.  
 DE Maize W64A CCoAOMT2 gene deletion mutant #2.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Percent Similarity: 48.39% Conservative: 44  
 Best Local Similarity: 32.62% Mismatches: 72  
 Query Match: 26.14% Indels: 72  
 RESULT 131  
 ID ADK69925 standard; DNA; 1196 BP.  
 DE Maize W64A CCoAOMT2 gene insertion mutant #3.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Percent Similarity: 46.67% Conservative: 38  
 Best Local Similarity: 33.33% Mismatches: 74  
 Query Match: 26.14% Indels: 78  
 RESULT 132  
 ID ADK69918 standard; DNA; 1172 BP.  
 DE Maize W64A CCoAOMT2 gene deletion mutant #1.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Percent Similarity: 48.21% Conservative: 44  
 Best Local Similarity: 32.50% Mismatches: 72  
 Query Match: 26.10% Indels: 73  
 RESULT 133  
 ID ADK69919 standard; DNA; 1181 BP.  
 DE Maize W64A CCoAOMT2 gene substitution mutant #1.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Percent Similarity: 48.21% Conservative: 44  
 Best Local Similarity: 32.50% Mismatches: 72  
 Query Match: 26.10% Indels: 73  
 RESULT 134  
 ID ADK69920 standard; DNA; 1181 BP.  
 DE Maize W64A CCoAOMT2 gene substitution mutant #2.  
 PN FR2833615-A1.

PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Percent Similarity: 48.21% Conservative: 44  
 Best Local Similarity: 32.50% Mismatches: 72  
 Query Match: 26.10% Indels: 73  
 RESULT 135  
 ID ADK69928 standard; DNA; 1181 BP.  
 DE Maize W64A CCoAOMT2 gene substitution mutant #7.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Percent Similarity: 48.21% Conservative: 44  
 Best Local Similarity: 32.50% Mismatches: 72  
 Query Match: 26.10% Indels: 73  
 RESULT 136  
 ID ADK69923 standard; DNA; 1181 BP.  
 DE Maize W64A CCoAOMT2 gene substitution mutant #5.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Percent Similarity: 48.21% Conservative: 44  
 Best Local Similarity: 32.50% Mismatches: 72  
 Query Match: 26.10% Indels: 73  
 RESULT 137  
 ID ADK69904 standard; DNA; 1181 BP.  
 DE Maize W64A CCoAOMT2 gene, seq id 1.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Percent Similarity: 48.21% Conservative: 44  
 Best Local Similarity: 32.50% Mismatches: 72  
 Query Match: 26.10% Indels: 73  
 RESULT 138  
 ID ADK69922 standard; DNA; 1181 BP.  
 DE Maize W64A CCoAOMT2 gene substitution mutant #4.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Percent Similarity: 48.21% Conservative: 44  
 Best Local Similarity: 32.50% Mismatches: 72  
 Query Match: 26.10% Indels: 73  
 RESULT 139  
 ID ADK69924 standard; DNA; 1181 BP.  
 DE Maize W64A CCoAOMT2 gene substitution mutant #6.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Percent Similarity: 48.21% Conservative: 44  
 Best Local Similarity: 32.50% Mismatches: 72  
 Query Match: 26.10% Indels: 73  
 RESULT 140  
 ID ADK69929 standard; DNA; 1181 BP.  
 DE Maize W64A CCoAOMT2 gene substitution mutant #8.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Percent Similarity: 48.21% Conservative: 44  
 Best Local Similarity: 32.50% Mismatches: 72  
 Query Match: 26.10% Indels: 73  
 RESULT 141  
 ID ADK69921 standard; DNA; 1181 BP.  
 DE Maize W64A CCoAOMT2 gene substitution mutant #3.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Percent Similarity: 48.21% Conservative: 44  
 Best Local Similarity: 32.50% Mismatches: 72  
 Query Match: 26.10% Indels: 73  
 RESULT 142  
 ID ADK69930 standard; DNA; 1181 BP.  
 DE Maize W64A CCoAOMT2 gene substitution mutant #9.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.

PA (GENO-) GENOPLANTE-VALOR SAS.  
 Percent Similarity: 48.21% Conservative: 44  
 Best Local Similarity: 32.50% Mismatches: 72  
 Query Match: 26.10% Indels: 73  
 RESULT 143  
 ID ADK69917 standard; DNA; 1186 BP.  
 DE Maize W64A CCoAOMT2 gene insertion mutant #1.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Percent Similarity: 48.21% Conservative: 44  
 Best Local Similarity: 32.50% Mismatches: 72  
 Query Match: 26.10% Indels: 73  
 RESULT 144  
 ID ADH02845 standard; cDNA; 888 BP.  
 DE Petunia E20 cDNA #SEQ ID 4.  
 PN WO2003062428-A1.  
 PD 31-JUL-2003.  
 PA (ITFL-) INT FLOWER DEV PTY LTD.  
 Percent Similarity: 54.39% Conservative: 40  
 Best Local Similarity: 37.66% Mismatches: 88  
 Query Match: 25.99% Indels: 21  
 RESULT 145  
 ID ADH02842 standard; cDNA; 969 BP.  
 DE Petunia dife cDNA #SEQ ID 1.  
 PN WO2003062428-A1.  
 PD 31-JUL-2003.  
 PA (ITFL-) INT FLOWER DEV PTY LTD.  
 Percent Similarity: 54.39% Conservative: 40  
 Best Local Similarity: 37.66% Mismatches: 88  
 Query Match: 25.99% Indels: 21  
 RESULT 146  
 ID AAA14651 standard; DNA; 77536 BP.  
 DE Nucleotide sequence of the FK-520 biosynthetic gene cluster.  
 Percent Similarity: 51.97% Conservative: 31  
 Best Local Similarity: 38.43% Mismatches: 104  
 Query Match: 25.91% Indels: 6  
 RESULT 147  
 ID ADK69926 standard; DNA; 1199 BP.  
 DE Maize W64A CCoAOMT2 gene insertion mutant #4.  
 PN FR2833615-A1.  
 PD 20-JUN-2003.  
 PA (GENO-) GENOPLANTE-VALOR SAS.  
 Percent Similarity: 47.20% Conservative: 44  
 Best Local Similarity: 31.82% Mismatches: 72  
 Query Match: 25.87% Indels: 79  
 RESULT 148  
 ID ABS63422 standard; cDNA; 982 BP.  
 DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAPALSKI J A.  
 Percent Similarity: 55.14% Conservative: 37  
 Best Local Similarity: 37.85% Mismatches: 86  
 Query Match: 25.39% Indels: 10  
 RESULT 149  
 ID AAL61224 standard; DNA; 82746 BP.  
 DE Actinosynnema pretiosum ansamitocin biosynthetic gene cluster I.  
 PN WO2003045312-A2.  
 PD 05-JUN-2003.  
 PA (UNIW ) UNIV WASHINGTON.  
 Percent Similarity: 52.63% Conservative: 28  
 Best Local Similarity: 40.35% Mismatches: 98  
 Query Match: 25.32% Indels: 10  
 RESULT 150  
 ID ADH02867 standard; cDNA; 1079 BP.  
 DE Petunia E33 (corrected) cDNA #SEQ ID 26.  
 PN WO2003062428-A1.  
 PD 31-JUL-2003.  
 PA (ITFL-) INT FLOWER DEV PTY LTD.  
 Percent Similarity: 57.59% Conservative: 47

Best Local Similarity: 36.61% Mismatches: 84  
Query Match: 25.28% Indels: 11  
RESULT 151  
ID ABN87110 standard; cDNA; 758 BP.  
DE Lolium perenne LpCCoAMTA partial nucleotide sequence SEQ ID NO:4.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Percent Similarity: 51.82% Conservative: 42  
Best Local Similarity: 34.82% Mismatches: 86  
Query Match: 25.17% Indels: 33  
RESULT 152  
ID ABN87115 standard; cDNA; 793 BP.  
DE Lolium perenne LpCCoAMTA partial nucleotide sequence SEQ ID NO:9.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Percent Similarity: 55.56% Conservative: 40  
Best Local Similarity: 37.04% Mismatches: 76  
Query Match: 24.91% Indels: 20  
RESULT 153  
ID ABN87126 standard; cDNA; 689 BP.  
DE Lolium perenne LpCCoAMTC nucleotide sequence SEQ ID NO:21.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Percent Similarity: 55.94% Conservative: 30  
Best Local Similarity: 41.09% Mismatches: 72  
Query Match: 24.80% Indels: 17  
RESULT 154  
ID ABN87112 standard; cDNA; 765 BP.  
DE Lolium perenne LpCCoAMTA partial nucleotide sequence SEQ ID NO:6.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Percent Similarity: 58.33% Conservative: 37  
Best Local Similarity: 39.06% Mismatches: 72  
Query Match: 24.46% Indels: 8  
RESULT 155  
ID ADH02847 standard; cDNA; 1077 BP.  
DE Petunia E33 cDNA #SEQ ID 5.  
PN WO2003062428-A1.  
PD 31-JUL-2003.  
PA (ITFL-) INT FLOWER DEV PTY LTD.  
Percent Similarity: 56.70% Conservative: 46  
Best Local Similarity: 36.16% Mismatches: 86  
Query Match: 24.42% Indels: 11  
RESULT 156  
ID ADH02884 standard; cDNA; 943 BP.  
DE Fuchsia FMT full (3289) cDNA #SEQ ID 43.  
PN WO2003062428-A1.  
PD 31-JUL-2003.  
PA (ITFL-) INT FLOWER DEV PTY LTD.  
Percent Similarity: 57.47% Conservative: 48  
Best Local Similarity: 35.75% Mismatches: 82  
Query Match: 24.35% Indels: 12  
RESULT 157  
ID ADH02882 standard; cDNA; 841 BP.  
DE Fuchsia FMT (3282) cDNA #SEQ ID 41.  
PN WO2003062428-A1.  
PD 31-JUL-2003.  
PA (ITFL-) INT FLOWER DEV PTY LTD.  
Percent Similarity: 58.82% Conservative: 44  
Best Local Similarity: 37.25% Mismatches: 74  
Query Match: 24.20% Indels: 10  
RESULT 158  
ID AAC47161 standard; DNA; 738 BP.  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 52786.  
PN EP1033405-A2.

PD 06-SEP-2000.  
Percent Similarity: 56.42% Conservative: 44  
Best Local Similarity: 36.24% Mismatches: 85  
Query Match: 24.13% Indels: 10  
RESULT 159  
ID AAC47930 standard; DNA; 833 BP.  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 55635.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Percent Similarity: 56.42% Conservative: 44  
Best Local Similarity: 36.24% Mismatches: 85  
Query Match: 24.13% Indels: 10  
RESULT 160  
ID ABN87111 standard; cDNA; 774 BP.  
DE Lolium perenne LpCCoAMTA partial nucleotide sequence SEQ ID NO:5.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Percent Similarity: 57.81% Conservative: 37  
Best Local Similarity: 38.54% Mismatches: 73  
Query Match: 24.09% Indels: 8  
RESULT 161  
ID ABN87113 standard; cDNA; 777 BP.  
DE Lolium perenne LpCCoAMTA partial nucleotide sequence SEQ ID NO:7.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Percent Similarity: 54.63% Conservative: 40  
Best Local Similarity: 36.11% Mismatches: 78  
Query Match: 24.01% Indels: 20  
RESULT 162  
ID ABN87114 standard; cDNA; 792 BP.  
DE Lolium perenne LpCCoAMTA partial nucleotide sequence SEQ ID NO:8.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Percent Similarity: 54.63% Conservative: 40  
Best Local Similarity: 36.11% Mismatches: 78  
Query Match: 23.94% Indels: 20  
RESULT 163  
ID ABN87122 standard; cDNA; 789 BP.  
DE Lolium perenne LpCCoAMTB partial nucleotide sequence SEQ ID NO:17.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Percent Similarity: 52.77% Conservative: 37  
Best Local Similarity: 37.02% Mismatches: 94  
Query Match: 23.90% Indels: 18  
RESULT 164  
ID ADR65555 standard; cDNA; 749 BP.  
DE Cotton cDNA sequence, SEQ ID 6336.  
PN US2004181830-A1.  
PD 16-SEP-2004.  
PA (KOVA/) KOVALIC D K.  
PA (ZHOU/) ZHOU Y.  
PA (CAOY/) CAO Y.  
Percent Similarity: 55.67% Conservative: 44  
Best Local Similarity: 33.99% Mismatches: 74  
Query Match: 23.83% Indels: 16  
RESULT 165  
ID ABN87121 standard; cDNA; 773 BP.  
DE Lolium perenne LpCCoAMTB partial nucleotide sequence SEQ ID NO:16.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Percent Similarity: 54.25% Conservative: 33  
Best Local Similarity: 38.68% Mismatches: 86  
Query Match: 23.45% Indels: 12

RESULT 166  
ID ADS72763 standard; cDNA; 257 BP.  
DE Human kidney tumour specific cDNA, SEQ ID 1360.  
PN US2003109434-A1.  
PD 12-JUN-2003.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 23.38%  
Indels: 0  
Conservative: 0  
Mismatch: 0

RESULT 167  
ID AB213934 standard; DNA; 699 BP.  
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 1739.  
PN WO200216655-A2.  
PD 28-FEB-2002.  
PA (SCRI-) SCRIPPS RES INST.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Percent Similarity: 55.00%  
Best Local Similarity: 34.09%  
Query Match: 23.19%  
Indels: 15  
Conservative: 46  
Mismatch: 84

RESULT 168  
ID ADG87603 standard; cDNA; 699 BP.  
DE A. thaliana RPP7/RPP8-upregulated pathogen infection-related gene #45.  
PN WO20022675-A2.  
PD 21-MAR-2002.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
PA (UYNC-) UNIV NORTH CAROLINA.  
PA (GLAZ/) GLAZEBROOK J.  
PA (WANG/) WANG X.  
PA (DANG/) DANG J L.  
PA (EULG/) EULGEM T.  
PA (ZHUT/) ZHU T.  
Percent Similarity: 55.00%  
Best Local Similarity: 34.09%  
Query Match: 23.19%  
Indels: 15  
Conservative: 46  
Mismatch: 84

RESULT 169  
ID ADG87604 standard; cDNA; 699 BP.  
DE A. thaliana RPP7/RPP8-upregulated pathogen infection-related gene #46.  
PN WO20022675-A2.  
PD 21-MAR-2002.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
PA (UYNC-) UNIV NORTH CAROLINA.  
PA (GLAZ/) GLAZEBROOK J.  
PA (WANG/) WANG X.  
PA (DANG/) DANG J L.  
PA (EULG/) EULGEM T.  
PA (ZHUT/) ZHU T.  
Percent Similarity: 55.00%  
Best Local Similarity: 34.09%  
Query Match: 23.19%  
Indels: 15  
Conservative: 46  
Mismatch: 84

RESULT 170  
ID ADA67907 standard; DNA; 699 BP.  
DE Arabidopsis thaliana gene, SEQ ID 151.  
PN WO200300898-A1.  
PD 03-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Percent Similarity: 55.00%  
Best Local Similarity: 34.09%  
Query Match: 23.19%  
Indels: 15  
Conservative: 46  
Mismatch: 84

RESULT 171  
ID ADS72855 standard; cDNA; 257 BP.  
DE Human kidney tumour specific cDNA, SEQ ID 1452.  
PN US2003109434-A1.  
PD 12-JUN-2003.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 98.39%  
Best Local Similarity: 98.39%  
Query Match: 23.01%  
Indels: 0  
Conservative: 0  
Mismatch: 1

RESULT 172  
ID AAL61190 standard; DNA; 504 BP.  
DE Actinomyces pretiosum O-methyltransferase gene.  
PN WO2003045312-A2.  
PD 05-JUN-2003.  
PA (UNIW) UNIV WASHINGTON.

Percent Similarity: 57.32%  
Best Local Similarity: 43.29%  
Query Match: 22.30%  
Indels: 3  
Conservative: 23  
Mismatch: 67

RESULT 173  
ID AAV23875 standard; DNA; 1075 BP.  
DE Plant OMT enzyme DNA sequence.  
PN WO9811205-A2.  
PD 19-MAR-1998.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
Percent Similarity: 50.41%  
Best Local Similarity: 31.30%  
Query Match: 22.23%  
Indels: 23  
Conservative: 47  
Mismatch: 99

RESULT 174  
ID AAZ06878 standard; cDNA; 1075 BP.  
DE Pine O-methyl transferase (OMT) partial cDNA 4.  
PN US952486-A.  
PD 14-SEP-1999.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
Percent Similarity: 50.41%  
Best Local Similarity: 31.30%  
Query Match: 22.23%  
Indels: 23  
Conservative: 47  
Mismatch: 99

RESULT 175  
ID AAA67962 standard; DNA; 1075 BP.  
DE Pinus radiata OMT nucleotide sequence SEQ ID NO:55.  
PN WO200022099-A1.  
PD 20-APR-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Percent Similarity: 50.41%  
Best Local Similarity: 31.30%  
Query Match: 22.23%  
Indels: 23  
Conservative: 47  
Mismatch: 99

RESULT 176  
ID ADD41712 standard; DNA; 1075 BP.  
DE O-methyl transferase DNA #8.  
PN US2003131373-A1.  
PD 10-JUL-2003.  
PA (BLOK/) BLOKSBERG L N.  
PA (HAVU/) HAVUKKALA I.  
Percent Similarity: 50.41%  
Best Local Similarity: 31.30%  
Query Match: 22.23%  
Indels: 23  
Conservative: 47  
Mismatch: 99

RESULT 177  
ID AAX28142 standard; DNA; 3072 BP.  
DE CCoAOMT promoter, PtCCOAMT2.  
PN WO9909188-A2.  
PD 25-FEB-1999.  
PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.  
Percent Similarity: 43.80%  
Best Local Similarity: 27.91%  
Query Match: 22.19%  
Indels: 82  
Conservative: 41  
Mismatch: 63

RESULT 178  
ID ACL23248 standard; DNA; 509 BP.  
DE DNA clone originating in barley containing SNP encoding sequence #13239.  
PN WO2003057877-A1.  
PD 17-JUL-2003.  
PA (UYNI-) UNIV JAPAN OKAYAMA.  
Percent Similarity: 57.23%  
Best Local Similarity: 39.76%  
Query Match: 22.15%  
Indels: 7  
Conservative: 29  
Mismatch: 64

RESULT 179  
ID AAQ14978 standard; DNA; 1810 BP.  
DE AGYA Gene.  
PN EP459525-A.  
PD 04-DEC-1991.  
PA (SAOC) MERCIAN CORP.  
Percent Similarity: 49.76%  
Best Local Similarity: 39.02%  
Query Match: 21.89%  
Indels: 34  
Conservative: 22  
Mismatch: 69

RESULT 180  
ID AAV23874 standard; DNA; 1074 BP.  
DE Plant OMT enzyme DNA sequence.



RESULT 194

ID ADH02862 standard; cDNA; 780 BP.  
DE Fuchsia FMT cDNA #SEQ ID 21.  
PN W02003062428-A1.  
PD 31-JUL-2003.  
PA (ITFL-) INT FLOWER DEV PTY LTD.  
Percent Similarity: 57.50%  
Best Local Similarity: 38.12%  
Query Match: 19.81%  
Conservative: 31  
Mismatches: 60  
Indels: 8

RESULT 195

ID ABD00975 standard; DNA; 675 BP.  
DE Klebsiella pneumoniae polynucleotide seqid 6750.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 53.33%  
Best Local Similarity: 35.56%  
Query Match: 19.21%  
Conservative: 32  
Mismatches: 76  
Indels: 8

RESULT 196

ID ADD34177 standard; DNA; 407 BP.  
DE Mouse mitochondrial DNA sequence SEQ ID NO:1955.  
PN W02003020220-A2.  
PD 13-MAR-2003.  
PA (UYEM-) UNIV EMORY.  
Percent Similarity: 85.71%  
Best Local Similarity: 79.33%  
Query Match: 18.69%  
Conservative: 4  
Mismatches: 9  
Indels: 0

RESULT 197

ID AAV23845 standard; DNA; 760 BP.  
DE Plant OMT enzyme DNA sequence.  
PN W09811205-A2.  
PD 19-MAR-1998.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Percent Similarity: 58.92%  
Best Local Similarity: 37.31%  
Query Match: 16.72%  
Conservative: 29  
Mismatches: 52  
Indels: 3

RESULT 198

ID AAZ06846 standard; cDNA; 760 BP.  
DE Eucalyptus O-methyl transferase (OMT) partial cDNA 4.  
PN US9552486-A.  
PD 14-SEP-1999.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Percent Similarity: 58.96%  
Best Local Similarity: 37.31%  
Query Match: 16.72%  
Conservative: 29  
Mismatches: 52  
Indels: 3

RESULT 199

ID AAA69584 standard; cDNA; 760 BP.  
DE Eucalyptus grandis cinnamoyl-CoA reductase cDNA SEQ ID NO:58.  
PN W02003036081-A2.  
PD 22-JUN-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Percent Similarity: 58.96%  
Best Local Similarity: 37.31%  
Query Match: 16.72%  
Conservative: 29  
Mismatches: 52  
Indels: 3

RESULT 200

ID AAA67932 standard; DNA; 760 BP.  
DE Eucalyptus grandis OMT nucleotide sequence SEQ ID NO:25.  
PN W020022099-A1.  
PD 20-APR-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Percent Similarity: 58.96%  
Best Local Similarity: 37.31%  
Query Match: 16.72%  
Conservative: 29  
Mismatches: 52  
Indels: 3

RESULT 201

ID ADD41682 standard; DNA; 760 BP.  
DE O-methyl transferase DNA #5.  
PN US2003131373-A1.  
PD 10-JUL-2003.  
PA (BLOK/) BLOKSBERG L N.  
Percent Similarity: 58.96%  
Best Local Similarity: 37.31%  
Query Match: 16.72%  
Conservative: 29  
Mismatches: 52  
Indels: 3

<hr/>							
PA	(HAVU/) HAVUKKALA I.						
Percent Similarity:	58.96%					Conservative:	29
Best Local Similarity:	37.31%					Mismatches:	52
Query Match:	16.72%					Indels:	3
RESULT 202							
ID	ARS63430 standard; cDNA; 534 BP.						
DE	DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).						
PN	US20020281693-A1.						
PD	27-JUN-2002.						
PA	(CAHO/) CAHOON R E.						
PA	(FADE/) FADER G M.						
PA	(RAFA/) RAFALSKI J A.						
Percent Similarity:	58.71%					Conservative:	35
Best Local Similarity:	36.13%					Mismatches:	56
Query Match:	16.68%					Indels:	8
RESULT 203							
ID	ARN87119 standard; cDNA; 628 BP.						
DE	Lolium perenne LpCOMTB partial nucleotide sequence SEQ ID NO:14.						
PN	WO200228594-A1.						
PD	04-APR-2002.						
PA	(AGRI-) AGRIC VICTORIA SERVICES PTY LTD.						
PA	(AGR-) AGRESEARCH LTD.						
Percent Similarity:	51.93%					Conservative:	30
Best Local Similarity:	35.36%					Mismatches:	75
Query Match:	16.46%					Indels:	13
RESULT 204							
ID	ACL23249 standard; DNA; 542 BP.						
DE	DNA clone originating in barley containing SNP encoding sequence #13240.						
PN	WO2003057877-A1.						
PD	17-JUL-2003.						
PA	(UYNI-) UNIV JAPAN OKAYAMA.						
Percent Similarity:	55.70%					Conservative:	28
Best Local Similarity:	37.97%					Mismatches:	59
Query Match:	15.82%					Indels:	13
RESULT 205							
ID	ABS63423 standard; cDNA; 528 BP.						
DE	DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCONT).						
PN	US2002081693-A1.						
PD	27-JUN-2002.						
PA	(CAHO/) CAHOON R E.						
PA	(FADE/) FADER G M.						
PA	(RAFA/) RAFALSKI J A.						
Percent Similarity:	59.52%					Conservative:	27
Best Local Similarity:	38.10%					Mismatches:	45
Query Match:	15.41%					Indels:	6
RESULT 206							
Percent Similarity:	54.29%					Conservative:	37
Best Local Similarity:	33.14%					Mismatches:	69
Query Match:	15.08%					Indels:	11
RESULT 207							
Percent Similarity:	54.29%					Conservative:	37
Best Local Similarity:	33.14%					Mismatches:	69
Query Match:	15.08%					Indels:	11
RESULT 208							
ID	AAA68101 standard; DNA; 399 BP.						
DE	E. grandis caffeoyl CoA methyl transferase DNA sequence SEQ ID NO:194.						
PN	WO200022099-A1.						
PD	20-APR-2000.						
PA	(GENE-) GENESIS RES & DEV CORP LTD.						
PA	(FLET-) FLETCHER CHALLENGE FORESTS LTD.						
Percent Similarity:	62.93%					Conservative:	27
Best Local Similarity:	39.66%					Mismatches:	33
Query Match:	15.04%					Indels:	11
RESULT 209							
ID	ADD41851 standard; DNA; 399 BP.						
DE	Caffeoyl CoA methyl transferase DNA #2.						
PN	US2003131373-A1.						
PD	10-JUL-2003.						
PA	(BLOK-) BLOKSBERG L N.						
PA	(HAVU/) HAVUKKALA I.						
Percent Similarity:	62.93%					Conservative:	27
Best Local Similarity:	39.66%					Mismatches:	33
Query Match:	15.04%					Indels:	11



```

RESULT 210
ID ADA31006 standard; DNA; 588 BP.
DE DNA encoding Acinetobacter baumannii protein #2293.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 50.24%
Best Local Similarity: 33.66%
Query Match: 15.00%
Conservative: 34
Mismatch: 65
Indels: 37
RESULT 211
ID ACN56145 standard; cDNA; 525 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-032-Q6-N6-D4, SEQ:10926.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FING/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Percent Similarity: 57.02%
Best Local Similarity: 33.88%
Query Match: 14.48%
Conservative: 28
Mismatch: 45
Indels: 7
RESULT 212
ID ABN87109 standard; cDNA; 557 BP.
DE Lolium perenne LpCoAMTA partial nucleotide sequence SEQ ID NO:3.
PN WO200226994-A1.
PD 04-APR-2002.
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA (AGRE-) AGRESEARCH LTD.
Percent Similarity: 54.35%
Best Local Similarity: 34.06%
Query Match: 14.30%
Conservative: 28
Mismatch: 52
Indels: 11
RESULT 213
ID AAS96694 standard; DNA; 8580 BP.
DE Arabidopsis DMT4 (IDMT4) DNA.
PN WO200180626-A1.
PD 01-NOV-2001.
PA (REGC) UNIV CALIFORNIA.
Percent Similarity: 39.59%
Best Local Similarity: 25.89%
Query Match: 14.11%
Conservative: 27
Mismatch: 51
Indels: 69
RESULT 214
ID ADM39547 standard; DNA; 8580 BP.
DE DMT polynucleotide #9.
PN US2003135890-A1.
PD 17-JUL-2003.
PA (FISC/) FISCHER R.
PA (CHOI/) CHOI Y.
PA (HANN/) HANNON M.
PA (OKAM/) OKAMURO J.
PA (TATA/) TATARINOVA T.
Percent Similarity: 39.59%
Best Local Similarity: 25.89%
Query Match: 14.11%
Conservative: 27
Mismatch: 51
Indels: 69
RESULT 215
ID AAA68012 standard; DNA; 594 BP.
DE Eucalyptus grandis OMT nucleotide sequence SEQ ID NO:105.
PN WO200022099-A1.
PD 20-APR-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Percent Similarity: 61.17%
Best Local Similarity: 36.89%
Query Match: 13.63%
Conservative: 25
Mismatch: 38
Indels: 2
RESULT 216
ID ADD41762 standard; DNA; 594 BP.
DE O-methyl transferase DNA #11.
PN US2003131373-A1.
PD 10-JUL-2003.
PA (BLOK/) BLOKSBERG L N.
PA (HAVU/) HAVUKKALA I.
Percent Similarity: 61.17%
Best Local Similarity: 36.89%
Query Match: 13.63%
Conservative: 25
Mismatch: 38
Indels: 2
RESULT 217
ID ADB06101 standard; DNA; 798 BP.
DE Alloiococcus otitis antigenic protein encoding DNA SEQ ID NO:41.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Percent Similarity: 47.98%
Best Local Similarity: 32.32%
Query Match: 13.55%
Conservative: 31
Mismatch: 72
Indels: 31
RESULT 218
ID ADB12064 standard; DNA; 1754382 BP.
DE Alloiococcus otitis entire genome sequence SEQ ID NO:6651.
PN WO2003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Percent Similarity: 47.98%
Best Local Similarity: 32.32%
Query Match: 13.55%
Conservative: 31
Mismatch: 72
Indels: 31
RESULT 219
ID ABS63421 standard; cDNA; 505 BP.
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).
PN US2002081693-A1.
PD 27-JUN-2002.
PA (CAHO/) CAHOON R E.
PA (FADE/) FADER G M.
PA (RAFA/) RAFALSKI J A.
Percent Similarity: 51.92%
Best Local Similarity: 32.69%
Query Match: 13.51%
Conservative: 30
Mismatch: 56
Indels: 19
RESULT 220
ID AAV23843 standard; DNA; 607 BP.
DE Plant OMT enzyme DNA sequence.
PN WO9811205-A2.
PD 19-MAR-1998.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Percent Similarity: 61.22%
Best Local Similarity: 37.76%
Query Match: 13.40%
Conservative: 23
Mismatch: 36
Indels: 2
RESULT 221
ID AAZ06844 standard; cDNA; 607 BP.
DE Eucalyptus O-methyl transferase (OMT) partial cDNA 2.
PN US9592486-A.
PD 14-SEP-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Percent Similarity: 61.22%
Best Local Similarity: 37.76%
Query Match: 13.40%
Conservative: 23
Mismatch: 36
Indels: 2
RESULT 222
ID AAA69594 standard; cDNA; 607 BP.
DE Eucalyptus grandis O-methyltransferase cDNA SEQ ID NO:68.
PN WO200036081-A2.
PD 22-JUN-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Percent Similarity: 61.22%
Best Local Similarity: 37.76%
Query Match: 13.40%
Conservative: 23
Mismatch: 36
Indels: 2
RESULT 223
ID AAA67930 standard; DNA; 607 BP.
DE Eucalyptus grandis OMT nucleotide sequence SEQ ID NO:23.
PN WO200022099-A1.
PD 20-APR-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Percent Similarity: 61.22%
Best Local Similarity: 37.76%
Query Match: 13.40%
Conservative: 23
Mismatch: 36
Indels: 2
RESULT 224
ID ADD41680 standard; DNA; 607 BP.
DE O-methyl transferase DNA #3.
PN US2003131373-A1.

```

PD 10-JUL-2003.  
 PA (BLOK/) BLOKSBERG L N.  
 PA (HAVU/) HAVUKKALA I.  
 Percent Similarity: 61.22%  
 Best Local Similarity: 37.76%  
 Mismatches: 36  
 Indels: 2  
 Query Match:  
 RESULT 225  
 ID AAS9516 standard; DNA; 2955 BP.  
 DE Propionibacterium acnes immunogenic protein encoding DNA #11.  
 PN WO200181581-A2.  
 PD 01-NOV-2001.  
 PA (CORI-) CORIXA CORP.  
 Percent Similarity: 45.54%  
 Best Local Similarity: 28.57%  
 Mismatches: 91  
 Indels: 32  
 Query Match:  
 RESULT 226  
 ID ACF64445 standard; DNA; 29255 BP.  
 DE Propionibacterium acnes DNA contig sequence #11.  
 PN WO2003033515-A1.  
 PD 24-APR-2003.  
 PA (CORI-) CORIXA CORP.  
 Percent Similarity: 45.54%  
 Best Local Similarity: 28.57%  
 Mismatches: 91  
 Indels: 32  
 Query Match:  
 RESULT 227  
 ID ADA4866 standard; DNA; 584 BP.  
 DE Banana gene conferring disease resistance in plants.  
 PN WO200300906-A2.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Percent Similarity: 46.67%  
 Best Local Similarity: 33.33%  
 Mismatches: 38  
 Indels: 34  
 Query Match:  
 RESULT 228  
 ID ABS63411 standard; cDNA; 510 BP.  
 DE DNA encoding rice caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAPA/) RAPALSKI J A.  
 Percent Similarity: 54.93%  
 Best Local Similarity: 35.92%  
 Mismatches: 45  
 Indels: 20  
 Query Match:  
 RESULT 229  
 ID ABS63426 standard; cDNA; 600 BP.  
 DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAPA/) RAPALSKI J A.  
 Percent Similarity: 48.84%  
 Best Local Similarity: 36.63%  
 Mismatches: 57  
 Indels: 32  
 Query Match:  
 RESULT 230  
 ID AAA31496 standard; DNA; 451 BP.  
 DE Plant microsatellite marker #457.  
 PN WO9967421-A1.  
 PD 29-DEC-1999.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FOREST LTD.  
 Percent Similarity: 59.18%  
 Best Local Similarity: 37.76%  
 Mismatches: 38  
 Indels: 2  
 Query Match:  
 RESULT 231  
 ID AAA68102 standard; DNA; 296 BP.  
 DE E. grandis caffeoyl CoA methyl transferase DNA sequence SEQ ID NO:195.  
 PN WO200022099-A1.  
 PD 20-APR-2000.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Percent Similarity: 62.89%  
 Mismatches: 42  
 Indels: 6  
 Query Match:  
 RESULT 232  
 ID AAA67960 standard; DNA; 562 BP.  
 DE Pinus radiata OMT nucleotide sequence SEQ ID NO:53.  
 PN WO200022099-A1.  
 PD 20-APR-2000.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Percent Similarity: 58.26%  
 Best Local Similarity: 33.04%  
 Mismatches: 42  
 Indels: 6  
 Query Match:  
 RESULT 233  
 ID AAA67960 standard; DNA; 562 BP.  
 DE Pinus radiata OMT nucleotide sequence SEQ ID NO:54.  
 PN WO200036081-A2.  
 PD 22-JUN-2000.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Percent Similarity: 58.26%  
 Best Local Similarity: 33.04%  
 Mismatches: 42  
 Indels: 6  
 Query Match:  
 RESULT 234  
 ID AAV23873 standard; DNA; 562 BP.  
 DE Plant OMT enzyme DNA sequence.  
 PN WO9811205-A2.  
 PD 19-MAR-1998.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Percent Similarity: 58.26%  
 Best Local Similarity: 33.04%  
 Mismatches: 42  
 Indels: 6  
 Query Match:  
 RESULT 235  
 ID AAZ06876 standard; cDNA; 562 BP.  
 DE Pine O-methyl transferase (OMT) partial cDNA 2.  
 PN US9592486-A.  
 PD 14-SEP-1999.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Percent Similarity: 58.26%  
 Best Local Similarity: 33.04%  
 Mismatches: 42  
 Indels: 6  
 Query Match:  
 RESULT 236  
 ID AAA69580 standard; cDNA; 562 BP.  
 DE Pinus radiata O-methyltransferase cDNA SEQ ID NO:54.  
 PN WO200036081-A2.  
 PD 22-JUN-2000.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Percent Similarity: 58.26%  
 Best Local Similarity: 33.04%  
 Mismatches: 42  
 Indels: 6  
 Query Match:  
 RESULT 237  
 ID AAA67960 standard; DNA; 562 BP.  
 DE Pinus radiata OMT nucleotide sequence SEQ ID NO:53.  
 PN WO200022099-A1.  
 PD 20-APR-2000.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Percent Similarity: 58.26%  
 Best Local Similarity: 33.04%  
 Mismatches: 42  
 Indels: 6  
 Query Match:  
 RESULT 238  
 ID ADD41710 standard; DNA; 562 BP.  
 DE O-methyl transferase DNA #6.  
 PN US200313173-A1.  
 PD 10-JUL-2003.  
 PA (BLOK/) BLOKSBERG L N.  
 PA (HAVU/) HAVUKKALA I.  
 Percent Similarity: 58.26%  
 Best Local Similarity: 33.04%  
 Mismatches: 42  
 Indels: 6  
 Query Match:  
 RESULT 239  
 ID ADP95323 standard; cDNA; 447 BP.

Best Local Similarity: 39.18%  
 Mismatches: 32  
 Indels: 4  
 Query Match:  
 RESULT 232  
 ID ADD41852 standard; DNA; 296 BP.  
 DE Caffeoyl CoA methyl transferase DNA #3.  
 PN US200313173-A1.  
 PD 10-JUL-2003.  
 PA (BLOK/) BLOKSBERG L N.  
 PA (HAVU/) HAVUKKALA I.  
 Percent Similarity: 62.89%  
 Best Local Similarity: 39.18%  
 Mismatches: 32  
 Indels: 4  
 Query Match:  
 RESULT 233  
 ID ABQ81846 standard; DNA; 349980 BP.  
 DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1102.  
 PN EP1227152-A1.  
 PD 31-JUL-2002.  
 PA (NEST) SOC. PROD NESTLE SA.  
 Percent Similarity: 42.31%  
 Best Local Similarity: 27.31%  
 Mismatches: 137  
 Indels: 13  
 Query Match:  
 RESULT 234  
 ID AAV23873 standard; DNA; 562 BP.  
 DE Plant OMT enzyme DNA sequence.  
 PN WO9811205-A2.  
 PD 19-MAR-1998.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Percent Similarity: 58.26%  
 Best Local Similarity: 33.04%  
 Mismatches: 42  
 Indels: 6  
 Query Match:  
 RESULT 235  
 ID AAZ06876 standard; cDNA; 562 BP.  
 DE Pine O-methyl transferase (OMT) partial cDNA 2.  
 PN US9592486-A.  
 PD 14-SEP-1999.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Percent Similarity: 58.26%  
 Best Local Similarity: 33.04%  
 Mismatches: 42  
 Indels: 6  
 Query Match:  
 RESULT 236  
 ID AAA69580 standard; cDNA; 562 BP.  
 DE Pinus radiata O-methyltransferase cDNA SEQ ID NO:54.  
 PN WO200036081-A2.  
 PD 22-JUN-2000.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Percent Similarity: 58.26%  
 Best Local Similarity: 33.04%  
 Mismatches: 42  
 Indels: 6  
 Query Match:  
 RESULT 237  
 ID AAA67960 standard; DNA; 562 BP.  
 DE Pinus radiata OMT nucleotide sequence SEQ ID NO:53.  
 PN WO200022099-A1.  
 PD 20-APR-2000.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Percent Similarity: 58.26%  
 Best Local Similarity: 33.04%  
 Mismatches: 42  
 Indels: 6  
 Query Match:  
 RESULT 238  
 ID ADD41710 standard; DNA; 562 BP.  
 DE O-methyl transferase DNA #6.  
 PN US200313173-A1.  
 PD 10-JUL-2003.  
 PA (BLOK/) BLOKSBERG L N.  
 PA (HAVU/) HAVUKKALA I.  
 Percent Similarity: 58.26%  
 Best Local Similarity: 33.04%  
 Mismatches: 42  
 Indels: 6  
 Query Match:  
 RESULT 239  
 ID ADP95323 standard; cDNA; 447 BP.

DE Cotton expressed sequence tag, EST, #4334.  
 PN US2004123338-A1.  
 PD 24-JUN-2004.  
 PA (FINC/) FINCHER K L.  
 Percent Similarity: 60.42% Conservative: 22  
 Best Local Similarity: 37.50% Mismatches: 36  
 Query Match: 12.66% Indels: 2  
 RESULT 240  
 ID ABX09141 standard; DNA; 75216 BP.  
 DE Mycobacterium tuberculosis H37Rv BAC clone BAC-Rv230.  
 PN WO200274903-A2.  
 PD 26-SEP-2002.  
 PA (INSP ) INST PASTEUR.  
 Percent Similarity: 41.32% Conservative: 33  
 Best Local Similarity: 29.86% Mismatches: 134  
 Query Match: 12.66% Indels: 37  
 RESULT 241  
 Percent Similarity: 41.32% Conservative: 33  
 Best Local Similarity: 29.86% Mismatches: 134  
 Query Match: 12.66% Indels: 37  
 RESULT 242  
 Percent Similarity: 41.32% Conservative: 33  
 Best Local Similarity: 29.86% Mismatches: 134  
 Query Match: 12.66% Indels: 37  
 RESULT 243  
 ID ABQ68900 standard; DNA; 1289 BP.  
 DE Listeria monocytogenes 4b contig DNA sequence #1666.  
 PN WO200228891-A2.  
 PD 11-APR-2002.  
 PA (INSP ) INST PASTEUR.  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 Percent Similarity: 43.94% Conservative: 36  
 Best Local Similarity: 27.10% Mismatches: 96  
 Query Match: 12.58% Indels: 24  
 RESULT 244  
 Percent Similarity: 44.95% Conservative: 37  
 Best Local Similarity: 27.98% Mismatches: 88  
 Query Match: 12.58% Indels: 32  
 RESULT 245  
 ID ABQ70732 standard; DNA; 2233 BP.  
 DE Listeria monocytogenes 4b contig DNA sequence #674.  
 PN WO200228891-A2.  
 PD 11-APR-2002.  
 PA (INSP ) INST PASTEUR.  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 Percent Similarity: 43.93% Conservative: 36  
 Best Local Similarity: 27.10% Mismatches: 96  
 Query Match: 12.51% Indels: 24  
 RESULT 246  
 ID AA668100 standard; DNA; 399 BP.  
 DE E. grandis caffeoyl CoA methyl transferase DNA sequence SEQ ID NO:193.  
 PN WO200022099-A1.  
 PD 20-APR-2000.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Percent Similarity: 61.86% Conservative: 21  
 Best Local Similarity: 40.21% Mismatches: 27  
 Query Match: 12.21% Indels: 11  
 RESULT 247  
 ID ADD41850 standard; DNA; 399 BP.  
 DE Caffeoyl CoA methyl transferase DNA #1.  
 PN US200313173-A1.  
 PD 10-JUL-2003.  
 PA (BLOK/) BLOKSBERG L N.  
 PA (HAVU/) HAVUKKALA I.  
 Percent Similarity: 61.86% Conservative: 21  
 Best Local Similarity: 40.21% Mismatches: 27  
 Query Match: 12.21% Indels: 11  
 RESULT 248  
 Percent Similarity: 41.84% Conservative: 37  
 Best Local Similarity: 26.36% Mismatches: 93  
 Query Match: 12.21% Indels: 46  
 RESULT 249

Percent Similarity: 41.84% Conservative: 37  
 Best Local Similarity: 26.36% Mismatches: 93  
 Query Match: 12.21% Indels: 46  
 RESULT 250  
 ID ADA31376 standard; DNA; 702 BP.  
 DE DNA encoding Acinetobacter baumannii protein #2663.  
 PN US6562958-B1.  
 PD 13-MAY-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 42.92% Conservative: 37  
 Best Local Similarity: 26.03% Mismatches: 104  
 Query Match: 12.10% Indels: 21  
 RESULT 251  
 Percent Similarity: 51.18% Conservative: 38  
 Best Local Similarity: 28.82% Mismatches: 72  
 Query Match: 12.10% Indels: 11  
 RESULT 252  
 ID ABX62366 standard; DNA; 415 BP.  
 DE Arabidopsis thaliana expressed sequence related polynucleotide #481.  
 PN US2002040490-A1.  
 PD 04-APR-2002.  
 PA (GORL/) GORLACH J.  
 PA (ANY/) AN Y.  
 PA (HAMI/) HAMILTON C M.  
 PA (PRIC/) PRICE J L.  
 PA (RAIN/) RAINES T M.  
 PA (YUY/) YU Y.  
 PA (RAME/) RAMEAKA J G.  
 PA (PAGE/) PAGE A.  
 PA (MATH/) MATHAW A V.  
 PA (LEDF/) LEDFORD B L.  
 PA (WOES/) WOESSNER J P.  
 PA (HAAS/) HAAS W D.  
 PA (GARC/) GARCIA C A.  
 PA (KRIC/) KRICKER M.  
 PA (SLAT/) SLATER T.  
 PA (DAVI/) DAVIS K R.  
 PA (ALLE/) ALLEN K.  
 PA (HOFF/) HOFFMAN N.  
 PA (HURB/) HURBAN P.  
 Percent Similarity: 54.10% Conservative: 26  
 Best Local Similarity: 32.79% Mismatches: 45  
 Query Match: 11.88% Indels: 11  
 RESULT 253  
 ID ADB74386 standard; DNA; 38675 BP.  
 DE Mycobacterium leprae DNA #20.  
 PN US6583266-B1.  
 PD 24-JUN-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 40.42% Conservative: 43  
 Best Local Similarity: 25.44% Mismatches: 128  
 Query Match: 11.76% Indels: 44  
 RESULT 254  
 ID ADH82166 standard; DNA; 801 BP.  
 DE Enterococcus faecalis polynucleotide #51.  
 PN US6617156-B1.  
 PD 09-SEP-2003.  
 PA (DOUC/) DOUCETTE-STAMM L A.  
 PA (BUSH/) BUSH D.  
 Percent Similarity: 41.38% Conservative: 37  
 Best Local Similarity: 25.43% Mismatches: 112  
 Query Match: 11.69% Indels: 24  
 RESULT 255  
 ID AAX13116 standard; DNA; 19024 BP.  
 DE Enterococcus faecalis genome contig SEQ ID NO:179.  
 PN WO9850555-A2.  
 PD 12-NOV-1998.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 41.38% Conservative: 37  
 Best Local Similarity: 25.43% Mismatches: 112  
 Query Match: 11.62% Indels: 24  
 RESULT 256  
 ID ABS98911 standard; DNA; 19024 BP.

DE Enterococcus faecalis contig sequence #179.  
 PN US200210116-A1.  
 PD 29-AUG-2002.  
 PA (KUNS/) KUNSCH C A.  
 PA (DILL/) DILLON P J.  
 PA (BARA/) BARASH S.  
 Percent Similarity: 41.38%  
 Best Local Similarity: 25.43%  
 Query Match: 11.62%  
 Conservative: 37  
 Mismatches: 112  
 Indels: 24  
 RESULT 257  
 ID ABS63414 standard; cDNA; 508 BP.  
 DE DNA encoding rice caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Percent Similarity: 51.28%  
 Best Local Similarity: 37.61%  
 Query Match: 11.13%  
 Conservative: 16  
 Mismatches: 39  
 Indels: 19  
 RESULT 258  
 ID ACL23251 standard; DNA; 422 BP.  
 DE DNA clone originating in barley containing SNP encoding sequence #13242.  
 PN WO2003057877-A1.  
 PD 17-JUL-2003.  
 PA (UYNI-) UNIV JAPAN OKAYAMA.  
 Percent Similarity: 58.02%  
 Best Local Similarity: 39.51%  
 Query Match: 10.87%  
 Conservative: 15  
 Mismatches: 28  
 Indels: 6  
 RESULT 259  
 ID AAF08409 standard; cDNA; 645 BP.  
 DE Fusarium venenatum EST SEQ ID NO:932.  
 PN WO200056762-A2.  
 PD 28-SEP-2000.  
 PA (NOVO) NOVO NORDISK INC.  
 PA (NOVO) NOVO NORDISK AS.  
 Percent Similarity: 48.35%  
 Best Local Similarity: 26.92%  
 Query Match: 10.46%  
 Conservative: 39  
 Mismatches: 79  
 Indels: 16  
 RESULT 260  
 ID ADR65553 standard; cDNA; 409 BP.  
 DE Cotton cDNA sequence, SEQ ID 6334.  
 PN US2004181830-A1.  
 PD 16-SEP-2004.  
 PA (KOVA/) KOVALIC D K.  
 PA (ZHOU/) ZHOU Y.  
 PA (CAOY/) CAO Y.  
 Percent Similarity: 54.00%  
 Best Local Similarity: 35.00%  
 Query Match: 10.13%  
 Conservative: 19  
 Mismatches: 38  
 Indels: 8  
 RESULT 261  
 ID ABN69362 standard; DNA; 705 BP.  
 DE Streptococcus polynucleotide SEQ ID NO 6637.  
 PN WO200234771-A2.  
 PD 02-MAY-2002.  
 PA (CHIR-) CHIRON SPA.  
 PA (GENO-) INST GENOMIC RES.  
 Percent Similarity: 44.06%  
 Best Local Similarity: 25.25%  
 Query Match: 10.13%  
 Conservative: 38  
 Mismatches: 87  
 Indels: 26  
 RESULT 262  
 ID ABX72177 standard; cDNA; 894 BP.  
 DE Human NOVX polynucleotide #8.  
 PN WO200281498-A2.  
 PD 17-OCT-2002.  
 PA (CURA-) CURAGEN CORP.  
 Percent Similarity: 40.00%  
 Best Local Similarity: 29.17%  
 Query Match: 9.53%  
 Conservative: 26  
 Mismatches: 79  
 Indels: 65  
 RESULT 263  
 ID AAD13478 standard; DNA; 2316 BP.  
 DE Catechol-O-methyltransferase-like human enzyme encoding DNA.  
 PN WO200157220-A2.  
 PD 09-AUG-2001.  
 PA (LEXI-) LEXICON GENETICS INC.  
 Percent Similarity: 39.54%  
 Best Local Similarity: 31.56%  
 Query Match: 9.53%  
 Conservative: 21  
 Mismatches: 100  
 Indels: 61  
 RESULT 264  
 ID ABK74977 standard; DNA; 534 BP.  
 DE Bacillus licheniformis genomic sequence tag (GST) #2268.  
 PN WO200229113-A2.  
 PD 11-APR-2002.  
 PA (NOVO) NOVOZYMES BIOTECH INC.  
 PA (NOVO) NOVOZYMES AS.  
 Percent Similarity: 44.81%  
 Best Local Similarity: 25.68%  
 Query Match: 9.42%  
 Conservative: 35  
 Mismatches: 88  
 Indels: 13  
 RESULT 265  
 ID AAD13476 standard; cDNA; 777 BP.  
 DE Catechol-O-methyltransferase-like human enzyme encoding cDNA #1.  
 PN WO200157220-A2.  
 PD 09-AUG-2001.  
 PA (LEXI-) LEXICON GENETICS INC.  
 Percent Similarity: 39.58%  
 Best Local Similarity: 29.17%  
 Query Match: 9.38%  
 Conservative: 25  
 Mismatches: 80  
 Indels: 65  
 RESULT 266  
 ID AAD33497 standard; cDNA; 777 BP.  
 DE Human drug metabolising enzyme (DME-18) cDNA.  
 PN WO200212467-A2.  
 PD 14-FEB-2002.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Percent Similarity: 39.58%  
 Best Local Similarity: 29.17%  
 Query Match: 9.38%  
 Conservative: 25  
 Mismatches: 80  
 Indels: 65  
 RESULT 267  
 ID ABX72178 standard; cDNA; 897 BP.  
 DE Human NOVX polynucleotide #9.  
 PN WO200281498-A2.  
 PD 17-OCT-2002.  
 PA (CURA-) CURAGEN CORP.  
 Percent Similarity: 39.58%  
 Best Local Similarity: 29.17%  
 Query Match: 9.38%  
 Conservative: 25  
 Mismatches: 80  
 Indels: 65  
 RESULT 268  
 ID ABN69361 standard; DNA; 705 BP.  
 DE Streptococcus polynucleotide SEQ ID NO 6635.  
 PN WO200234771-A2.  
 PD 02-MAY-2002.  
 PA (CHIR-) CHIRON SPA.  
 PA (GENO-) INST GENOMIC RES.  
 Percent Similarity: 43.28%  
 Best Local Similarity: 23.95%  
 Query Match: 9.34%  
 Conservative: 46  
 Mismatches: 84  
 Indels: 51  
 RESULT 269  
 Percent Similarity: 43.28%  
 Best Local Similarity: 23.95%  
 Query Match: 9.34%  
 Conservative: 46  
 Mismatches: 84  
 Indels: 51  
 RESULT 270  
 ID ADS65765 standard; cDNA; 242 BP.  
 DE Corn seedling-derived polynucleotide (cpds), SEQ ID 781.  
 PN US2003237110-A9.  
 PD 25-DEC-2003.  
 PA (INCY-) INCYTE PHARM INC.  
 Percent Similarity: 53.85%  
 Best Local Similarity: 37.18%  
 Query Match: 9.27%  
 Conservative: 13  
 Mismatches: 35  
 Indels: 1  
 RESULT 271  
 ID ABN87123 standard; cDNA; 532 BP.  
 DE Lolium perenne LpCCoMTb partial nucleotide sequence, SEQ ID NO:18.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Percent Similarity: 52.69%  
 Conservative: 19

Best Local Similarity: 32.26% Mismatches: 38  
 Query Match: 9.23% Indels: 7  
 RESULT 272  
 ID ABN87124 standard; cDNA; 532 BP.  
 DE Lolium perenne LpCCoMTB partial nucleotide sequence SEQ ID NO:19.  
 PN WO20026994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Percent Similarity: 52.69% Conservative: 19  
 Best Local Similarity: 32.26% Mismatches: 38  
 Query Match: 9.23% Indels: 7  
 RESULT 273  
 ID ADC92983 standard; DNA; 498 BP.  
 DE E. faecium DNA sequence SEQ ID 2610.  
 PN US6583275-B1.  
 PD 24-JUN-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 45.78% Conservative: 29  
 Best Local Similarity: 28.31% Mismatches: 74  
 Query Match: 9.16% Indels: 16  
 RESULT 274  
 ID ABN91349 standard; DNA; 699 BP.  
 DE Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:812.  
 PN US6380370-B1.  
 PD 30-APR-2002.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 44.83% Conservative: 38  
 Best Local Similarity: 22.99% Mismatches: 86  
 Query Match: 9.16% Indels: 10  
 RESULT 275  
 ID AAH54424 standard; DNA; 3673 BP.  
 DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3788.  
 PN WO200134809-A2.  
 PD 17-MAY-2001.  
 PA (GLAX) GLAXO GROUP LTD.  
 Percent Similarity: 44.83% Conservative: 38  
 Best Local Similarity: 22.99% Mismatches: 86  
 Query Match: 9.16% Indels: 10  
 RESULT 276  
 ID AAA31117 standard; DNA; 402 BP.  
 DE Plant microsatellite marker #78.  
 PN WO9967421-A1.  
 PD 29-DEC-1999.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FOREST LTD.  
 Percent Similarity: 57.32% Conservative: 15  
 Best Local Similarity: 39.02% Mismatches: 32  
 Query Match: 9.08% Indels: 3  
 RESULT 277  
 ID ABX06678 standard; DNA; 711 BP.  
 DE S. pneumoniae type 4 strain coding region #966.  
 PN WO200277021-A2.  
 PD 03-OCT-2002.  
 PA (CHIR-) CHIRON SPA.  
 PA (GENO-) INST GENOMIC RES.  
 Percent Similarity: 46.11% Conservative: 36  
 Best Local Similarity: 26.11% Mismatches: 66  
 Query Match: 9.05% Indels: 31  
 RESULT 278  
 ID ADR92174 standard; DNA; 726 BP.  
 DE Novel S. pneumoniae DNA sequence, SEQ ID 809.  
 PN US6800744-B1.  
 PD 05-OCT-2004.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 46.11% Conservative: 36  
 Best Local Similarity: 26.11% Mismatches: 66  
 Query Match: 9.05% Indels: 31  
 RESULT 279  
 ID AAV52241 standard; DNA; 11309 BP.  
 DE Streptococcus pneumoniae genome fragment SEQ ID NO:108.  
 PN WO9818931-A2.  
 PD 07-MAY-1998.

PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 46.11% Conservative: 36  
 Best Local Similarity: 26.11% Mismatches: 66  
 Query Match: 9.05% Indels: 31  
 RESULT 280  
 Percent Similarity: 46.11% Conservative: 36  
 Best Local Similarity: 26.11% Mismatches: 66  
 Query Match: 9.05% Indels: 31  
 RESULT 281  
 ID AAZ54186 standard; DNA; 918 BP.  
 DE Neisseria gonorrhoeae ORF 695 partial DNA sequence SEQ ID NO:2321.  
 PN WO9957280-A2.  
 PD 11-NOV-1999.  
 PA (CHIR) CHIRON CORP.  
 PA (GENO-) INST GENOMIC RES.  
 Percent Similarity: 60.00% Conservative: 17  
 Best Local Similarity: 35.71% Mismatches: 18  
 Query Match: 8.94% Indels: 10  
 RESULT 282  
 ID AAZ54188 standard; DNA; 921 BP.  
 DE Neisseria meningitidis ORF 695 partial DNA sequence SEQ ID NO:2325.  
 PN WO9957280-A2.  
 PD 11-NOV-1999.  
 PA (CHIR) CHIRON CORP.  
 PA (GENO-) INST GENOMIC RES.  
 Percent Similarity: 60.61% Conservative: 16  
 Best Local Similarity: 36.36% Mismatches: 24  
 Query Match: 8.94% Indels: 2  
 RESULT 283  
 ID ABX17318 standard; cDNA; 2712 BP.  
 DE Human cancer promoting protein PP7517.  
 PN CN1351082-A.  
 PD 29-MAY-2002.  
 PA (SHAN-) SHANGHAI INST ONCOLOGY.  
 Percent Similarity: 40.19% Conservative: 25  
 Best Local Similarity: 28.50% Mismatches: 81  
 Query Match: 8.90% Indels: 47  
 RESULT 284  
 ID ACN44729 standard; cDNA; 1253 BP.  
 DE Mouse mRNA sequence MCT7005.  
 PN WO2003073826-A2.  
 PD 12-SEP-2003.  
 PA (SAGR-) SAGRES DISCOVERY.  
 Percent Similarity: 33.56% Conservative: 40  
 Best Local Similarity: 20.13% Mismatches: 111  
 Query Match: 8.82% Indels: 87  
 RESULT 285  
 ID AAD13477 standard; cDNA; 507 BP.  
 DE Catechol-O-methyltransferase-like human enzyme encoding cDNA #2.  
 PN WO200157220-A2.  
 PD 09-AUG-2001.  
 PA (LEXI-) LEXICON GENETICS INC.  
 Percent Similarity: 45.52% Conservative: 17  
 Best Local Similarity: 32.84% Mismatches: 53  
 Query Match: 8.79% Indels: 20  
 RESULT 286  
 ID AAZ54187 standard; DNA; 918 BP.  
 DE Neisseria meningitidis ORF 695 partial DNA sequence SEQ ID NO:2323.  
 PN WO9957280-A2.  
 PD 11-NOV-1999.  
 PA (CHIR) CHIRON CORP.  
 PA (GENO-) INST GENOMIC RES.  
 Percent Similarity: 60.61% Conservative: 16  
 Best Local Similarity: 36.36% Mismatches: 24  
 Query Match: 8.79% Indels: 2  
 RESULT 287  
 ID AAH66205 standard; DNA; 639 BP.  
 DE C. glutamicum coding sequence fragment SEQ ID NO:1240.  
 PN EP1108790-A2.  
 PD 20-JUN-2001.  
 PA (KYOW) KYOWA HAKKO KOGYO KK.  
 Percent Similarity: 39.70% Conservative: 28  
 Best Local Similarity: 25.63% Mismatches: 82

Query Match: 8.56% Indels: 38  
 RESULT 288  
 ID ACA00413 standard; DNA; 639 BP.  
 DE C. glutamicum derived ORF SEQ ID 404.  
 PN DE10128510-A1.  
 PD 19-DEC-2002.  
 PA (DEGS ) DEGUSSA AG.  
 Percent Similarity: 39.70%  
 Best Local Similarity: 25.63%  
 Query Match: 8.56%  
 Indels: 38  
 RESULT 289  
 ID ADD13690 standard; DNA; 769 BP.  
 DE C. glutamicum homeostasis and adaptation associated DNA SEQ ID 91.  
 PN WO2003040290-A2.  
 PD 15-MAY-2003.  
 PA (BADI ) BASF AG.  
 Percent Similarity: 39.70%  
 Best Local Similarity: 25.63%  
 Query Match: 8.56%  
 Indels: 38  
 RESULT 290  
 ID AAH68527 standard; DNA; 349980 BP.  
 DE C glutamicum coding sequence fragment SEQ ID NO: 7062.  
 PN EPI108790-A2.  
 PD 20-JUN-2001.  
 PA (KIOW ) KYOWA HAKKO KOGYO KK.  
 Percent Similarity: 39.70%  
 Best Local Similarity: 25.63%  
 Query Match: 8.56%  
 Indels: 38  
 RESULT 291  
 ID ACF72506 standard; DNA; 636 BP.  
 DE Staphylococcus aureus DNA #186.  
 PN WO200294868-A2.  
 PD 28-NOV-2002.  
 PA (CHIR-) CHIRON SPA.  
 Percent Similarity: 42.01%  
 Best Local Similarity: 21.92%  
 Query Match: 8.49%  
 Indels: 28  
 RESULT 292  
 ID ABL12193 standard; cDNA; 5514 BP.  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 31061.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Percent Similarity: 42.33%  
 Best Local Similarity: 29.63%  
 Query Match: 8.49%  
 Indels: 39  
 RESULT 293  
 ID AAC89765 standard; cDNA; 178 BP.  
 DE Human gastrointestinal inflammation-related cDNA, SEQ ID NO: 34.  
 PN WO200073324-A2.  
 PD 07-DEC-2000.  
 PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.  
 Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Query Match: 8.41%  
 Indels: 0  
 RESULT 296  
 ID ABN87116 standard; cDNA; 457 BP.  
 DE Lolium perenne LpCCoAWta partial nucleotide sequence SEQ ID NO:10.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 Percent Similarity: 54.93%  
 Best Local Similarity: 35.21%  
 Query Match: 8.41%  
 Indels: 6

RESULT 297  
 ID AAD35115 standard; DNA; 2086 BP.  
 DE Corynebacterium glutamicum sigE gene.  
 PN WO200218428-A2.  
 PD 07-MAR-2002.  
 PA (DEGS ) DEGUSSA AG.  
 Percent Similarity: 39.80%  
 Best Local Similarity: 25.51%  
 Query Match: 8.34%  
 Indels: 38  
 RESULT 298  
 ID ABQ90300 standard; DNA; 4029 BP.  
 DE M. capsulatus gene #285 for DNA array.  
 PN WO200253655-A2.  
 PD 18-JUL-2002.  
 PA (UNIF-) UNIFOB STIFTELSEN UNIV BERGEN.  
 PA (TIGR-) TIGR.  
 Percent Similarity: 37.63%  
 Best Local Similarity: 25.44%  
 Query Match: 8.30%  
 Indels: 83  
 RESULT 299  
 ID AAH53823 standard; DNA; 495 BP.  
 DE S. epidermidis open reading frame nucleotide sequence SEQ ID NO:3039.  
 PN WO200134809-A2.  
 PD 17-MAY-2001.  
 PA (GLAX ) GLAXO GROUP LTD.  
 Percent Similarity: 44.24%  
 Best Local Similarity: 22.42%  
 Query Match: 8.27%  
 Indels: 10  
 RESULT 300  
 ID ADB74275 standard; DNA; 38494 BP.  
 DE Mycobacterium leprae DNA #2.  
 PN US6583266-B1.  
 PD 24-JUN-2003.  
 PA (GENE-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 50.00%  
 Best Local Similarity: 33.33%  
 Query Match: 8.27%  
 Indels: 0  
 RESULT 301  
 ID AAA68082 standard; DNA; 236 BP.  
 DE Pinus radiata OMT nucleotide sequence SEQ ID NO:175.  
 PN WO200022099-A1.  
 PD 20-APR-2000.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Percent Similarity: 54.55%  
 Best Local Similarity: 29.87%  
 Query Match: 8.19%  
 Indels: 8  
 RESULT 302  
 ID ADD41832 standard; DNA; 236 BP.  
 DE O-methyl transferase DNA #16.  
 PN US200313173-A1.  
 PD 10-JUL-2003.  
 PA (BLOK/) BLOKBERG L N.  
 PA (HAVU/) HAVUKKALA I.  
 Percent Similarity: 54.55%  
 Best Local Similarity: 29.87%  
 Query Match: 8.19%  
 Indels: 8  
 RESULT 303  
 ID ADS59333 standard; cDNA; 624 BP.  
 DE Bacterial polynucleotide #11320.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Percent Similarity: 37.20%  
 Best Local Similarity: 21.74%  
 Query Match: 8.12%  
 Indels: 50  
 RESULT 304  
 ID AAQ13306 standard; DNA; 1107 BP.  
 DE Human catechol-O-methyltransferase gene.

PN W09111513-A.  
 PD 08-AUG-1991.  
 PA (ORIN ) ORION YHYMAE OY.  
 Percent Similarity: 38.72% Conservative: 41  
 Best Local Similarity: 23.31% Mismatches: 118  
 Query Match: 8.08% Indels: 45  
 RESULT 305  
 ID ACN40883 standard; cDNA; 1289 BP.  
 DE Tumour-associated antigenic target (TAT) cDNA DNA226561, SEQ ID NO:5956.  
 PN W02004030615-A2.  
 PD 15-APR-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 38.72% Conservative: 41  
 Best Local Similarity: 23.31% Mismatches: 118  
 Query Match: 8.08% Indels: 45  
 RESULT 306  
 ID ADP45594 standard; DNA; 133100 BP.  
 DE Human NUMA1/FLJ20625/LOC220074 region gDNA.  
 Percent Similarity: 41.83% Conservative: 28  
 Best Local Similarity: 28.37% Mismatches: 81  
 Query Match: 8.04% Indels: 41  
 RESULT 307  
 ID ABZ83278 standard; cDNA; 1024 BP.  
 DE Toxicologically relevant human nucleotide sequence #437.  
 PN W02003016500-A2.  
 PD 27-FEB-2003.  
 PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.  
 Percent Similarity: 38.72% Conservative: 41  
 Best Local Similarity: 23.31% Mismatches: 118  
 Query Match: 8.00% Indels: 45  
 RESULT 308  
 ID ADE84973 standard; DNA; 1206 BP.  
 DE Farnesyl transferase inhibitor modulated leukemia associated gene #192.  
 PN W02003038129-A2.  
 PD 08-MAY-2003.  
 PA (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.  
 Percent Similarity: 38.72% Conservative: 41  
 Best Local Similarity: 23.31% Mismatches: 118  
 Query Match: 8.00% Indels: 45  
 RESULT 309  
 ID ADQ85986 standard; cDNA; 1291 BP.  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #2858.  
 PN W02004060270-A2.  
 PD 22-JUL-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 38.72% Conservative: 41  
 Best Local Similarity: 23.31% Mismatches: 118  
 Query Match: 8.00% Indels: 45  
 RESULT 310  
 ID ACN44731 standard; cDNA; 1311 BP.  
 DE Human mRNA sequence hCT1955643.  
 PN W02003073826-A2.  
 PD 12-SEP-2003.  
 PA (SAGR-) SAGRES DISCOVERY.  
 Percent Similarity: 38.72% Conservative: 41  
 Best Local Similarity: 23.31% Mismatches: 118  
 Query Match: 8.00% Indels: 45  
 RESULT 311  
 ID ABX63642 standard; cDNA; 1327 BP.  
 DE Human cDNA #642 differentially expressed in activated vascular tissue.  
 PN US2002137081-A1.  
 PD 26-SEP-2002.  
 PA (BAND/) BANDMAN O.  
 Percent Similarity: 38.72% Conservative: 41  
 Best Local Similarity: 23.31% Mismatches: 118  
 Query Match: 8.00% Indels: 45  
 RESULT 312  
 ID ADS69859 standard; cDNA; 253 BP.  
 DE Corn seedling-derived polynucleotide (cpds), SEQ ID 4875.  
 PN US2003237110-A9.  
 PD 25-DEC-2003.

PA (INCY-) INCYTE PHARM INC.  
 Percent Similarity: 52.44% Conservative: 9  
 Best Local Similarity: 41.46% Mismatches: 34  
 Query Match: 7.97% Indels: 5  
 RESULT 313  
 ID AB251068 standard; cDNA; 836 BP.  
 DE Aspergillus oryzae polynucleotide SEQ ID NO 181.  
 PN W0200279476-A1.  
 PD 10-OCT-2002.  
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
 PA (NARE-) NAT RES INST BREWING.  
 PA (NORQ ) NAT FOOD RES INST MIN AGRIC.  
 Percent Similarity: 40.96% Conservative: 21  
 Best Local Similarity: 28.31% Mismatches: 57  
 Query Match: 7.97% Indels: 41  
 RESULT 314  
 ID AAC77872 standard; cDNA; 1350 BP.  
 DE Human cancer associated gene sequence SEQ ID NO:266.  
 PN W0200055350-A1.  
 PD 21-SEP-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 39.84% Conservative: 38  
 Best Local Similarity: 24.70% Mismatches: 116  
 Query Match: 7.89% Indels: 35  
 RESULT 315  
 ID AAA31195 standard; DNA; 356 BP.  
 DE Plant microsatellite marker #156.  
 PN W09967421-A1.  
 PD 29-DEC-1999.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FOREST LTD.  
 Percent Similarity: 52.87% Conservative: 16  
 Best Local Similarity: 34.48% Mismatches: 33  
 Query Match: 7.82% Indels: 9  
 RESULT 316  
 ID AAD35116 standard; DNA; 457 BP.  
 DE Corynebacterium glutamicum sigE gene upstream region DNA.  
 PN W0200218428-A2.  
 PD 07-MAR-2002.  
 PA (DEGS ) DEGUSSA AG.  
 Percent Similarity: 44.37% Conservative: 26  
 Best Local Similarity: 26.06% Mismatches: 59  
 Query Match: 7.82% Indels: 20  
 RESULT 317  
 ID AC51621 standard; DNA; 834 BP.  
 DE Prokaryotic essential gene #33278.  
 PN W0200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 38.11% Conservative: 33  
 Best Local Similarity: 26.57% Mismatches: 95  
 Query Match: 7.71% Indels: 82  
 RESULT 318  
 ID ADB58045 standard; DNA; 1531 BP.  
 DE Toxicity-related gene, SEQ ID 3071.  
 PN W02003064624-A2.  
 PD 07-AUG-2003.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 43.19% Conservative: 41  
 Best Local Similarity: 23.94% Mismatches: 92  
 Query Match: 7.71% Indels: 31  
 RESULT 319  
 ID ADB52519 standard; DNA; 1531 BP.  
 DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3061.  
 PN W02003065993-A2.  
 PD 14-AUG-2003.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 43.19% Conservative: 41  
 Best Local Similarity: 23.94% Mismatches: 92  
 Query Match: 7.71% Indels: 31  
 RESULT 320  
 ID ACN40884 standard; cDNA; 1067 BP.  
 DE Tumour-associated antigenic target (TAT) cDNA DNA326926, SEQ ID NO:5958.



PN W02004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 40.51%  
Best Local Similarity: 24.05%  
Query Match: 7.67%  
RESULT 321  
ID ADK16023 standard; DNA; 64492 BP.  
DE Streptomyces halstedii vincenistatin gene cluster seq id 1.  
PN US2004053274-A1.  
PD 18-MAR-2004.  
PA (TOKD ) TOKYO INST TECHNOLOGY.  
Percent Similarity: 30.15%  
Best Local Similarity: 22.77%  
Query Match: 7.67%  
RESULT 322  
ID AAQ13305 standard; DNA; 1591 BP.  
DE Rat catechol-O-methyltransferase gene.  
PN W09111513-A.  
PD 08-AUG-1991.  
PA (ORIN ) ORION YHTWAE OY.  
Percent Similarity: 43.19%  
Best Local Similarity: 23.94%  
Query Match: 7.63%  
RESULT 323  
ID ADQ67408 standard; cDNA; 3003 BP.  
DE Novel human cDNA sequence #2381.  
PN EP1440981-A2.  
PD 28-JUL-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Percent Similarity: 37.29%  
Best Local Similarity: 27.12%  
Query Match: 7.63%  
RESULT 324  
ID AAS83954 standard; cDNA; 4083 BP.  
DE DNA encoding novel human diagnostic protein #19758.  
PN W0200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 37.29%  
Best Local Similarity: 27.12%  
Query Match: 7.63%  
RESULT 325  
ID AAQ88760 standard; DNA; 1813 BP.  
DE Human ubiquitous nuclear receptor protein DNA.  
PN W09513373-A1.  
PD 18-MAY-1995.  
PA (ARCH-) ARCH DEV CORP.  
Percent Similarity: 34.41%  
Best Local Similarity: 25.59%  
Query Match: 7.59%  
RESULT 326  
ID AAT79634 standard; DNA; 1898 BP.  
DE DNA encoding human ubiquitous nuclear receptor polypeptide.  
PN US539616-A.  
PD 17-JUN-1997.  
PA (ARCH-) ARCH DEV CORP.  
Percent Similarity: 34.21%  
Best Local Similarity: 25.73%  
Query Match: 7.59%  
RESULT 327  
ID AAT7617 standard; cDNA to mRNA; 1688 BP.  
DE Steroid hormone receptor analogue ECDN small mol. variant cDNA.  
PN W09609324-A1.  
PD 28-MAR-1996.  
PA (CANC-) CANCER INST.  
PA (EISA ) EISAI CO LTD.  
Percent Similarity: 37.41%  
Best Local Similarity: 25.90%  
Query Match: 7.56%  
RESULT 328  
ID ACC85541 standard; DNA; 2505 BP.  
DE T thermophilus strain GK24 DNA polymerase gene SEQ ID NO: 1.

PN W02003048309-A2.  
PD 12-JUN-2003.  
PA (APPL-) APPLERA CORP.  
Percent Similarity: 36.73%  
Best Local Similarity: 26.19%  
Query Match: 7.56%  
RESULT 329  
ID ACC85544 standard; DNA; 2505 BP.  
DE T thermophilus strain GK24 variant DNA polymerase gene SEQ ID NO: 4.  
PN W02003048309-A2.  
PD 12-JUN-2003.  
PA (APPL-) APPLERA CORP.  
Percent Similarity: 36.73%  
Best Local Similarity: 26.19%  
Query Match: 7.56%  
RESULT 330  
ID ABZ11775 standard; cDNA; 1564 BP.  
DE Human polynucleotide SEQ ID NO 657.  
PN W0200270539-A2.  
PD 12-SEP-2002.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 31.96%  
Best Local Similarity: 24.63%  
Query Match: 7.52%  
RESULT 331  
ID ADM44293 standard; cDNA; 1786 BP.  
DE Novel human arginine-rich protein cDNA #657.  
PN US2004053250-A1.  
PD 18-MAR-2004.  
PA (TANG/) TANG Y T.  
PA (XUEA/) XUE A.  
PA (DRMA/) DRMANAC R T.  
Percent Similarity: 31.96%  
Best Local Similarity: 24.63%  
Query Match: 7.52%  
RESULT 332  
ID ADC30127 standard; cDNA; 3298 BP.  
DE Human novel cDNA sequence, SEQ ID NO:209.  
PN W02003029271-A2.  
PD 10-APR-2003.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 37.09%  
Best Local Similarity: 28.17%  
Query Match: 7.52%  
RESULT 333  
ID ACF36088 standard; DNA; 1815 BP.  
DE Human LXR beta polypeptide encoding DNA.  
PN W02003059884-A1.  
PD 24-JUL-2003.  
PA (XCEP-) X-CEPTOR THERAPEUTICS INC.  
Percent Similarity: 37.68%  
Best Local Similarity: 27.90%  
Query Match: 7.48%  
RESULT 334  
ID ACF04414 standard; DNA; 1815 BP.  
DE Human liver X receptor LXR beta coding sequence.  
PN W02003060078-A2.  
PD 24-JUL-2003.  
PA (XCEP-) X-CEPTOR THERAPEUTICS INC.  
Percent Similarity: 37.68%  
Best Local Similarity: 27.90%  
Query Match: 7.48%  
RESULT 335  
ID ADQ83721 standard; cDNA; 1986 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #535.  
PN W02004060270-A2.  
PD 22-JUL-2004.  
PA (GETH ) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 37.68%  
Best Local Similarity: 27.90%  
Query Match: 7.48%

RESULT 336  
ID ADQ87023 standard; cDNA; 1986 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3899.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH ) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 37.68%  
Best Local Similarity: 27.90%  
Conservative: 27  
Mismatches: 108  
Indels: 64  
Query Match: 7.48%  
RESULT 337  
ID ACN40662 standard; cDNA; 1986 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA326744, SEQ ID NO:5578.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 37.68%  
Best Local Similarity: 27.90%  
Conservative: 27  
Mismatches: 108  
Indels: 64  
Query Match: 7.48%  
RESULT 338  
ID ADL12925 standard; cDNA; 1987 BP.  
DE Human steroid-induced C3A liver cell cDNA #654.  
PN US6673549-B1.  
PD 06-JAN-2004.  
PA (INCV-) INCYTE CORP.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 37.68%  
Best Local Similarity: 27.90%  
Conservative: 27  
Mismatches: 108  
Indels: 64  
Query Match: 7.48%  
RESULT 339  
ID ADQ89943 standard; DNA; 7531 BP.  
DE Antagonist of cell cycle progression nucleotide sequence #187.  
PN WO2004063362-A2.  
PD 29-JUL-2004.  
PA (CYCL-) CYCLACEL LTD.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 33.23%  
Best Local Similarity: 24.70%  
Conservative: 28  
Mismatches: 85  
Indels: 134  
Query Match: 7.45%  
RESULT 340  
ID AAT88206 standard; cDNA; 8460 BP.  
DE cDNA for protein (OA-519) cross-reactive with hpr gene product.  
PN US5665874-A.  
PD 09-SEP-1997.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 33.23%  
Best Local Similarity: 24.70%  
Conservative: 28  
Mismatches: 85  
Indels: 134  
Query Match: 7.45%  
RESULT 341  
ID ACC49471 standard; cDNA; 8460 BP.  
DE Human fatty acid synthase encoding cDNA.  
PN WO2003023355-A2.  
PD 20-MAR-2003.  
PA (BURN-) BURNHAM INST.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 33.23%  
Best Local Similarity: 24.70%  
Conservative: 28  
Mismatches: 85  
Indels: 134  
Query Match: 7.45%  
RESULT 342  
ID ACA64923 standard; DNA; 8460 BP.  
DE Human breast carcinoma fatty acid synthase DNA corresponding to U29344.  
PN DE10127572-A1.  
PD 05-DEC-2002.  
PA (PATH-) PATHOARRAY GMBH.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 33.23%  
Best Local Similarity: 24.70%  
Conservative: 28  
Mismatches: 85  
Indels: 134  
Query Match: 7.45%  
RESULT 343  
ID ACF63393 standard; DNA; 8460 BP.  
DE Human fatty acid synthase gene SEQ ID NO:115.  
PN WO2003006478-A1.  
PD 23-JAN-2003.  
PA (OLIG-) OLIGOS ETC INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 33.23%  
Best Local Similarity: 24.70%  
Conservative: 28  
Mismatches: 85  
Indels: 134  
Query Match: 7.45%

Query Match: 7.45%  
Indels: 134  
RESULT 344  
ID ADO21281 standard; cDNA; 8460 BP.  
DE DNA encoding human fatty acid synthase.  
PN US2004077570-A1.  
PD 22-APR-2004.  
PA (FREI/) FREIER S M.  
PA (DOBI/) DOBIE K W.  
PA (BHAM/) BHANOT S.  
Percent Similarity: 33.23%  
Best Local Similarity: 24.70%  
Conservative: 28  
Mismatches: 85  
Indels: 134  
Query Match: 7.45%  
RESULT 345  
ID ADP13456 standard; DNA; 8460 BP.  
DE Renal cell carcinoma differentially expressed gene #192.  
PN WO2004048933-A2.  
PD 10-JUN-2004.  
PA (AMHP ) WYETH.  
PA (TWIN/) TWINE N C.  
PA (BURC/) BURCZYNSKI M E.  
PA (TREP/) TREPICCHIO W L.  
PA (DORN/) DORNER A.  
PA (STOV/) STOVER J A.  
PA (SLON/) SLONI D K.  
Percent Similarity: 33.23%  
Best Local Similarity: 24.70%  
Conservative: 28  
Mismatches: 85  
Indels: 134  
Query Match: 7.45%  
RESULT 346  
ID ADQ89779 standard; DNA; 8460 BP.  
DE Antagonist of cell cycle progression nucleotide sequence #105.  
PN WO2004063362-A2.  
PD 29-JUL-2004.  
PA (CYCL-) CYCLACEL LTD.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 33.23%  
Best Local Similarity: 24.70%  
Conservative: 28  
Mismatches: 85  
Indels: 134  
Query Match: 7.45%  
RESULT 347  
ID AAV74506 standard; DNA; 13715 BP.  
DE Staphylococcus aureus contig SEQ ID #195.  
PN EP786519-A2.  
PD 30-JUL-1997.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 39.27%  
Best Local Similarity: 21.46%  
Conservative: 39  
Mismatches: 105  
Indels: 28  
Query Match: 7.45%  
RESULT 348  
ID ABD07304 standard; DNA; 2469 BP.  
DE Pseudomonas aeruginosa polynucleotide #5908.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 37.37%  
Best Local Similarity: 27.40%  
Conservative: 28  
Mismatches: 107  
Indels: 69  
Query Match: 7.41%  
RESULT 349  
ID ABD11218 standard; DNA; 636 BP.  
DE Pseudomonas aeruginosa polynucleotide #9822.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 43.88%  
Best Local Similarity: 28.78%  
Conservative: 21  
Mismatches: 58  
Indels: 20  
Query Match: 7.37%  
RESULT 350  
ID ABD11311 standard; DNA; 1275 BP.  
DE Pseudomonas aeruginosa polynucleotide #9915.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 43.88%  
Best Local Similarity: 28.78%  
Conservative: 21  
Mismatches: 58  
Indels: 20  
Query Match: 7.37%  
RESULT 351

ID ABD11556 standard; DNA; 1443 BP.  
 DE Pseudomonas aeruginosa polynucleotide #10160.  
 PN US551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 43.88% Conservative: 21  
 Best Local Similarity: 28.78% Mismatches: 58  
 Query Match: 7.37% Indels: 20  
 RESULT 352  
 ID AAQ24322 standard; DNA; 1635 BP.  
 DE Mutant thermostable DNA polymerase p205A292.  
 PN WO9206200-A.  
 PD 16-APR-1992.  
 PA (CETU) CETUS CORP.  
 Percent Similarity: 37.98% Conservative: 37  
 Best Local Similarity: 25.09% Mismatches: 112  
 Query Match: 7.37% Indels: 67  
 RESULT 353  
 ID AAQ24321 standard; DNA; 1899 BP.  
 DE Mutant thermostable DNA polymerase p205d2-203.  
 PN WO9206200-A.  
 PD 16-APR-1992.  
 PA (CETU) CETUS CORP.  
 Percent Similarity: 37.98% Conservative: 37  
 Best Local Similarity: 25.09% Mismatches: 112  
 Query Match: 7.37% Indels: 67  
 RESULT 354  
 ID ABK84201 standard; cDNA; 2010 BP.  
 DE Human cDNA differentially expressed in granulocytic cells #772.  
 PN WO200228999-A2.  
 PD 11-APR-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 37.76% Conservative: 29  
 Best Local Similarity: 27.62% Mismatches: 111  
 Query Match: 7.37% Indels: 67  
 RESULT 355  
 ID ADJ14181 standard; DNA; 2010 BP.  
 DE DNA encoding human liver X receptor LXR beta.  
 PN US2004018560-A1.  
 PD 29-JAN-2004.  
 PA (BLED/) BLED SOE R K.  
 PA (MILL/) MILLER A.  
 PA (MOOR/) MOORE J T.  
 PA (MOOR/) MOORE L.  
 PA (WILL/) WILLIAMS S P.  
 PA (WISE/) WISELY G B.  
 Percent Similarity: 37.76% Conservative: 29  
 Best Local Similarity: 27.62% Mismatches: 111  
 Query Match: 7.37% Indels: 67  
 RESULT 356  
 ID ADMA1245 standard; DNA; 2010 BP.  
 DE Human liver X receptor beta gene.  
 PN EPI398032-A1.  
 PD 17-MAR-2004.  
 PA (PHEN-) PHENEX PHARM AG.  
 Percent Similarity: 37.76% Conservative: 29  
 Best Local Similarity: 27.62% Mismatches: 111  
 Query Match: 7.37% Indels: 67  
 RESULT 357  
 ID AAQ63134 standard; cDNA; 2030 BP.  
 DE Human recombinant steroid hormone receptor NERI cDNA.  
 PN WO9407916-A1.  
 PD 14-APR-1994.  
 PA (MERI) MERCK & CO INC.  
 Percent Similarity: 37.76% Conservative: 29  
 Best Local Similarity: 27.62% Mismatches: 111  
 Query Match: 7.37% Indels: 67  
 RESULT 358  
 ID AAT18996 standard; DNA; 2030 BP.  
 DE Human steroid receptor NER gene.  
 PN WO9613519-A1.  
 PD 09-MAY-1996.  
 PA (MERI) MERCK & CO INC.

PA (MEDI-) MEDICAL COLLEGE PENNSYLVANIA.  
 Percent Similarity: 37.76% Conservative: 29  
 Best Local Similarity: 27.62% Mismatches: 111  
 Query Match: 7.37% Indels: 67  
 RESULT 359  
 ID AAT30031 standard; DNA; 2030 BP.  
 DE NER receptor potentiator DNA.  
 PN WO9613257-A1.  
 PD 09-MAY-1996.  
 PA (MERI) MERCK & CO INC.  
 Percent Similarity: 37.76% Conservative: 29  
 Best Local Similarity: 27.62% Mismatches: 111  
 Query Match: 7.37% Indels: 67  
 RESULT 360  
 ID AAQ24320 standard; DNA; 2043 BP.  
 DE Mutant thermostable DNA polymerase p205d2-155.  
 PN WO9206200-A.  
 PD 16-APR-1992.  
 PA (CETU) CETUS CORP.  
 Percent Similarity: 37.98% Conservative: 37  
 Best Local Similarity: 25.09% Mismatches: 112  
 Query Match: 7.37% Indels: 67  
 RESULT 361  
 ID AAQ24013 standard; DNA; 2277 BP.  
 DE Mutant thermostable DNA polymerase p205d2-77.  
 PN WO9206200-A.  
 PD 16-APR-1992.  
 PA (CETU) CETUS CORP.  
 Percent Similarity: 37.98% Conservative: 37  
 Best Local Similarity: 25.09% Mismatches: 112  
 Query Match: 7.37% Indels: 67  
 RESULT 362  
 ID AAQ24012 standard; DNA; 2370 BP.  
 DE Mutant thermostable DNA polymerase p205d2-46.  
 PN WO9206200-A.  
 PD 16-APR-1992.  
 PA (CETU) CETUS CORP.  
 Percent Similarity: 37.98% Conservative: 37  
 Best Local Similarity: 25.09% Mismatches: 112  
 Query Match: 7.37% Indels: 67  
 RESULT 363  
 ID AAQ24011 standard; DNA; 2505 BP.  
 DE Mutant thermostable DNA polymerase from Thermus species 205.  
 PN WO9206200-A.  
 PD 16-APR-1992.  
 PA (CETU) CETUS CORP.  
 Percent Similarity: 37.98% Conservative: 37  
 Best Local Similarity: 25.09% Mismatches: 112  
 Query Match: 7.37% Indels: 67  
 RESULT 364  
 ID ADG64486 standard; DNA; 2685 BP.  
 DE Chimeric thermostable DNA polymerase CS8 encoding DNA SEQ ID NO:171.  
 PN EPI350841-A2.  
 PD 08-OCT-2003.  
 PA (HOFF) ROCHE DIAGNOSTICS GMBH.  
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.  
 Percent Similarity: 37.98% Conservative: 37  
 Best Local Similarity: 25.09% Mismatches: 112  
 Query Match: 7.37% Indels: 67  
 RESULT 365  
 ID ADG64462 standard; DNA; 2685 BP.  
 DE Chimeric thermostable DNA polymerase CS7 encoding DNA SEQ ID NO:147.  
 PN EPI350841-A2.  
 PD 08-OCT-2003.  
 PA (HOFF) ROCHE DIAGNOSTICS GMBH.  
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.  
 Percent Similarity: 37.98% Conservative: 37  
 Best Local Similarity: 25.09% Mismatches: 112  
 Query Match: 7.37% Indels: 67  
 RESULT 366  
 ID ADA13364 standard; cDNA; 2877 BP.  
 DE Human intracellular signalling molecule INTSIG-1 cDNA, SEQ ID NO:46.

```

PN WO2003031568-A2.
PD 17-APR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 36.80%
Best Local Similarity: 27.14%
Query Match: 7.37%
RESULT 367
ID ADQ84658 standard; cDNA; 8450 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1472.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH ) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Percent Similarity: 34.27%
Best Local Similarity: 24.92%
Query Match: 7.37%
RESULT 368
ID ADQ86657 standard; cDNA; 8450 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3531.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH ) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Percent Similarity: 34.27%
Best Local Similarity: 24.92%
Query Match: 7.37%
RESULT 369
ID ADQ85543 standard; cDNA; 8450 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #2357.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH ) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Percent Similarity: 34.27%
Best Local Similarity: 24.92%
Query Match: 7.37%
RESULT 370
ID ACN40305 standard; cDNA; 8450 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA326430, SEQ ID NO:5010.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 34.27%
Best Local Similarity: 24.92%
Query Match: 7.37%
RESULT 371
ID ADR65924 standard; DNA; 8455 BP.
DE Human prostatic carcinoma derived DNA SEQ ID 120 #1.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Percent Similarity: 34.27%
Best Local Similarity: 24.92%
Query Match: 7.37%
RESULT 372
ID ADR66827 standard; DNA; 8455 BP.
DE Human prostatic carcinoma derived DNA SEQ ID 120 #4.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Percent Similarity: 34.27%
Best Local Similarity: 24.92%
Query Match: 7.37%
RESULT 373
ID ADMA1248 standard; DNA; 8461 BP.
DE Human fatty acid synthase gene.
PN EPI398032-A1.
PD 17-MAR-2004.
PA (PHEN-) PHENEX PHARM AG.
Percent Similarity: 34.27%
Best Local Similarity: 24.92%
Query Match: 7.37%
RESULT 374
ID ADR67189 standard; DNA; 8461 BP.
DE Human bladder cancer associated nucleotide sequence.
PN WO2004076613-A2.
PD 10-SEP-2004.
PA (HERR/) HERR A.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (STAU/) STAUB E.
PA (PILA/) PILARSKY C.
PA (SPEC/) SPECHT T.
Percent Similarity: 34.27%
Best Local Similarity: 24.92%
Query Match: 7.37%
RESULT 375
ID AAA37760 standard; DNA; 8519 BP.
DE Human fatty acid synthase (FAS) coding sequence.
PN WO200051430-A1.
PD 08-SEP-2000.
PA (SMIK ) SMITHKLINE BEECHAM CORP.
Percent Similarity: 34.27%
Best Local Similarity: 24.92%
Query Match: 7.37%
RESULT 376
ID AAK73222 standard; DNA; 15914 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28034.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 34.70%
Best Local Similarity: 24.66%
Query Match: 7.37%
RESULT 377
ID ABD10818 standard; DNA; 855 BP.
DE Pseudomonas aeruginosa polynucleotide #9422.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 38.56%
Best Local Similarity: 28.39%
Query Match: 7.33%
RESULT 379
ID ABD10851 standard; DNA; 1101 BP.
DE Pseudomonas aeruginosa polynucleotide #9455.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 38.56%
Best Local Similarity: 28.39%
Query Match: 7.33%
RESULT 380
ID ADB62413 standard; cDNA; 2384 BP.
DE Human cDNA encoding clone FCBBF30220050.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 39.32%
Best Local Similarity: 27.67%
Query Match: 7.33%

```

Query Match: 7.33% Indels: 51  
 RESULT 381  
 ID AAX07131 standard; DNA; 3147 BP.  
 DE Staphylococcus aureus mutant P14B25 virulence gene.  
 PN WO9001473-A2.  
 PD 14-JAN-1999.  
 PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
 Percent Similarity: 41.31% Conservative: 29  
 Best Local Similarity: 27.70% Mismatches: 63  
 Query Match: 7.33% Indels: 64  
 RESULT 382  
 ID AAS52328 standard; DNA; 3147 BP.  
 DE E. coli DNA for cellular proliferation protein #50.  
 PN WO200170955-A2.  
 PD 27-SEP-2001.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 41.31% Conservative: 29  
 Best Local Similarity: 27.70% Mismatches: 63  
 Query Match: 7.33% Indels: 64  
 RESULT 383  
 ID AAH81417 standard; DNA; 3147 BP.  
 DE Escherichia coli protein encoding nucleotide sequence SEQ ID NO:216.  
 PN WO200148209-A2.  
 PD 05-JUL-2001.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 41.31% Conservative: 29  
 Best Local Similarity: 27.70% Mismatches: 63  
 Query Match: 7.33% Indels: 64  
 RESULT 384  
 ID ACA32390 standard; DNA; 3147 BP.  
 DE Prokaryotic essential gene #14047.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 41.31% Conservative: 29  
 Best Local Similarity: 27.70% Mismatches: 63  
 Query Match: 7.33% Indels: 64  
 RESULT 385  
 ID AAA14651 standard; DNA; 77536 BP.  
 DE Nucleotide sequence of the FK-520 biosynthetic gene cluster.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 37.44% Conservative: 24  
 Best Local Similarity: 26.48% Mismatches: 85  
 Query Match: 7.33% Indels: 52  
 RESULT 386  
 ID ACA44128 standard; DNA; 828 BP.  
 DE Prokaryotic essential gene #25785.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 36.36% Conservative: 16  
 Best Local Similarity: 30.04% Mismatches: 79  
 Query Match: 7.30% Indels: 84  
 RESULT 387  
 ID ABD01505 standard; DNA; 1713 BP.  
 DE Pseudomonas aeruginosa polynucleotide #109.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 36.16% Conservative: 26  
 Best Local Similarity: 26.57% Mismatches: 73  
 Query Match: 7.30% Indels: 101  
 RESULT 388  
 ID AAHL6078 standard; cDNA; 1782 BP.  
 DE Human cDNA sequence SEQ ID NO:14776.  
 PN EP1074617-A2.  
 PD 07-FEB-2001.  
 PA (HELI-) HELIX RES INST.  
 Percent Similarity: 31.67% Conservative: 24  
 Best Local Similarity: 24.63% Mismatches: 125  
 Query Match: 7.30% Indels: 108  
 RESULT 389  
 ID ACC78000 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.

PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 37.37% Conservative: 34  
 Best Local Similarity: 25.61% Mismatches: 115  
 Query Match: 7.30% Indels: 68  
 RESULT 390  
 ID ADP64454 standard; DNA; 76994 BP.  
 DE Sorangium cellulosum disorazole polyketide synthase gene cluster DNA.  
 PN WO2004053065-A2.  
 PD 24-JUN-2004.  
 PA (KOSA-) KOSAN BIOSCIENCES INC.  
 Percent Similarity: 32.34% Conservative: 36  
 Best Local Similarity: 21.66% Mismatches: 79  
 Query Match: 7.30% Indels: 149  
 RESULT 391  
 ID ABD10747 standard; DNA; 657 BP.  
 DE Pseudomonas aeruginosa polynucleotide #9351.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 38.50% Conservative: 23  
 Best Local Similarity: 28.32% Mismatches: 83  
 Query Match: 7.26% Indels: 56  
 RESULT 392  
 ID AAZ91260 standard; DNA; 1632 BP.  
 DE Acetohydroxyacid synthase nucleotide sequence SEQ ID NO:14.  
 PN WO200004158-A2.  
 PD 27-JAN-2000.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Percent Similarity: 38.33% Conservative: 34  
 Best Local Similarity: 26.48% Mismatches: 124  
 Query Match: 7.26% Indels: 53  
 RESULT 393  
 ID AAT27616 standard; cDNA to mRNA; 1979 BP.  
 DE Human foetal lung steroid hormone receptor analogue ECDN cDNA.  
 PN WO9609324-A1.  
 PD 28-MAR-1996.  
 PA (CANC-) CANCER INST.  
 Percent Similarity: 37.77% Conservative: 26  
 Best Local Similarity: 28.42% Mismatches: 105  
 Query Match: 7.26% Indels: 68  
 RESULT 394  
 ID ABD13152 standard; DNA; 2232 BP.  
 DE Pseudomonas aeruginosa polynucleotide #11756.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 38.11% Conservative: 28  
 Best Local Similarity: 28.32% Mismatches: 112  
 Query Match: 7.26% Indels: 67  
 RESULT 395  
 ID ABD13005 standard; DNA; 2274 BP.  
 DE Pseudomonas aeruginosa polynucleotide #11609.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 38.11% Conservative: 28  
 Best Local Similarity: 28.32% Mismatches: 112  
 Query Match: 7.26% Indels: 67  
 RESULT 396  
 ID ACC85543 standard; DNA; 2505 BP.  
 DE T thermophilus strain lb21 DNA polymerase gene SEQ ID NO: 3.  
 PN WO2003048309-A2.  
 PD 12-JUN-2003.  
 PA (APPL-) APPLERA CORP.  
 Percent Similarity: 37.33% Conservative: 34  
 Best Local Similarity: 25.68% Mismatches: 111  
 Query Match: 7.26% Indels: 74  
 RESULT 397  
 ID ACC85542 standard; DNA; 2505 BP.  
 DE T thermophilus strain RQ-1 DNA polymerase gene SEQ ID NO: 2.

```

PN WO2003048309-A2.
PD 12-JUN-2003.
PA (APPL-) APPLERA CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.68%
Query Match: 7.26%
Indels: 74
Conservative: 32
Mismatch: 113
Indels: 74
RESULT 398
ID ACC85547 standard; DNA; 2505 BP.
DE T thermophilus strain GK24 variant DNA polymerase gene SEQ ID NO: 7.
PN WO2003048309-A2.
PD 12-JUN-2003.
PA (APPL-) APPLERA CORP.
Percent Similarity: 36.39%
Best Local Similarity: 26.19%
Query Match: 7.26%
Indels: 78
Conservative: 30
Mismatch: 111
Indels: 78
RESULT 399
ID ACC85545 standard; DNA; 2505 BP.
DE T thermophilus strain RQ-1 variant DNA polymerase gene SEQ ID NO: 5.
PN WO2003048309-A2.
PD 12-JUN-2003.
PA (APPL-) APPLERA CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.68%
Query Match: 7.26%
Indels: 74
Conservative: 32
Mismatch: 113
Indels: 74
RESULT 400
ID ACC85550 standard; DNA; 2505 BP.
DE T thermophilus strain GK24 variant DNA polymerase gene SEQ ID NO: 10.
PN WO2003048309-A2.
PD 12-JUN-2003.
PA (APPL-) APPLERA CORP.
Percent Similarity: 36.39%
Best Local Similarity: 26.19%
Query Match: 7.26%
Indels: 78
Conservative: 30
Mismatch: 111
Indels: 78
RESULT 401
ID ACC85546 standard; DNA; 2505 BP.
DE T thermophilus strain 1b21 variant DNA polymerase gene SEQ ID NO: 6.
PN WO2003048309-A2.
PD 12-JUN-2003.
PA (APPL-) APPLERA CORP.
Percent Similarity: 37.33%
Best Local Similarity: 25.68%
Query Match: 7.26%
Indels: 74
Conservative: 34
Mismatch: 111
Indels: 74
RESULT 402
ID ABD13232 standard; DNA; 2613 BP.
DE Pseudomonas aeruginosa polynucleotide #11836.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 38.11%
Best Local Similarity: 28.32%
Query Match: 7.26%
Indels: 67
Conservative: 28
Mismatch: 112
Indels: 67
RESULT 403
ID ACC77974 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Query Match: 7.26%
Indels: 74
Conservative: 33
Mismatch: 113
Indels: 74
RESULT 404
ID ACC77971 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.99%
Best Local Similarity: 25.34%
Query Match: 7.26%
Indels: 74
Conservative: 34
Mismatch: 112
Indels: 74
RESULT 405
ID AA291253 standard; DNA; 24494 BP.
DE Bacterium 2412.1 fumonisin-catabolising gene cluster.
PN WO200004158-A2.
PD 27-JAN-2000.
PA (PION-) PIONEER HI-BRED INT INC.
Percent Similarity: 38.33%
Best Local Similarity: 26.48%
Query Match: 7.26%
Indels: 53
Conservative: 34
Mismatch: 124
Indels: 53
RESULT 406
ID AAQ46806 standard; DNA; 29879 BP.
DE eryA region of S. erythraea chromosome.
PN WO9313663-A1.
PD 22-JUL-1993.
PA (ABBO) ABBOTT LAB.
Percent Similarity: 33.03%
Best Local Similarity: 24.62%
Query Match: 7.26%
Indels: 130
Conservative: 28
Mismatch: 93
Indels: 130
RESULT 407
ID ABD11655 standard; DNA; 1086 BP.
DE Pseudomonas aeruginosa polynucleotide #10259.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 40.35%
Best Local Similarity: 26.32%
Query Match: 7.22%
Indels: 49
Conservative: 40
Mismatch: 122
Indels: 49
RESULT 408
ID ABD11993 standard; DNA; 1101 BP.
DE Pseudomonas aeruginosa polynucleotide #10597.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 40.35%
Best Local Similarity: 26.32%
Query Match: 7.22%
Indels: 49
Conservative: 40
Mismatch: 122
Indels: 49
RESULT 409
ID ACA45703 standard; DNA; 1104 BP.
DE Prokaryotic essential gene #27360.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 44.22%
Best Local Similarity: 26.63%
Query Match: 7.22%
Indels: 39
Conservative: 35
Mismatch: 72
Indels: 39
RESULT 410
ID AAA81453 standard; DNA; 36471 BP.
DE N. meningitidis partial DNA sequence gnm_1 SEQ ID NO:1.
PN WO200022430-A2.
PD 20-APR-2000.
PA (CHIR) CHIRON CORP.
Percent Similarity: 35.76%
Best Local Similarity: 23.84%
Query Match: 7.22%
Indels: 92
Conservative: 36
Mismatch: 103
Indels: 92
RESULT 411
ID AAF21611 standard; DNA; 349980 BP.
DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:112.
PN WO200066791-A1.
PD 09-NOV-2000.
PA (CHIR) CHIRON CORP.
Percent Similarity: 35.76%
Best Local Similarity: 23.84%
Query Match: 7.22%
Indels: 92
Conservative: 36
Mismatch: 103
Indels: 92
RESULT 412
ID ABD13494 standard; DNA; 783 BP.
DE Pseudomonas aeruginosa polynucleotide #12098.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 35.43%
Best Local Similarity: 25.98%
Query Match: 7.19%
Indels: 71
Conservative: 24
Mismatch: 93
Indels: 71

```

RESULT 414  
 ID ABD13569 standard; DNA; 984 BP.  
 DE Pseudomonas aeruginosa polynucleotide #12173.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 35.43% Conservative: 24  
 Best Local Similarity: 25.98% Mismatches: 93  
 Query Match: 7.19% Indels: 71

RESULT 415  
 ID ABD13816 standard; DNA; 1254 BP.  
 DE Pseudomonas aeruginosa polynucleotide #12420.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 36.03% Conservative: 23  
 Best Local Similarity: 27.57% Mismatches: 125  
 Query Match: 7.19% Indels: 50

RESULT 416  
 ID ACC77992 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 7.19% Indels: 74

RESULT 417  
 ID ABD07318 standard; DNA; 3135 BP.  
 DE Pseudomonas aeruginosa polynucleotide #5922.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 37.17% Conservative: 27  
 Best Local Similarity: 27.14% Mismatches: 101  
 Query Match: 7.15% Indels: 68

RESULT 418  
 ID ADC59447 standard; DNA; 15534 BP.  
 DE Human epiplakin-encoding cDNA.  
 PN JP2003047469-A.  
 PD 18-FEB-2003.  
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
 Percent Similarity: 34.68% Conservative: 28  
 Best Local Similarity: 25.25% Mismatches: 101  
 Query Match: 7.15% Indels: 93

RESULT 419  
 ID ADJ75047 standard; DNA; 15534 BP.  
 DE Marker gene SEQ ID NO:299.  
 PN EP1394274-A2.  
 PD 03-MAR-2004.  
 PA (GENO-) GENOX RES INC.  
 Percent Similarity: 34.68% Conservative: 28  
 Best Local Similarity: 25.25% Mismatches: 101  
 Query Match: 7.15% Indels: 93

RESULT 420  
 ID ACF12853 standard; cDNA; 15952 BP.  
 DE Human cervical cancer cell marker encoding cDNA SEQ ID NO:51.  
 PN WO2002101075-A2.  
 PD 19-DEC-2002.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Percent Similarity: 34.68% Conservative: 28  
 Best Local Similarity: 25.25% Mismatches: 101  
 Query Match: 7.15% Indels: 93

RESULT 421  
 ID ABD09003 standard; DNA; 852 BP.  
 DE Pseudomonas aeruginosa polynucleotide #7607.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 39.39% Conservative: 20  
 Best Local Similarity: 27.27% Mismatches: 71  
 Query Match: 7.11% Indels: 29

RESULT 422

ID ADS62025 standard; cDNA; 1272 BP.  
 DE Bacterial polynucleotide #14012.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Percent Similarity: 38.03% Conservative: 18  
 Best Local Similarity: 30.34% Mismatches: 114  
 Query Match: 7.11% Indels: 33

RESULT 423  
 ID ABD05329 standard; DNA; 1452 BP.  
 DE Pseudomonas aeruginosa polynucleotide #3933.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 38.89% Conservative: 34  
 Best Local Similarity: 26.30% Mismatches: 95  
 Query Match: 7.11% Indels: 70

RESULT 424  
 ID AAT27255 standard; DNA; 1794 BP.  
 DE DNA polymerase I exonuclease-free fragment.  
 PN WO9614405-A2.  
 PD 17-MAY-1996.  
 PA (MOLE-) MOLECULAR BIOLOGY RESOURCES INC.  
 Percent Similarity: 36.99% Conservative: 33  
 Best Local Similarity: 25.68% Mismatches: 112  
 Query Match: 7.11% Indels: 74

RESULT 425  
 ID AAT32327 standard; DNA; 1794 BP.  
 DE Thermus flavus DNA polymerase I exonuclease free fragment.  
 PN WO9614417-A1.  
 PD 17-MAY-1996.  
 PA (MOLE-) MOLECULAR BIOLOGY RESOURCES INC.  
 Percent Similarity: 36.99% Conservative: 33  
 Best Local Similarity: 25.68% Mismatches: 112  
 Query Match: 7.11% Indels: 74

RESULT 426  
 ID ADN96193 standard; cDNA; 1837 BP.  
 DE Human NOVX polynucleotide #124.  
 PN US2004067490-A1.  
 PD 08-APR-2004.  
 PA (ZHON/) ZHONG M.  
 PA (LILL/) LI L.  
 PA (GORM/) GORMAN L.  
 PA (SPYT/) SPYTEK K A.  
 PA (KEKO/) KEKUDA R.  
 PA (TAUP/) TAUPIER R J.  
 PA (ANDE/) ANDERSON D W.  
 PA (VERN/) VERNET C A M.  
 PA (CATT/) CATTERTON E.  
 PA (MILL/) MILLER C E.  
 PA (SHEN/) SHENOY S G.  
 PA (PATT/) PATTURAJAN M.  
 PA (PENA/) PENA C E A.  
 PA (TCHE/) TCHERNEV V T.  
 PA (PADI/) PADIGARU M.  
 PA (GUSE/) GUSEV V Y.  
 PA (MALY/) MALYANKAR U M.  
 PA (BURG/) BURGESS C E.  
 PA (GERL/) GERLACH V.  
 PA (CASM/) CASMAN S J.  
 PA (RIEG/) RIEGER D K.  
 PA (GROS/) GROSSE W M.  
 PA (SMIT/) SMITHSON G.  
 PA (PEYM/) PEYMAN J A.  
 PA (STAR/) STARLING G.  
 PA (ROTH/) ROTHENBERG M E.  
 PA (LARO/) LAROCHELLE W J.  
 PA (SHIM/) SHIMKETS R A.  
 PA (CRAB/) CRABTREE J.



PA (RAST/) RASTELLI L.  
 PA (VOSS/) VOSS E Z.  
 PA (BOLD/) BOLDOG F L.  
 PA (EDIN/) EDINGER S R.  
 PA (MILL/) MILLET I.  
 PA (MACD/) MACDOUGALL J R.  
 PA (ELLE/) ELLERMAN K.  
 PA (CHAP/) CHAPOVAL A.  
 Percent Similarity: 32.99%  
 Best Local Similarity: 24.40%  
 Query Match: 7.11%  
 Indels: 102  
 Conservative: 25  
 Mismatches: 93

RESULT 427  
 ID AAS54053 standard; DNA; 2553 BP.  
 DE Pseudomonas aeruginosa DNA for cellular proliferation protein #184.  
 PN WO200170955-A2.  
 PD 27-SEP-2001.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 36.26%  
 Best Local Similarity: 27.47%  
 Query Match: 7.11%  
 Indels: 76  
 Conservative: 24  
 Mismatches: 99

RESULT 428  
 ID ACA42124 standard; DNA; 2553 BP.  
 DE Prokaryotic essential gene #23781.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 36.26%  
 Best Local Similarity: 27.47%  
 Query Match: 7.11%  
 Indels: 76  
 Conservative: 24  
 Mismatches: 99

RESULT 429  
 ID AAZ48661 standard; DNA; 2942 BP.  
 DE L. mycophilus chitinase gene, N4-7 chia.  
 PN WO9555833-A2.  
 PD 04-NOV-1999.  
 PA (RUTF) UNIV RUTGERS STATE NEW JERSEY.  
 Percent Similarity: 35.89%  
 Best Local Similarity: 27.42%  
 Query Match: 7.11%  
 Indels: 68  
 Conservative: 21  
 Mismatches: 92

RESULT 430  
 ID AAT27254 standard; DNA; 3048 BP.  
 DE DNA polymerase I holoenzyme coding sequence.  
 PN WO9614405-A2.  
 PD 17-MAY-1996.  
 PA (MOLE-) MOLECULAR BIOLOGY RESOURCES INC.  
 Percent Similarity: 36.99%  
 Best Local Similarity: 25.68%  
 Query Match: 7.11%  
 Indels: 74  
 Conservative: 33  
 Mismatches: 112

RESULT 431  
 ID ACC78014 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64%  
 Best Local Similarity: 25.34%  
 Query Match: 7.11%  
 Indels: 74  
 Conservative: 33  
 Mismatches: 113

RESULT 432  
 ID ACC78011 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64%  
 Best Local Similarity: 25.34%  
 Query Match: 7.11%  
 Indels: 74  
 Conservative: 33  
 Mismatches: 113

RESULT 433  
 ID ACC77998 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.99%  
 Best Local Similarity: 25.68%  
 Query Match: 7.11%  
 Indels: 112  
 Conservative: 33  
 Mismatches: 112

Query Match: 7.11%  
 Indels: 74

RESULT 434  
 ID ABD05402 standard; DNA; 4284 BP.  
 DE Pseudomonas aeruginosa polynucleotide #4006.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 38.89%  
 Best Local Similarity: 26.30%  
 Query Match: 7.11%  
 Indels: 70  
 Conservative: 34  
 Mismatches: 95

RESULT 435  
 ID ABQ55289 standard; cDNA; 553 BP.  
 DE Human ovarian antigen HCOQX38 cDNA, SEQ ID NO:1169.  
 PN WO200200677-A1.  
 PD 03-JAN-2002.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 45.69%  
 Best Local Similarity: 25.00%  
 Query Match: 7.07%  
 Indels: 4  
 Conservative: 24  
 Mismatches: 59

RESULT 436  
 ID AAH13983 standard; cDNA; 1416 BP.  
 DE Human cDNA sequence SEQ ID NO:11048.  
 PN EP1074617-A2.  
 PD 07-FEB-2001.  
 PA (HELI-) HELIX RES INST.  
 Percent Similarity: 37.13%  
 Best Local Similarity: 24.89%  
 Query Match: 7.07%  
 Indels: 55  
 Conservative: 29  
 Mismatches: 94

RESULT 437  
 ID ACA27231 standard; DNA; 1948 BP.  
 DE Prokaryotic essential gene #8888.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 29.66%  
 Best Local Similarity: 22.57%  
 Query Match: 7.07%  
 Indels: 172  
 Conservative: 27  
 Mismatches: 96

RESULT 438  
 ID ADA52678 standard; cDNA; 2597 BP.  
 DE Human coding sequence, SEQ ID 246.  
 PN EP1293569-A2.  
 PD 19-MAR-2003.  
 PA (HELI-) HELIX RES INST.  
 Percent Similarity: 37.13%  
 Best Local Similarity: 24.89%  
 Query Match: 7.07%  
 Indels: 55  
 Conservative: 29  
 Mismatches: 94

RESULT 439  
 ID ADD69665 standard; cDNA; 3153 BP.  
 DE Human REMAP cDNA - SEQ ID 94.  
 PN WO2003048305-A2.  
 PD 12-JUN-2003.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Percent Similarity: 39.81%  
 Best Local Similarity: 26.07%  
 Query Match: 7.07%  
 Indels: 55  
 Conservative: 29  
 Mismatches: 72

RESULT 440  
 ID ADD24914 standard; DNA; 4184 BP.  
 DE DNA encoding Escherichia coli intracellular protease #6.  
 PN US2003036176-A1.  
 PD 20-FEB-2003.  
 PA (BOWE/) BOWER S G.  
 PA (RAMS/) RAMSEIER T M.  
 Percent Similarity: 36.84%  
 Best Local Similarity: 25.39%  
 Query Match: 7.07%  
 Indels: 97  
 Conservative: 37  
 Mismatches: 109

RESULT 441  
 ID ADQ85412 standard; cDNA; 4962 BP.  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #2226.  
 PN WO2004060270-A2.  
 PD 22-JUL-2004.  
 PA (GETH) GENENTECH INC.  
 PA (WUTD/) WU T D.  
 Query Match: 7.07%  
 Indels: 97  
 Conservative: 37  
 Mismatches: 109

PA (ZHOU/) ZHOU Y.  
 Percent Similarity: 37.13% Conservative: 29  
 Best Local Similarity: 24.89% Mismatches: 94  
 Query Match: 7.07% Indels: 55  
 RESULT 442  
 ID AAF6431 standard; DNA; 349980 BP.  
 DE *Pyrococcus abyssi* genomic fragment #1.  
 PN FR2792651-A1.  
 PD 27-OCT-2000.  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 PA (IFRE-) IPREMER INST FR RECH EXPL MER.  
 Percent Similarity: 36.00% Conservative: 43  
 Best Local Similarity: 20.36% Mismatches: 100  
 Query Match: 7.07% Indels: 76  
 RESULT 443  
 ID AAQ14176 standard; cDNA; 2304 BP.  
 DE Clone pXR2C8 encoding insect steroid receptor XR2C.  
 PN WO9114695-A.  
 PD 03-OCT-1991.  
 PA (SALK ) SALK INST BIOLOGICAL STUDIES.  
 Percent Similarity: 34.46% Conservative: 28  
 Best Local Similarity: 25.00% Mismatches: 109  
 Query Match: 7.04% Indels: 85  
 RESULT 444  
 ID AAQ55374 standard; DNA; 2304 BP.  
 DE pXR2C8 DNA.  
 PN WO9401558-A2.  
 PD 20-JAN-1994.  
 PA (SALK ) SALK INST BIOLOGICAL STUDIES.  
 Percent Similarity: 34.46% Conservative: 28  
 Best Local Similarity: 25.00% Mismatches: 109  
 Query Match: 7.04% Indels: 85  
 RESULT 445  
 ID AAT76787 standard; DNA; 2304 BP.  
 DE Insect XR2C receptor coding sequence.  
 PN US5841652-A.  
 PD 24-JUN-1997.  
 PA (SALK ) SALK INST BIOLOGICAL STUDIES.  
 Percent Similarity: 34.46% Conservative: 28  
 Best Local Similarity: 25.00% Mismatches: 109  
 Query Match: 7.04% Indels: 85  
 RESULT 446  
 ID AAT99959 standard; DNA; 2304 BP.  
 DE D. melanogaster XR2C retinoid-like receptor DNA.  
 PN US568691-A.  
 PD 18-NOV-1997.  
 PA (SALK ) SALK INST BIOLOGICAL STUDIES.  
 Percent Similarity: 34.46% Conservative: 28  
 Best Local Similarity: 25.00% Mismatches: 109  
 Query Match: 7.04% Indels: 85  
 RESULT 447  
 ID ABL07559 standard; cDNA; 2483 BP.  
 DE *Drosophila melanogaster* expressed polynucleotide SEQ ID NO 17159.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Percent Similarity: 34.46% Conservative: 28  
 Best Local Similarity: 25.00% Mismatches: 109  
 Query Match: 7.04% Indels: 85  
 RESULT 448  
 ID ACC77970 standard; DNA; 3221 BP.  
 DE *Thermus thermophilus* mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 7.04% Indels: 74  
 RESULT 449  
 ID ACC77978 standard; DNA; 3221 BP.  
 DE *Thermus thermophilus* mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.

PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 7.04% Indels: 74  
 RESULT 450  
 ID ACC77991 standard; DNA; 3221 BP.  
 DE *Thermus thermophilus* mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 7.04% Indels: 74  
 RESULT 451  
 ID ACC77984 standard; DNA; 3221 BP.  
 DE *Thermus thermophilus* mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 7.04% Indels: 74  
 RESULT 452  
 ID ABL07558 standard; cDNA; 4483 BP.  
 DE *Drosophila melanogaster* expressed polynucleotide SEQ ID NO 17156.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Percent Similarity: 34.46% Conservative: 28  
 Best Local Similarity: 25.00% Mismatches: 109  
 Query Match: 7.04% Indels: 85  
 RESULT 453  
 ID ABL07492 standard; cDNA; 18737 BP.  
 DE *Drosophila melanogaster* expressed polynucleotide SEQ ID NO 16958.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Percent Similarity: 34.46% Conservative: 28  
 Best Local Similarity: 25.00% Mismatches: 109  
 Query Match: 7.04% Indels: 85  
 RESULT 454  
 ID ABL07530 standard; cDNA; 18737 BP.  
 DE *Drosophila melanogaster* expressed polynucleotide SEQ ID NO 17072.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Percent Similarity: 34.46% Conservative: 28  
 Best Local Similarity: 25.00% Mismatches: 109  
 Query Match: 7.04% Indels: 85  
 RESULT 455  
 ID ACA43915 standard; DNA; 717 BP.  
 DE *Prokaryotic essential gene* #25572.  
 PN WO20027183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 34.08% Conservative: 22  
 Best Local Similarity: 25.84% Mismatches: 84  
 Query Match: 7.00% Indels: 93  
 RESULT 456  
 ID AAS65542 standard; cDNA; 825 BP.  
 DE DNA encoding novel human diagnostic protein #1346.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 44.79% Conservative: 11  
 Best Local Similarity: 33.33% Mismatches: 33  
 Query Match: 7.00% Indels: 20  
 RESULT 457  
 ID AAQ80524 standard; DNA; 1410 BP.  
 DE Oxidoreducing avermectin DNA from *S. avermetilis* ATCC31271.  
 PN JP06189774-A.  
 PD 12-JUL-1994.  
 PA (KITA ) KITASATO KENKYUSHO SH.

Percent Similarity: 35.48% Conservative: 32  
 Best Local Similarity: 24.01% Mismatches: 104  
 Query Match: 7.00% Indels: 76  
 RESULT 458  
 ID ABD13438 standard; DNA; 1527 BP.  
 DE Pseudomonas aeruginosa polynucleotide #12042.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 37.62% Conservative: 23  
 Best Local Similarity: 26.67% Mismatches: 78  
 Query Match: 7.00% Indels: 53  
 RESULT 459  
 ID ABD01627 standard; DNA; 1962 BP.  
 DE Pseudomonas aeruginosa polynucleotide #231.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 36.64% Conservative: 24  
 Best Local Similarity: 28.42% Mismatches: 118  
 Query Match: 7.00% Indels: 67  
 RESULT 460  
 ID ABD13335 standard; DNA; 2313 BP.  
 DE Pseudomonas aeruginosa polynucleotide #11939.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 37.62% Conservative: 23  
 Best Local Similarity: 26.67% Mismatches: 78  
 Query Match: 7.00% Indels: 53  
 RESULT 461  
 ID ADO22115 standard; DNA; 4618 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4935.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Percent Similarity: 37.33% Conservative: 22  
 Best Local Similarity: 27.19% Mismatches: 79  
 Query Match: 7.00% Indels: 57  
 RESULT 462  
 ID ADR44308 standard; DNA; 9576 BP.  
 DE Mosquito leucine-rich repeat protein gene sequence SEQ ID NO:54.  
 PN EP1452183-A1.  
 PD 01-SEP-2004.  
 PA (EMBL-) EMBL.  
 Percent Similarity: 36.54% Conservative: 45  
 Best Local Similarity: 22.12% Mismatches: 99  
 Query Match: 7.00% Indels: 99  
 RESULT 463  
 ID ABD10637 standard; DNA; 1233 BP.  
 DE Pseudomonas aeruginosa polynucleotide #9241.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 31.86% Conservative: 26  
 Best Local Similarity: 24.65% Mismatches: 100  
 Query Match: 6.96% Indels: 147  
 RESULT 464  
 ID ABD10108 standard; DNA; 1980 BP.  
 DE Pseudomonas aeruginosa polynucleotide #8712.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 30.93% Conservative: 17  
 Best Local Similarity: 25.09% Mismatches: 78  
 Query Match: 6.96% Indels: 123  
 RESULT 465  
 ID ACC85548 standard; DNA; 2505 BP.  
 DE T thermophilus strain RQ-1 variant DNA polymerase gene SEQ ID NO: 8.  
 PN WO2003048309-A2.  
 PD 12-JUN-2003.  
 PA (APPL-) APPLERA CORP.  
 Percent Similarity: 36.30% Conservative: 31

Best Local Similarity: 25.68% Mismatches: 114  
 Query Match: 6.96% Indels: 74  
 RESULT 466  
 ID ACC85552 standard; DNA; 2505 BP.  
 DE T thermophilus strain 1b21 variant DNA polymerase gene SEQ ID NO: 12.  
 PN WO2003048309-A2.  
 PD 12-JUN-2003.  
 PA (APPL-) APPLERA CORP.  
 Percent Similarity: 36.99% Conservative: 33  
 Best Local Similarity: 25.68% Mismatches: 112  
 Query Match: 6.96% Indels: 74  
 RESULT 467  
 ID ACC85549 standard; DNA; 2505 BP.  
 DE T thermophilus strain 1b21 variant DNA polymerase gene SEQ ID NO: 9.  
 PN WO2003048309-A2.  
 PD 12-JUN-2003.  
 PA (APPL-) APPLERA CORP.  
 Percent Similarity: 36.99% Conservative: 33  
 Best Local Similarity: 25.68% Mismatches: 112  
 Query Match: 6.96% Indels: 74  
 RESULT 468  
 ID ACC85551 standard; DNA; 2505 BP.  
 DE T thermophilus strain RQ-1 variant DNA polymerase gene SEQ ID NO: 11.  
 PN WO2003048309-A2.  
 PD 12-JUN-2003.  
 PA (APPL-) APPLERA CORP.  
 Percent Similarity: 36.30% Conservative: 31  
 Best Local Similarity: 25.68% Mismatches: 114  
 Query Match: 6.96% Indels: 74  
 RESULT 469  
 ID ACC78001 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.96% Indels: 74  
 RESULT 470  
 ID ACC78002 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.96% Indels: 74  
 RESULT 471  
 ID ACC77983 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.96% Indels: 74  
 RESULT 472  
 ID ACC77987 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.96% Indels: 74  
 RESULT 473  
 ID ACC77996 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.96% Indels: 74

Query Match: 6.96% Indels: 74  
 RESULT 474  
 ID ACC78013 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64%  
 Best Local Similarity: 25.34%  
 Query Match: 6.96%  
 Indels: 74  
 Conservative: 33  
 Mismatches: 113  
 Indels: 74  
 RESULT 475  
 ID AAV62176 standard; DNA; 117213 BP.  
 DE HSV-2 strain SB5 Contig ID 15 DNA sequence.  
 Percent Similarity: 34.46%  
 Best Local Similarity: 27.03%  
 Query Match: 6.96%  
 Indels: 86  
 Conservative: 22  
 Mismatches: 109  
 Indels: 86  
 RESULT 476  
 ID AAD25519 standard; DNA; 154746 BP.  
 DE Human herpesvirus 2 complete DNA genome.  
 PN WO200176643-A1.  
 PD 18-OCT-2001.  
 PA (BAYU) BAYLOR COLLEGE MEDICINE.  
 Percent Similarity: 34.46%  
 Best Local Similarity: 27.03%  
 Query Match: 6.96%  
 Indels: 86  
 Conservative: 22  
 Mismatches: 109  
 Indels: 86  
 RESULT 477  
 ID ABD03356 standard; DNA; 1701 BP.  
 DE Pseudomonas aeruginosa polynucleotide #1960.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 37.13%  
 Best Local Similarity: 25.41%  
 Query Match: 6.92%  
 Indels: 75  
 Conservative: 36  
 Mismatches: 119  
 Indels: 75  
 RESULT 478  
 ID ABD10467 standard; DNA; 1848 BP.  
 DE Pseudomonas aeruginosa polynucleotide #9071.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 32.06%  
 Best Local Similarity: 25.95%  
 Query Match: 6.92%  
 Indels: 110  
 Conservative: 16  
 Mismatches: 68  
 Indels: 110  
 RESULT 479  
 ID AAV39834 standard; cDNA; 1898 BP.  
 DE Mouse protein phosphatase 2A subunit encoding cDNA.  
 PN WO9824915-A1.  
 PD 11-JUN-1998.  
 PA (VEHE-) VER HET NEDERLANDS KANKER INST.  
 PA (PROL-) PROLIFIX LTD.  
 Percent Similarity: 36.02%  
 Best Local Similarity: 28.39%  
 Query Match: 6.92%  
 Indels: 70  
 Conservative: 18  
 Mismatches: 81  
 Indels: 70  
 RESULT 480  
 ID ADS58106 standard; cDNA; 1908 BP.  
 DE Bacterial polynucleotide #10093.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY) CAO Y.  
 PA (HINK) HINKLE G J.  
 PA (SLAT) SLATER S C.  
 PA (CHEN) CHEN X.  
 PA (GOLD) GOLDMAN B S.  
 Percent Similarity: 39.93%  
 Best Local Similarity: 26.12%  
 Query Match: 6.92%  
 Indels: 75  
 Conservative: 37  
 Mismatches: 87  
 Indels: 75  
 RESULT 481  
 ID AAV39835 standard; cDNA; 1988 BP.  
 DE Mouse protein phosphatase 2A subunit variant encoding cDNA.  
 PN WO9824915-A1.  
 PD 11-JUN-1998.  
 PA (VEHE-) VER HET NEDERLANDS KANKER INST.  
 PA (PROL-) PROLIFIX LTD.

Percent Similarity: 36.02%  
 Best Local Similarity: 28.39%  
 Query Match: 6.92%  
 Indels: 70  
 Conservative: 18  
 Mismatches: 81  
 Indels: 70  
 RESULT 482  
 ID ABD03306 standard; DNA; 2169 BP.  
 DE Pseudomonas aeruginosa polynucleotide #1910.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 37.13%  
 Best Local Similarity: 25.41%  
 Query Match: 6.92%  
 Indels: 75  
 Conservative: 36  
 Mismatches: 119  
 Indels: 75  
 RESULT 483  
 ID ABA97187 standard; DNA; 2326 BP.  
 DE Goat lactoferrin-associated DNA.  
 PN KR98043944-A.  
 PD 05-SEP-1998.  
 PA (KOAD) KOREA ADV INST SCI & TECHNOLOGY.  
 Percent Similarity: 37.01%  
 Best Local Similarity: 27.05%  
 Query Match: 6.92%  
 Indels: 75  
 Conservative: 28  
 Mismatches: 103  
 Indels: 75  
 RESULT 484  
 ID ABD03441 standard; DNA; 2946 BP.  
 DE Pseudomonas aeruginosa polynucleotide #2045.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 37.13%  
 Best Local Similarity: 25.41%  
 Query Match: 6.92%  
 Indels: 75  
 Conservative: 36  
 Mismatches: 119  
 Indels: 75  
 RESULT 485  
 ID AAQ3954 standard; DNA; 3221 BP.  
 DE Heat stable DNA polymerase coding sequence.  
 PN JP05317058-A.  
 PD 03-DEC-1993.  
 PA (TOYM) TOYOBO KK.  
 Percent Similarity: 35.64%  
 Best Local Similarity: 23.27%  
 Query Match: 6.92%  
 Indels: 77  
 Conservative: 34  
 Mismatches: 101  
 Indels: 77  
 RESULT 486  
 ID ACC77985 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.99%  
 Best Local Similarity: 25.34%  
 Query Match: 6.92%  
 Indels: 74  
 Conservative: 34  
 Mismatches: 112  
 Indels: 74  
 RESULT 487  
 ID ACC77994 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.99%  
 Best Local Similarity: 25.34%  
 Query Match: 6.92%  
 Indels: 74  
 Conservative: 34  
 Mismatches: 112  
 Indels: 74  
 RESULT 488  
 ID ACC77979 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.99%  
 Best Local Similarity: 25.34%  
 Query Match: 6.92%  
 Indels: 74  
 Conservative: 34  
 Mismatches: 112  
 Indels: 74  
 RESULT 489  
 ID ADR06764 standard; cDNA; 3470 BP.  
 DE Full length human cDNA useful for treating neurological disease Seq 270.  
 PN EP1447413-A2.  
 PD 18-AUG-2004.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 Percent Similarity: 40.00%  
 Indels: 16  
 Conservative: 16

Best Local Similarity: 30.00% Mismatches: 65  
Query Match: 6.92% Indels: 31  
RESULT 490  
ID AB211703 standard; cDNA; 3744 BP.  
DE Human polynucleotide SEQ ID NO 585.  
PN WO200270539-A2.  
PD 12-SEP-2002.  
PA (HYPF-) HYSFO INC.  
Percent Similarity: 40.00% Conservative: 16  
Best Local Similarity: 30.00% Mismatches: 65  
Query Match: 6.92% Indels: 31  
RESULT 491  
ID ADM44221 standard; cDNA; 3744 BP.  
DE Novel human arginine-rich protein cDNA #585.  
PN US2004053250-A1.  
PD 18-MAR-2004. Y T.  
PA (TANG/) TANG Y T.  
PA (XUEA/) XUE A.  
PA (DRMA/) DRMANAC R T.  
Percent Similarity: 40.00% Conservative: 16  
Best Local Similarity: 30.00% Mismatches: 65  
Query Match: 6.92% Indels: 31  
RESULT 492  
ID ADR24447 standard; DNA; 4018 BP.  
DE Breast cancer prognosis marker #308.  
PN WO2004065545-A2.  
PD 05-AUG-2004.  
PA (ROSE-) ROSETTA INPHARMATICS LLC.  
PA (NECA-) NETHERLANDS CANCER INST.  
Percent Similarity: 40.00% Conservative: 16  
Best Local Similarity: 30.00% Mismatches: 65  
Query Match: 6.92% Indels: 31  
RESULT 493  
ID ABQ83861 standard; DNA; 5032 BP.  
DE Human MDT-3 encoding cDNA SEQ ID NO:26.  
PN WO200278420-A2.  
PD 10-OCT-2002.  
PA (INCV-) INCVTE GENOMICS INC.  
Percent Similarity: 40.00% Conservative: 16  
Best Local Similarity: 30.00% Mismatches: 65  
Query Match: 6.92% Indels: 31  
RESULT 494  
ID ABV77879 standard; DNA; 5591 BP.  
DE Hypoxia-induced protein coding sequence #7.  
PN WO200246465-A2.  
PD 13-JUN-2002.  
PA (OXFO-) OXFORD BIOMEDICA UK LTD.  
Percent Similarity: 40.00% Conservative: 16  
Best Local Similarity: 30.00% Mismatches: 65  
Query Match: 6.92% Indels: 31  
RESULT 495  
ID ADI82477 standard; DNA; 5592 BP.  
DE Human modifier of p21 (ME21) gene sequence SeqID43.  
PN WO2004005486-A2.  
PD 15-JAN-2004.  
PA (EXEL-) EXELIXIS INC.  
Percent Similarity: 40.00% Conservative: 16  
Best Local Similarity: 30.00% Mismatches: 65  
Query Match: 6.92% Indels: 31  
RESULT 496  
ID ADQ86758 standard; cDNA; 5592 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3633.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH-) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 40.00% Conservative: 16  
Best Local Similarity: 30.00% Mismatches: 65  
Query Match: 6.92% Indels: 31  
RESULT 497  
ID ADQ84279 standard; cDNA; 5592 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1093.

PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH-) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 40.00% Conservative: 16  
Best Local Similarity: 30.00% Mismatches: 65  
Query Match: 6.92% Indels: 31  
RESULT 498  
ID ACN40426 standard; cDNA; 5592 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA326541, SEQ ID NO:5197.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH-) GENENTECH INC.  
Percent Similarity: 40.00% Conservative: 16  
Best Local Similarity: 30.00% Mismatches: 65  
Query Match: 6.92% Indels: 31  
RESULT 499  
ID ADP24535 standard; cDNA; 5595 BP.  
DE PRO polypeptide encoding cDNA SEQ ID NO:1713.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH-) GENENTECH INC.  
Percent Similarity: 40.00% Conservative: 16  
Best Local Similarity: 30.00% Mismatches: 65  
Query Match: 6.92% Indels: 31  
RESULT 500  
ID ADI23894 standard; DNA; 7788 BP.  
DE Streptomyces fradiae A541 locus ORF3.  
PN US2003198981-A1.  
PD 23-OCT-2003.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Percent Similarity: 36.24% Conservative: 33  
Best Local Similarity: 24.74% Mismatches: 114  
Query Match: 6.92% Indels: 70  
RESULT 501  
ID ADI23892 standard; DNA; 37360 BP.  
DE Streptomyces fradiae A541 locus contig 2.  
PN US2003198981-A1.  
PD 23-OCT-2003.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Percent Similarity: 36.24% Conservative: 33  
Best Local Similarity: 24.74% Mismatches: 114  
Query Match: 6.92% Indels: 70  
RESULT 502  
Percent Similarity: 30.90% Conservative: 12  
Best Local Similarity: 25.75% Mismatches: 73  
Query Match: 6.92% Indels: 88  
RESULT 503  
Percent Similarity: 30.90% Conservative: 12  
Best Local Similarity: 25.75% Mismatches: 73  
Query Match: 6.92% Indels: 88  
RESULT 504  
Percent Similarity: 30.90% Conservative: 12  
Best Local Similarity: 25.75% Mismatches: 73  
Query Match: 6.92% Indels: 88  
RESULT 505  
Percent Similarity: 30.90% Conservative: 12  
Best Local Similarity: 25.75% Mismatches: 73  
Query Match: 6.92% Indels: 88  
RESULT 506  
ID ADI22710 standard; DNA; 1052 BP.  
DE S. pristinaespiralis papM gene C658T mutant.  
PN WO2004003012-A2.  
PD 08-JAN-2004.  
PA (AVET-) AVENTIS PHARMA SA.  
Percent Similarity: 32.23% Conservative: 26  
Best Local Similarity: 22.71% Mismatches: 120  
Query Match: 6.89% Indels: 65  
RESULT 507  
ID ADI22712 standard; DNA; 1052 BP.  
DE S. pristinaespiralis papM gene C658T/G828A mutant.  
PN WO2004003012-A2.

```

PD 08-JAN-2004.
PA (AVET ) AVENTIS PHARMA SA.
Percent Similarity: 32.23% Conservative: 26
Best Local Similarity: 22.71% Mismatches: 120
Query Match: 6.89% Indels: 65
RESULT 508
ID ABD01646 standard; DNA; 1200 BP.
DE Pseudomonas aeruginosa polynucleotide #250.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 36.17% Conservative: 23
Best Local Similarity: 28.01% Mismatches: 114
Query Match: 6.89% Indels: 66
RESULT 509
ID ABD05045 standard; DNA; 1311 BP.
DE Pseudomonas aeruginosa polynucleotide #3649.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 37.06% Conservative: 33
Best Local Similarity: 25.52% Mismatches: 95
Query Match: 6.89% Indels: 86
RESULT 510
ID ADK56578 standard; DNA; 1828 BP.
DE Plant DNA sequence which confers altered metabolic characteristic #3961.
PN WO2003020936-A1.
PD 13-MAR-2003.
PA (DOWC ) DOW CHEM CO.
Percent Similarity: 34.20% Conservative: 38
Best Local Similarity: 21.82% Mismatches: 102
Query Match: 6.89% Indels: 100
RESULT 511
ID ADI91034 standard; DNA; 2433 BP.
DE Thermus sp polymerase nuclease domain chimera N1C4 DNA.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 512
ID ADI93026 standard; DNA; 2445 BP.
DE Thermus sp polymerase chimera S26 (K69E) DNA.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 513
ID ADI93022 standard; DNA; 2445 BP.
DE Thermus sp polymerase chimera S26 (FT) DNA.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 514
ID ADI93028 standard; DNA; 2445 BP.
DE Thermus sp polymerase chimera S26 (FT/K69E) DNA.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 515
ID ADI93018 standard; DNA; 2445 BP.
DE Thermus sp polymerase chimera S26 DNA.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 516
ID ADI93036 standard; DNA; 2493 BP.
DE Thermus sp polymerase nuclease domain chimera N2C3 DNA.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 517
ID ADI93032 standard; DNA; 2499 BP.
DE Thermus sp polymerase nuclease domain chimera N1A12 DNA.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 518
ID ADI92870 standard; DNA; 2508 BP.
DE Construct TthAKK A518L DNA SEQ ID 423.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 519
ID ADI92852 standard; DNA; 2508 BP.
DE Construct TthAKK E425V DNA SEQ ID 405.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 520
ID ADI92858 standard; DNA; 2508 BP.
DE Construct TthAKK A504F DNA SEQ ID 411.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 521
ID ADI92862 standard; DNA; 2508 BP.
DE Construct TthAKK A504F DNA SEQ ID 415.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 522
ID ADI92864 standard; DNA; 2508 BP.
DE Construct TthAKK A504S DNA SEQ ID 417.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 523
ID ADI92866 standard; DNA; 2508 BP.
DE Construct TthAKK S517G DNA SEQ ID 419.
PN WO200190337-A2.
PD 29-NOV-2001.

```

PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 524  
 ID ADI92856 standard; DNA; 2508 BP.  
 DE Construct TthAKK L422F/W430C DNA SEQ ID 409.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 525  
 ID ADI92886 standard; DNA; 2508 BP.  
 DE Construct TthAKK T508P DNA SEQ ID 439.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 526  
 ID ADI92848 standard; DNA; 2508 BP.  
 DE Construct TthAKK L429V DNA SEQ ID 401.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 527  
 ID ADI92873 standard; DNA; 2508 BP.  
 DE Construct TthAKK A518R DNA SEQ ID 426.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 528  
 ID ADI92878 standard; DNA; 2508 BP.  
 DE Construct TthAKK A504K DNA SEQ ID 431.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 529  
 ID ADI92854 standard; DNA; 2508 BP.  
 DE Construct TthAKK L422N/E425V DNA SEQ ID 407.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 530  
 ID AAV53995 standard; DNA; 2511 BP.  
 DE Nucleotide sequence of the structure specific endonuclease 2.  
 PN WO9823774-A1.  
 PD 04-JUN-1998.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.89% Indels: 74  
 RESULT 531  
 ID ABS68749 standard; DNA; 2511 BP.  
 DE DNA encoding Thermus thermophilus mutant DNA polymerase #2.  
 PN WO200263030-A2.  
 PD 15-AUG-2002.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34

Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.89% Indels: 74  
 RESULT 532  
 ID ADES3076 standard; DNA; 2511 BP.  
 DE FEN-1 related DNA used within the scope of the invention, #231.  
 PN WO200270755-A2.  
 PD 12-SEP-2002.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.89% Indels: 74  
 RESULT 533  
 ID ADI92709 standard; DNA; 2511 BP.  
 DE T. thermophilus polymerase Tth mutant SEQ ID 262.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.89% Indels: 74  
 RESULT 534  
 ID ADI92946 standard; DNA; 2514 BP.  
 DE Construct Tsc(K69B)TthAKK DNA SEQ ID 499.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 535  
 ID ADI92922 standard; DNA; 2514 BP.  
 DE Construct Tsc(1-167)TthAKK DNA SEQ ID 475.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 536  
 ID ADI92580 standard; DNA; 2514 BP.  
 DE Synthetic 5' nuclease DNA SEQ ID 133.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 537  
 ID ADI92901 standard; DNA; 2514 BP.  
 DE Construct Tsc(FT)TthAKK DNA SEQ ID 454.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 538  
 ID ADI92956 standard; DNA; 2517 BP.  
 DE Construct TagEFT-Tth(AKK)-B/M2 DNA SEQ ID 509.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 539  
 ID ADI92964 standard; DNA; 2517 BP.  
 DE Construct TagEFT-Tth(AKK)-D/M5 DNA SEQ ID 517.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74



Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 540  
 ID ADI92980 standard; DNA; 2517 BP.  
 DE Construct TagEFT-Tth(AKK)-H/M9 DNA SEQ ID 533.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 541  
 ID ADI92575 standard; DNA; 2517 BP.  
 DE Synthetic 5' nuclease DNA SEQ ID 128.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 542  
 ID ADI92960 standard; DNA; 2517 BP.  
 DE Construct TagEFT-Tth(AKK)-C/M3 DNA SEQ ID 513.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 543  
 ID ADI92972 standard; DNA; 2517 BP.  
 DE Construct TagEFT-Tth(AKK)-F/M7 DNA SEQ ID 525.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 544  
 ID ADI92516 standard; DNA; 2517 BP.  
 DE Synthetic 5' nuclease DNA SEQ ID 69.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.89% Indels: 74  
 RESULT 545  
 ID ADI92942 standard; DNA; 2517 BP.  
 DE Construct Tag(K69E)ThAKK DNA SEQ ID 495.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 546  
 ID ADI92984 standard; DNA; 2517 BP.  
 DE Construct TagEFT-Tth(AKK)-I/M10 DNA SEQ ID 537.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 547  
 ID ADI92948 standard; DNA; 2517 BP.  
 DE Construct TagEFT-Tth(AKK) DNA SEQ ID 501.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74

Query Match: 6.89% Indels: 74  
 RESULT 548  
 ID ADI92968 standard; DNA; 2517 BP.  
 DE Construct TagEFT-Tth(AKK)-E/M6 DNA SEQ ID 521.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 549  
 ID ADI92931 standard; DNA; 2517 BP.  
 DE Construct Tag(FT)ThAKK DNA SEQ ID 484.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 550  
 ID ADI92976 standard; DNA; 2517 BP.  
 DE Construct TagEFT-Tth(AKK)-G/M8 DNA SEQ ID 529.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 551  
 ID ADI93020 standard; DNA; 2520 BP.  
 DE Thermus sp polymerase chimera S36 DNA.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 552  
 ID ADI92952 standard; DNA; 2520 BP.  
 DE Construct TagEFT-Tth(AKK)-A/M1 DNA SEQ ID 505.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 553  
 ID ADI92669 standard; DNA; 2520 BP.  
 DE HCMV associated DNA SEQ ID 222.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 554  
 ID ADI93030 standard; DNA; 2520 BP.  
 DE Thermus sp polymerase nuclease domain chimera N3D7 DNA.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74  
 RESULT 555  
 ID ADI92990 standard; DNA; 2520 BP.  
 DE Construct TagEFT-Tth(AKK)-MI-10 DNA SEQ ID 543.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Query Match: 6.89% Indels: 74

RESULT 556  
 ID ADI92988 standard; DNA; 2520 BP.  
 DE Construct TscEFT-tth(AKK)-M1-9 DNA SEQ ID 541.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Indels: 74  
 Query Match:  
 RESULT 557  
 ID ADI93024 standard; DNA; 2520 BP.  
 DE Thermus sp polymerase chimera S36(FT) DNA.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Indels: 74  
 Query Match:  
 RESULT 558  
 ID ABS68757 standard; DNA; 2526 BP.  
 DE DNA encoding Thermus thermophilus mutant DNA polymerase #4.  
 PN WO200263030-A2.  
 PD 15-AUG-2002.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Indels: 74  
 Query Match:  
 RESULT 559  
 ID ABS68759 standard; DNA; 2526 BP.  
 DE DNA encoding Thermus thermophilus mutant DNA polymerase #5.  
 PN WO200263030-A2.  
 PD 15-AUG-2002.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Indels: 74  
 Query Match:  
 RESULT 560  
 ID ABS68751 standard; DNA; 2526 BP.  
 DE DNA encoding Thermus thermophilus mutant DNA polymerase #3.  
 PN WO200263030-A2.  
 PD 15-AUG-2002.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Indels: 74  
 Query Match:  
 RESULT 561  
 ID ABS68755 standard; DNA; 2526 BP.  
 DE DNA encoding Thermus thermophilus mutant DNA polymerase #3.  
 PN WO200263030-A2.  
 PD 15-AUG-2002.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Indels: 74  
 Query Match:  
 RESULT 562  
 ID ADI93005 standard; DNA; 2526 BP.  
 DE T. thermophilusTthAKK DNA fragment.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Indels: 74  
 Query Match:  
 RESULT 563  
 ID ADI92565 standard; DNA; 2526 BP.  
 DE Synthetic 5' nuclease DNA SEQ ID 118.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Indels: 74  
 Query Match:  
 RESULT 564

ADI92902 standard; DNA; 2526 BP.  
 DE Construct Tsc(167-333)TthAKK DNA SEQ ID 455.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Indels: 74  
 Query Match:  
 RESULT 565  
 ID ADI92838 standard; DNA; 2526 BP.  
 DE Construct TthAKK(N221H/R224Q) DNA SEQ ID 391.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Indels: 74  
 Query Match:  
 RESULT 566  
 ID ADI92564 standard; DNA; 2526 BP.  
 DE Synthetic 5' nuclease DNA SEQ ID 117.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Indels: 74  
 Query Match:  
 RESULT 567  
 ID ADI92566 standard; DNA; 2526 BP.  
 DE Synthetic 5' nuclease DNA SEQ ID 119.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Indels: 74  
 Query Match:  
 RESULT 568  
 ID ADI92830 standard; DNA; 2526 BP.  
 DE Construct TthAKK(P255L) DNA SEQ ID 383.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Indels: 74  
 Query Match:  
 RESULT 569  
 ID ADI92842 standard; DNA; 2526 BP.  
 DE Construct TthAKK(R251H) DNA SEQ ID 395.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Indels: 74  
 Query Match:  
 RESULT 570  
 ID ADI92899 standard; DNA; 2526 BP.  
 DE Construct Tth(K69E)AKK DNA SEQ ID 452.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Indels: 74  
 Query Match:  
 RESULT 571  
 ID ADI92579 standard; DNA; 2526 BP.  
 DE Synthetic 5' nuclease DNA SEQ ID 132.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.68% Conservative: 34  
 Best Local Similarity: 24.91% Mismatches: 111  
 Indels: 74  
 Query Match:  
 RESULT 572  
 ID ADI92714 standard; DNA; 2526 BP.

```

DE T. thermophilus Tth DN HT DNA SEQ ID 267.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.64% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 113
Query Match: 6.89% Indels: 74
RESULT 573
ID ADI92944 standard; DNA; 2526 BP.
DE Construct Tfi(K69E)/TthAKK DNA SEQ ID 497.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 574
ID ADI92826 standard; DNA; 2526 BP.
DE Construct TthAKK(N417K/L418K) DNA SEQ ID 379.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 575
ID ADI92918 standard; DNA; 2526 BP.
DE Construct Tsc(111-334)/TthAKK DNA SEQ ID 471.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 576
ID ADI92796 standard; DNA; 2526 BP.
DE Mutant Tsc construct mutagenic primer SEQ ID 349.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 577
ID ADI92822 standard; DNA; 2526 BP.
DE Construct TthAKK(P195K) DNA SEQ ID 375.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 578
ID ADI92906 standard; DNA; 2526 BP.
DE Construct Tsc(167-334)/TthAKK DNA SEQ ID 459.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 579
ID ADI92550 standard; DNA; 2526 BP.
DE Synthetic 5' nuclease DNA SEQ ID 103.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 580
ID ADI92551 standard; DNA; 2526 BP.
DE Synthetic 5' nuclease DNA SEQ ID 104.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 581
ID ADI92720 standard; DNA; 2526 BP.
DE T. thermophilus Tth DN RX HT DNA SEQ ID 273.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 582
ID ADI92820 standard; DNA; 2526 BP.
DE Construct TthAKK(P195A) DNA SEQ ID 373.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.64% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 113
Query Match: 6.89% Indels: 74
RESULT 583
ID ADI92846 standard; DNA; 2526 BP.
DE Construct TthAKK(P255L/R251H) DNA SEQ ID 399.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 584
ID ADI92834 standard; DNA; 2526 BP.
DE Construct TthAKK(F311Y) DNA SEQ ID 387.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 585
ID ADI92910 standard; DNA; 2532 BP.
DE Construct Tfi(222-334)/TthAKK DNA SEQ ID 463.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 586
ID ADI92914 standard; DNA; 2532 BP.
DE Construct Tfi(167-334)/TthAKK DNA SEQ ID 467.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 587
ID ADI93010 standard; DNA; 2619 BP.
DE Construct Afu328-Tth296(AKK) DNA.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 588
ID ADI93006 standard; DNA; 2643 BP.
DE Construct Afu336-Tth296(AKK) DNA.
PN WO200190337-A2.

```

```

PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 589
ID ADI92928 standard; DNA; 3135 BP.
DE Construct TthAKK-alpha peptide DNA SEQ ID 481.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.68% Conservative: 34
Best Local Similarity: 24.91% Mismatches: 111
Query Match: 6.89% Indels: 74
RESULT 590
ID ACC77865 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.49% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 113
Query Match: 6.89% Indels: 74
RESULT 591
ID ACC77880 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.49% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 113
Query Match: 6.89% Indels: 74
RESULT 592
ID ACC77960 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 113
Query Match: 6.89% Indels: 74
RESULT 593
ID ACC77936 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 37.89% Conservative: 36
Best Local Similarity: 25.26% Mismatches: 119
Query Match: 6.89% Indels: 60
RESULT 594
ID ACC77795 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 113
Query Match: 6.89% Indels: 74
RESULT 595
ID ACC78006 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 113
Query Match: 6.89% Indels: 74
RESULT 596
ID ACC77873 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.49% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 113
Query Match: 6.89% Indels: 74
RESULT 597
ID ACC77961 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 113
Query Match: 6.89% Indels: 74
RESULT 598
ID ACC77990 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 113
Query Match: 6.89% Indels: 74
RESULT 599
ID ACC78009 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 113
Query Match: 6.89% Indels: 74
RESULT 600
ID ACC77999 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 113
Query Match: 6.89% Indels: 74
RESULT 601
ID ACC77993 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 113
Query Match: 6.89% Indels: 74
RESULT 602
ID ACC77883 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 113
Query Match: 6.89% Indels: 74
RESULT 603
ID ACC77966 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.49% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 116
Query Match: 6.89% Indels: 74
RESULT 604
ID ACC78012 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 36.64% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 113
Query Match: 6.89% Indels: 74

```

Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.89% Indels: 74  
 RESULT 605  
 ID ACC77935 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 37.89% Conservative: 36  
 Best Local Similarity: 25.26% Mismatches: 119  
 Query Match: 6.89% Indels: 60  
 RESULT 606  
 ID ACC78003 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.89% Indels: 74  
 RESULT 607  
 ID ACC77976 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.89% Indels: 74  
 RESULT 608  
 ID ADS57429 standard; cDNA; 813 BP.  
 DE Bacterial polynucleotide #9416.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Percent Similarity: 38.68% Conservative: 32  
 Best Local Similarity: 25.51% Mismatches: 93  
 Query Match: 6.85% Indels: 56  
 RESULT 609  
 ID AAF26352 standard; DNA; 1035 BP.  
 DE P. putida oxygenase encoding DNA ORF04472.  
 PN WO200107629-A2.  
 PD 01-FEB-2001.  
 PA (TIGR-) TIGR INST GENOMIC RES.  
 PA (QUITA-) QUIAGEN GMBH.  
 PA (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MEH.  
 PA (DKFZ-) DKFZ DEUT KREBSFORSCHUNGSZENTRUM.  
 PA (MEDI-) MEDIZINISCHE HOCHSCHULE HANNOVER.  
 Percent Similarity: 33.21% Conservative: 22  
 Best Local Similarity: 24.91% Mismatches: 100  
 Query Match: 6.85% Indels: 77  
 RESULT 610  
 ID ACA31567 standard; DNA; 1130 BP.  
 DE Prokaryotic essential Gene #13224.  
 PN WO20027183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 37.62% Conservative: 27  
 Best Local Similarity: 24.78% Mismatches: 89  
 Query Match: 6.85% Indels: 42  
 RESULT 611  
 ID AAS72289 standard; cDNA; 1390 BP.  
 DE DNA encoding novel human diagnostic protein #8093.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 32.03% Conservative: 21  
 Best Local Similarity: 23.83% Mismatches: 75

Query Match: 6.85% Indels: 100  
 RESULT 612  
 ID ABD1414 standard; DNA; 1407 BP.  
 DE Pseudomonas aeruginosa polynucleotide #13018.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 38.41% Conservative: 31  
 Best Local Similarity: 28.15% Mismatches: 96  
 Query Match: 6.85% Indels: 90  
 RESULT 613  
 ID AD007762 standard; cDNA; 1932 BP.  
 DE Fly polynucleotide #43.  
 PN US2004071700-A1.  
 PD 15-APR-2004.  
 PA (LIFE-) LIFE SCI DEV CORP.  
 Percent Similarity: 33.33% Conservative: 29  
 Best Local Similarity: 23.05% Mismatches: 101  
 Query Match: 6.85% Indels: 87  
 RESULT 614  
 ID AAS94512 standard; cDNA; 2305 BP.  
 DE DNA encoding novel human diagnostic protein #30316.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 31.54% Conservative: 19  
 Best Local Similarity: 23.65% Mismatches: 94  
 Query Match: 6.85% Indels: 71  
 RESULT 615  
 ID ABL08195 standard; cDNA; 2396 BP.  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 19067.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Percent Similarity: 33.33% Conservative: 29  
 Best Local Similarity: 23.05% Mismatches: 101  
 Query Match: 6.85% Indels: 87  
 RESULT 616  
 ID ABL20321 standard; DNA; 2590 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 12436.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Percent Similarity: 33.33% Conservative: 29  
 Best Local Similarity: 23.05% Mismatches: 101  
 Query Match: 6.85% Indels: 87  
 RESULT 617  
 ID ABL20331 standard; DNA; 2894 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 12466.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Percent Similarity: 33.33% Conservative: 29  
 Best Local Similarity: 23.05% Mismatches: 101  
 Query Match: 6.85% Indels: 87  
 RESULT 618  
 ID ACC77995 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.99% Conservative: 34  
 Best Local Similarity: 25.34% Mismatches: 112  
 Query Match: 6.85% Indels: 74  
 RESULT 619  
 ID AAS84829 standard; cDNA; 3451 BP.  
 DE DNA encoding novel human diagnostic protein #20633.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 42.95% Conservative: 25  
 Best Local Similarity: 26.92% Mismatches: 58  
 Query Match: 6.85% Indels: 32

```

RESULT 620
ID ADR06934 standard; cDNA; 5008 BP.
DE Full length human cDNA useful for treating neurological disease Seq 440.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 36.21% Conservative: 26
Best Local Similarity: 27.57% Mismatches: 95
Query Match: 6.85% Indels: 98
RESULT 621
ID ACA44278 standard; DNA; 1116 BP.
DE Prokaryotic essential gene #25935.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 37.45% Conservative: 31
Best Local Similarity: 25.10% Mismatches: 76
Query Match: 6.81% Indels: 81
RESULT 622
ID ABD08133 standard; DNA; 1197 BP.
DE Pseudomonas aeruginosa polynucleotide #6737.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 38.19% Conservative: 31
Best Local Similarity: 25.98% Mismatches: 107
Query Match: 6.81% Indels: 51
RESULT 623
ID ABD08348 standard; DNA; 1272 BP.
DE Pseudomonas aeruginosa polynucleotide #6952.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 38.19% Conservative: 31
Best Local Similarity: 25.98% Mismatches: 107
Query Match: 6.81% Indels: 51
RESULT 624
ID ABZ38701 standard; DNA; 1560 BP.
DE N. gonorrhoeae nucleotide sequence SEQ ID 1991.
PN WO200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Percent Similarity: 38.21% Conservative: 33
Best Local Similarity: 24.80% Mismatches: 91
Query Match: 6.81% Indels: 61
RESULT 625
ID AAQ24328 standard; DNA; 1635 BP.
DE Mutant thermostable DNA polymerase pTHA292.
PN WO9206200-A.
PD 16-APR-1992.
PA (CETU) CETUS CORP.
Percent Similarity: 36.64% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 113
Query Match: 6.81% Indels: 74
RESULT 626
ID AAQ24327 standard; DNA; 1899 BP.
DE Mutant thermostable DNA polymerase pTHD2-203.
PN WO9206200-A.
PD 16-APR-1992.
PA (CETU) CETUS CORP.
Percent Similarity: 36.64% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 113
Query Match: 6.81% Indels: 74
RESULT 627
ID AAQ24326 standard; DNA; 2043 BP.
DE Mutant thermostable DNA polymerase pTHD2-155.
PN WO9206200-A.
PD 16-APR-1992.
PA (CETU) CETUS CORP.
Percent Similarity: 36.64% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 113
Query Match: 6.81% Indels: 74
RESULT 628
ID AAV53994 standard; DNA; 2511 BP.
DE AAV53994 standard; DNA; 2511 BP.
ID ACA42740 standard; DNA; 2253 BP.
DE Prokaryotic essential gene #24397.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 37.85% Conservative: 27
Best Local Similarity: 27.09% Mismatches: 101
Query Match: 6.81% Indels: 55
RESULT 629
ID AAQ24325 standard; DNA; 2277 BP.
DE Mutant thermostable DNA polymerase pTHD2-77.
PN WO9206200-A.
PD 16-APR-1992.
PA (CETU) CETUS CORP.
Percent Similarity: 36.64% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 113
Query Match: 6.81% Indels: 74
RESULT 630
ID ABD08178 standard; DNA; 2346 BP.
DE Pseudomonas aeruginosa polynucleotide #6782.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 38.19% Conservative: 31
Best Local Similarity: 25.98% Mismatches: 107
Query Match: 6.81% Indels: 51
RESULT 631
ID AAQ24324 standard; DNA; 2370 BP.
DE Mutant thermostable DNA polymerase pTHD2-46.
PN WO9206200-A.
PD 16-APR-1992.
PA (CETU) CETUS CORP.
Percent Similarity: 36.64% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 113
Query Match: 6.81% Indels: 74
RESULT 632
ID AD192526 standard; DNA; 2499 BP.
DE Synthetic 5' nuclease DNA SEQ ID 79.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.64% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 113
Query Match: 6.81% Indels: 74
RESULT 633
ID AAQ24323 standard; DNA; 2505 BP.
DE Mutant thermostable DNA polymerase from Thermus thermophilus.
PN WO9206200-A.
PD 16-APR-1992.
PA (CETU) CETUS CORP.
Percent Similarity: 36.64% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 113
Query Match: 6.81% Indels: 74
RESULT 634
ID AAV53993 standard; DNA; 2505 BP.
DE Nucleotide sequence of the nucleic acid 6.
PN WO9823774-A1.
PD 04-JUN-1998.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.64% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 113
Query Match: 6.81% Indels: 74
RESULT 635
ID AD192602 standard; DNA; 2505 BP.
DE T. thermophilus polymerase DNA SEQ ID 155.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 36.64% Conservative: 33
Best Local Similarity: 25.34% Mismatches: 113
Query Match: 6.81% Indels: 74
RESULT 636
ID AAV53994 standard; DNA; 2511 BP.
DE AAV53994 standard; DNA; 2511 BP.

```

DE Nucleotide sequence of the structure specific endonuclease 1.  
 PN WO9823774-A1.  
 PD 04-JUN-1998.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.81% Indels: 74  
 RESULT 637  
 ID ABS68747 standard; DNA; 2511 BP.  
 DE Thermus thermophilus DNA polymerase, PCR primer #4.  
 PN WO200263030-A2.  
 PD 15-AUG-2002.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.81% Indels: 74  
 RESULT 638  
 ID ADI92691 standard; DNA; 2511 BP.  
 DE T. thermophilus modified Tth polymerase DNA SEQ ID 244.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.81% Indels: 74  
 RESULT 639  
 ID AAQ12748 standard; DNA; 2640 BP.  
 DE T. thermophilus DNA polymerase I.  
 PN WO9109950-A.  
 PD 11-JUL-1991.  
 PA (CETU) CETUS CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.81% Indels: 74  
 RESULT 640  
 ID AAH14004 standard; cDNA; 2653 BP.  
 DE Human cDNA sequence SEQ ID NO:11090.  
 PN EP1074617-A2.  
 PD 07-FEB-2001.  
 PA (HELI-) HELIX RES INST..  
 Percent Similarity: 33.23% Conservative: 25  
 Best Local Similarity: 25.16% Mismatches: 98  
 Query Match: 6.81% Indels: 109  
 RESULT 641  
 ID AAD45690 standard; DNA; 2653 BP.  
 DE Human LBD54 DNA.  
 PN WO200270560-A2.  
 PD 12-SEP-2002.  
 PA (INPH-) INPHARMATICA LTD.  
 Percent Similarity: 33.23% Conservative: 25  
 Best Local Similarity: 25.16% Mismatches: 98  
 Query Match: 6.81% Indels: 109  
 RESULT 642  
 ID ADS99994 standard; DNA; 2669 BP.  
 DE Human therapeutic DNA - SEQ ID 231.  
 PN WO2004080148-A2.  
 PD 23-SEP-2004.  
 PA (NUVE-) NUVELO INC.  
 Percent Similarity: 33.23% Conservative: 25  
 Best Local Similarity: 25.16% Mismatches: 98  
 Query Match: 6.81% Indels: 109  
 RESULT 643  
 ID AAA30241 standard; DNA; 2943 BP.  
 DE Chimeric Pfu/T. thermophilus DNA polymerase coding sequence.  
 PN GB2344591-A.  
 PD 14-JUN-2000.  
 PA (BIOL-) BIOLINE LTD.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.81% Indels: 74  
 RESULT 644  
 ID ABD11116 standard; DNA; 3006 BP.  
 DE Pseudomonas aeruginosa polynucleotide #9720.

PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 31.97% Conservative: 28  
 Best Local Similarity: 22.45% Mismatches: 80  
 Query Match: 6.81% Indels: 120  
 RESULT 645  
 ID ACC78016 standard; DNA; 3210 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.81% Indels: 74  
 RESULT 646  
 ID AAO6261 standard; DNA; 3221 BP.  
 DE Thermus thermophilus thermostable DNA polymerase genomic DNA.  
 PN JP07163343-A.  
 PD 27-JUN-1995.  
 PA (TOYM) TOYOBO KK.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.81% Indels: 74  
 RESULT 647  
 ID ACC77892 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.81% Indels: 74  
 RESULT 648  
 ID ACC77919 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.81% Indels: 74  
 RESULT 649  
 ID ACC77962 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.81% Indels: 74  
 RESULT 650  
 ID ACC77972 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.81% Indels: 74  
 RESULT 651  
 ID ACC77874 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64% Conservative: 33  
 Best Local Similarity: 25.34% Mismatches: 113  
 Query Match: 6.81% Indels: 74  
 RESULT 652  
 ID ACC77915 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.



PA (INVI-) INVITROGEN CORP.	Conservative: 33
Percent Similarity:	36.64%
Best Local Similarity:	Mismatches: 113
Query Match:	Indels: 74
RESULT 661	
ID ACC77920 standard; DNA; 3221 BP.	
DE Thermus thermophilus mutant DNA polymerase encoding DNA.	
FN WO2003025132-A2.	
PD 27-MAR-2003.	
PA (INVI-) INVITROGEN CORP.	
Percent Similarity:	36.64%
Best Local Similarity:	Mismatches: 113
Query Match:	Indels: 74
RESULT 662	
ID ACC77977 standard; DNA; 3221 BP.	
DE Thermus thermophilus mutant DNA polymerase encoding DNA.	
FN WO2003025132-A2.	
PD 27-MAR-2003.	
PA (INVI-) INVITROGEN CORP.	
Percent Similarity:	36.64%
Best Local Similarity:	Mismatches: 113
Query Match:	Indels: 74
RESULT 663	
ID ACC77872 standard; DNA; 3221 BP.	
DE Thermus thermophilus mutant DNA polymerase encoding DNA.	
FN WO2003025132-A2.	
PD 27-MAR-2003.	
PA (INVI-) INVITROGEN CORP.	
Percent Similarity:	36.64%
Best Local Similarity:	Mismatches: 113
Query Match:	Indels: 74
RESULT 664	
ID ACC77879 standard; DNA; 3221 BP.	
DE Thermus thermophilus mutant DNA polymerase encoding DNA.	
FN WO2003025132-A2.	
PD 27-MAR-2003.	
PA (INVI-) INVITROGEN CORP.	
Percent Similarity:	36.64%
Best Local Similarity:	Mismatches: 113
Query Match:	Indels: 74
RESULT 665	
ID ACC77984 standard; DNA; 3221 BP.	
DE Thermus thermophilus mutant DNA polymerase encoding DNA.	
FN WO2003025132-A2.	
PD 27-MAR-2003.	
PA (INVI-) INVITROGEN CORP.	
Percent Similarity:	36.64%
Best Local Similarity:	Mismatches: 113
Query Match:	Indels: 74
RESULT 666	
ID ACC77911 standard; DNA; 3221 BP.	
DE Thermus thermophilus mutant DNA polymerase encoding DNA.	
FN WO2003025132-A2.	
PD 27-MAR-2003.	
PA (INVI-) INVITROGEN CORP.	
Percent Similarity:	36.64%
Best Local Similarity:	Mismatches: 113
Query Match:	Indels: 74
RESULT 667	
ID ACC77937 standard; DNA; 3221 BP.	
DE Thermus thermophilus mutant DNA polymerase encoding DNA.	
FN WO2003025132-A2.	
PD 27-MAR-2003.	
PA (INVI-) INVITROGEN CORP.	
Percent Similarity:	36.64%
Best Local Similarity:	Mismatches: 113
Query Match:	Indels: 74
RESULT 668	
ID ACC77967 standard; DNA; 3221 BP.	
DE Thermus thermophilus mutant DNA polymerase encoding DNA.	
FN WO2003025132-A2.	
PD 27-MAR-2003.	
PA (INVI-) INVITROGEN CORP.	
Percent Similarity:	36.64%
Best Local Similarity:	Mismatches: 113
Query Match:	Indels: 74
RESULT 669	
ID ACC77967 standard; DNA; 3221 BP.	
DE Thermus thermophilus mutant DNA polymerase encoding DNA.	
FN WO2003025132-A2.	
PD 27-MAR-2003.	
PA (INVI-) INVITROGEN CORP.	
Percent Similarity:	36.64%
Best Local Similarity:	Mismatches: 113
Query Match:	Indels: 74





ID	ACC77866 standard; DNA; 3221 BP.	
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.	
PN	WO2003025132-A2.	
PD	27-MAR-2003.	
PA	(INVI-) INVITROGEN CORP.	
Percent Similarity:	36.64%	Conservative: 33
Best Local Similarity:	25.34%	Mismatches: 113
Query Match:	6.81%	Indels: 74
RESULT 702		
ID	ACC77901 standard; DNA; 3221 BP.	
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.	
PN	WO2003025132-A2.	
PD	27-MAR-2003.	
PA	(INVI-) INVITROGEN CORP.	
Percent Similarity:	36.64%	Conservative: 33
Best Local Similarity:	25.34%	Mismatches: 113
Query Match:	6.81%	Indels: 74
RESULT 703		
ID	ACC77964 standard; DNA; 3221 BP.	
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.	
PN	WO2003025132-A2.	
PD	27-MAR-2003.	
PA	(INVI-) INVITROGEN CORP.	
Percent Similarity:	36.64%	Conservative: 33
Best Local Similarity:	25.34%	Mismatches: 113
Query Match:	6.81%	Indels: 74
RESULT 704		
ID	ACC77969 standard; DNA; 3221 BP.	
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.	
PN	WO2003025132-A2.	
PD	27-MAR-2003.	
PA	(INVI-) INVITROGEN CORP.	
Percent Similarity:	36.64%	Conservative: 33
Best Local Similarity:	25.34%	Mismatches: 113
Query Match:	6.81%	Indels: 74
RESULT 705		
ID	ACC77891 standard; DNA; 3221 BP.	
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.	
PN	WO2003025132-A2.	
PD	27-MAR-2003.	
PA	(INVI-) INVITROGEN CORP.	
Percent Similarity:	36.64%	Conservative: 33
Best Local Similarity:	25.34%	Mismatches: 113
Query Match:	6.81%	Indels: 74
RESULT 706		
ID	ACC77914 standard; DNA; 3221 BP.	
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.	
PN	WO2003025132-A2.	
PD	27-MAR-2003.	
PA	(INVI-) INVITROGEN CORP.	
Percent Similarity:	36.64%	Conservative: 33
Best Local Similarity:	25.34%	Mismatches: 113
Query Match:	6.81%	Indels: 74
RESULT 707		
ID	ACC77914 standard; DNA; 3221 BP.	
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.	
PN	WO2003025132-A2.	
PD	27-MAR-2003.	
PA	(INVI-) INVITROGEN CORP.	
Percent Similarity:	36.64%	Conservative: 33
Best Local Similarity:	25.34%	Mismatches: 113
Query Match:	6.81%	Indels: 74
RESULT 708		
ID	ACC78015 standard; DNA; 3221 BP.	
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.	
PN	WO2003025132-A2.	
PD	27-MAR-2003.	
PA	(INVI-) INVITROGEN CORP.	
Percent Similarity:	36.64%	Conservative: 33
Best Local Similarity:	25.34%	Mismatches: 113
Query Match:	6.81%	Indels: 74
RESULT 709		
ID	ACC77876 standard; DNA; 3221 BP.	
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.	
PN	WO2003025132-A2.	
PD	27-MAR-2003.	
PA	(INVI-) INVITROGEN CORP.	
Percent Similarity:	36.64%	Conservative: 33
Best Local Similarity:	25.34%	Mismatches: 113
Query Match:	6.81%	Indels: 74
RESULT 710		
ID	ACC77896 standard; DNA; 3221 BP.	
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.	
PN	WO2003025132-A2.	
PD	27-MAR-2003.	
PA	(INVI-) INVITROGEN CORP.	
Percent Similarity:	36.64%	Conservative: 33
Best Local Similarity:	25.34%	Mismatches: 113
Query Match:	6.81%	Indels: 74

PN	WO2003025132-A2.
PD	27-MAR-2003.
PA	(INVI-) INVITROGEN CORP.
Percent Similarity:	36.64%
Best Local Similarity:	25.34%
Query Match:	6.81%
RESULT 718	
ID	ACC77898 standard; DNA; 3221 BP.
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.
PN	WO2003025132-A2.
PD	27-MAR-2003.
PA	(INVI-) INVITROGEN CORP.
Percent Similarity:	36.64%
Best Local Similarity:	25.34%
Query Match:	6.81%
RESULT 719	
ID	ACC77893 standard; DNA; 3221 BP.
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.
PN	WO2003025132-A2.
PD	27-MAR-2003.
PA	(INVI-) INVITROGEN CORP.
Percent Similarity:	36.64%
Best Local Similarity:	25.34%
Query Match:	6.81%
RESULT 720	
ID	ACC77898 standard; DNA; 3221 BP.
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.
PN	WO2003025132-A2.
PD	27-MAR-2003.
PA	(INVI-) INVITROGEN CORP.
Percent Similarity:	36.64%
Best Local Similarity:	25.34%
Query Match:	6.81%
RESULT 721	
ID	ACC77903 standard; DNA; 3221 BP.
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.
PN	WO2003025132-A2.
PD	27-MAR-2003.
PA	(INVI-) INVITROGEN CORP.
Percent Similarity:	36.64%
Best Local Similarity:	25.34%
Query Match:	6.81%
RESULT 722	
ID	ACC77867 standard; DNA; 3221 BP.
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.
PN	WO2003025132-A2.
PD	27-MAR-2003.
PA	(INVI-) INVITROGEN CORP.
Percent Similarity:	36.64%
Best Local Similarity:	25.34%
Query Match:	6.81%
RESULT 723	
ID	ACC77870 standard; DNA; 3221 BP.
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.
PN	WO2003025132-A2.
PD	27-MAR-2003.
PA	(INVI-) INVITROGEN CORP.
Percent Similarity:	36.64%
Best Local Similarity:	25.34%
Query Match:	6.81%
RESULT 724	
ID	ACC77890 standard; DNA; 3221 BP.
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.
PN	WO2003025132-A2.
PD	27-MAR-2003.
PA	(INVI-) INVITROGEN CORP.
Percent Similarity:	36.64%
Best Local Similarity:	25.34%
Query Match:	6.81%
RESULT 725	
ID	ACC77965 standard; DNA; 3221 BP.
DE	Thermus thermophilus mutant DNA polymerase encoding DNA.
PN	WO2003025132-A2.
PD	27-MAR-2003.
PA	(INVI-) INVITROGEN CORP.
Percent Similarity:	36.64%
Best Local Similarity:	25.34%
Query Match:	6.81%

PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64% Conservative: 33  
Best Local Similarity: 25.34% Mismatches: 113  
Query Match: 6.81% Indels: 74  
RESULT 734  
ID ABD13665 standard; DNA; 1660 BP.  
DE Pseudomonas aeruginosa polynucleotide #12269.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 35.90% Conservative: 21  
Best Local Similarity: 26.92% Mismatches: 83  
Query Match: 6.81% Indels: 68  
RESULT 735  
ID ADD4868 standard; DNA; 5352 BP.  
DE Rat gene M34384, SEQ ID NO 14397.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GENO-) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Percent Similarity: 36.32% Conservative: 18  
Best Local Similarity: 28.25% Mismatches: 96  
Query Match: 6.81% Indels: 47  
RESULT 736  
ID ACAJ5857 standard; DNA; 846 BP.  
DE Prokaryotic essential gene #17514.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Percent Similarity: 33.74% Conservative: 19  
Best Local Similarity: 26.02% Mismatches: 74  
Query Match: 6.78% Indels: 90  
RESULT 737  
ID ACH97285 standard; DNA; 906 BP.  
DE Klebsiella pneumoniae polynucleotide seqid 3080.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 31.25% Conservative: 19  
Best Local Similarity: 24.26% Mismatches: 70  
Query Match: 6.78% Indels: 118  
RESULT 738  
ID ABD14669 standard; DNA; 966 BP.  
DE Pseudomonas aeruginosa polynucleotide #13273.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 36.55% Conservative: 16  
Best Local Similarity: 28.43% Mismatches: 86  
Query Match: 6.78% Indels: 39  
RESULT 739  
ID ABD08723 standard; DNA; 1083 BP.  
DE Pseudomonas aeruginosa polynucleotide #7327.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 36.72% Conservative: 23  
Best Local Similarity: 27.73% Mismatches: 101  
Query Match: 6.78% Indels: 62  
RESULT 740  
ID ABD16105 standard; DNA; 1200 BP.  
DE Pseudomonas aeruginosa polynucleotide #14709.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 38.60% Conservative: 29  
Best Local Similarity: 25.88% Mismatches: 91  
Query Match: 6.78% Indels: 49  
RESULT 741  
ID ABD16436 standard; DNA; 1290 BP.  
DE Pseudomonas aeruginosa polynucleotide #15040.  
PN US6551795-B1.  
PD 22-APR-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 38.60% Conservative: 29  
Best Local Similarity: 25.88% Mismatches: 91  
Query Match: 6.78% Indels: 49  
RESULT 742  
ID ABD15673 standard; DNA; 1299 BP.  
DE Pseudomonas aeruginosa polynucleotide #14277.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 35.00% Conservative: 20  
Best Local Similarity: 27.31% Mismatches: 108  
Query Match: 6.78% Indels: 61  
RESULT 743  
ID ABD14522 standard; DNA; 1428 BP.  
DE Pseudomonas aeruginosa polynucleotide #13126.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 38.86% Conservative: 14  
Best Local Similarity: 30.86% Mismatches: 77  
Query Match: 6.78% Indels: 31  
RESULT 744  
ID ABD16317 standard; DNA; 1449 BP.  
DE Pseudomonas aeruginosa polynucleotide #14921.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 38.60% Conservative: 29  
Best Local Similarity: 25.88% Mismatches: 91  
Query Match: 6.78% Indels: 49  
RESULT 745  
ID ACF39359 standard; DNA; 1509 BP.  
DE Mycobacterium tuberculosis mycobacterial antigen DNA SEQ ID NO:96.  
PN WO2003033530-A2.  
PD 24-APR-2003.  
PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.  
Percent Similarity: 37.84% Conservative: 16  
Best Local Similarity: 29.19% Mismatches: 83  
Query Match: 6.78% Indels: 32  
RESULT 746  
ID ABD14362 standard; DNA; 1515 BP.  
DE Pseudomonas aeruginosa polynucleotide #12966.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 38.86% Conservative: 14  
Best Local Similarity: 30.86% Mismatches: 77  
Query Match: 6.78% Indels: 31  
RESULT 747  
ID ACA53421 standard; DNA; 1590 BP.  
DE Prokaryotic essential gene #35078.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Percent Similarity: 34.89% Conservative: 28  
Best Local Similarity: 24.82% Mismatches: 74  
Query Match: 6.78% Indels: 107  
RESULT 748  
ID ABD15703 standard; DNA; 1824 BP.  
DE Pseudomonas aeruginosa polynucleotide #14307.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 35.00% Conservative: 20  
Best Local Similarity: 27.31% Mismatches: 108  
Query Match: 6.78% Indels: 61  
RESULT 749  
ID AAN70306 standard; DNA; 1906 BP.  
DE Sequence encoding bovine mullerian inhibiting substance (MIS)-like  
DE polypeptide and the promoter region based on genomic/cDNA fusion.  
PN EP221761-A.  
PD 13-MAY-1987.

```

PA (BIOJ ) BIOGEN NV.
PA (GEO ) GEN HOSPITAL CORP.
Percent Similarity: 32.72%
Best Local Similarity: 25.00%
Indels: 107
Query Match: 6.78%
RESULT 750
ID AAF60989 standard; DNA; 2085 BP.
DE P. putida KT2440-associated DNA ORF01994.
PN DE1935088-A1.
PD 01-FEB-2001.
PA (TIGR-) TIGR INST GENOMIC RES.
PA (QUIA-) QUIAGEN GMBH.
PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
PA (DKFZ-) DKFZ DEUT KREBSFORSCHUNGSZENTRUM.
PA (MEDI-) MEDIZINISCHE HOCHSCHULE HANNOVER.
Percent Similarity: 34.39%
Best Local Similarity: 26.67%
Indels: 71
Query Match: 6.78%
RESULT 751
ID ABS51351 standard; cDNA; 2299 BP.
DE cDNA encoding human secretory protein #49.
PN WO200257304-A2.
PD 25-JUL-2002.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 37.30%
Best Local Similarity: 24.18%
Indels: 76
Query Match: 6.78%
RESULT 752
ID AAZ34073 standard; cDNA; 2748 BP.
DE Human PRO846 nucleotide sequence.
PN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Indels: 100
Query Match: 6.78%
RESULT 753
ID AAA99905 standard; cDNA; 2749 BP.
DE cDNA encoding human protein PRO846.
PN WO200053757-A2.
PD 14-SEP-2000.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Indels: 100
Query Match: 6.78%
RESULT 754
ID AAA88517 standard; cDNA; 2749 BP.
DE Human PRO846 cDNA clone DNA44196-1353.
PN WO200053760-A2.
PD 14-SEP-2000.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Indels: 100
Query Match: 6.78%
RESULT 755
ID AAC78503 standard; cDNA; 2749 BP.
DE Human PRO846 (UNQ422) nucleotide sequence SEQ ID NO:215.
PN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Indels: 100
Query Match: 6.78%
RESULT 756
ID AAS21436 standard; cDNA; 2749 BP.
DE Human cDNA sequence encoding for PRO846 polypeptide.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Indels: 100
Query Match: 6.78%
RESULT 757
ID AAF44269 standard; cDNA; 2749 BP.
DE Human PRO846 nucleotide sequence SEQ ID NO:516.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Indels: 100
Query Match: 6.78%
RESULT 758
ID ABL88101 standard; cDNA; 2749 BP.
DE Human PRO846 cDNA sequence SEQ ID NO:59.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Indels: 100
Query Match: 6.78%
RESULT 759
ID ABL95590 standard; cDNA; 2749 BP.
DE Human angiogenesis related cDNA PRO846 SEQ ID NO: 59.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH ) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N E.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Indels: 100
Query Match: 6.78%
RESULT 760
ID ACAG3641 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Indels: 100
Query Match: 6.78%
RESULT 761
ID ACA4520 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Indels: 100
Query Match: 6.78%
RESULT 762
ID ACA03795 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Indels: 100
Query Match: 6.78%
RESULT 763
ID ACA71805 standard; cDNA; 2749 BP.
DE Human secreted and transmembrane polypeptide PRO846 cDNA.
PN US2002177553-A1.
PD 28-NOV-2002.

```



PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
Query Match:  
RESULT 764  
ID ABX89333 standard; cDNA; 2749 BP.  
DE DNA encoding novel secreted and transmembrane protein PRO846.  
PN US2003017563-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
Query Match:  
RESULT 765  
ID ABX92445 standard; cDNA; 2749 BP.  
DE cDNA encoding human PRO846 polypeptide.  
PN US2002169284-A1.  
PD 14-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
Query Match:  
RESULT 766  
ID ABX80979 standard; cDNA; 2749 BP.  
DE Human secreted/transmembrane protein cDNA, #183.  
PN US2003027162-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
Query Match:  
RESULT 767  
ID ACD4488 standard; cDNA; 2749 BP.  
DE cDNA encoding human PRO846 polypeptide.  
PN US2002127576-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
Query Match:  
RESULT 768  
ID ACD41987 standard; cDNA; 2749 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #193.  
PN US2003036179-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
Query Match:  
RESULT 769  
ID ACA66186 standard; cDNA; 2749 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO846.  
PN US2003004102-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
Query Match:  
RESULT 770  
ID ABX79659 standard; cDNA; 2749 BP.  
DE Human secreted/transmembrane protein cDNA, #183.  
PN US2002142961-A1.  
PD 03-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
Query Match:  
RESULT 771  
ID ACA93680 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003022187-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
Query Match:  
RESULT 772  
ID ABX81362 standard; DNA; 2749 BP.  
DE Human secreted or transmembrane protein related PCR primer #149.  
PN US2003027985-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
Query Match:  
RESULT 773  
ID ACA04216 standard; cDNA; 2749 BP.  
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 385.  
PN US2003032155-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
Query Match:  
RESULT 774  
ID ACA93178 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003017476-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
Query Match:  
RESULT 775  
ID ABX17262 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #147.  
PN US2002123463-A1.  
PD 05-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
Query Match:  
RESULT 776  
ID ACA68117 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2002177164-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
Query Match:  
RESULT 777  
ID ACA88566 standard; cDNA; 2749 BP.  
DE Human secreted and transmembrane polypeptide PRO846 cDNA.  
PN US2002197615-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
Query Match:  
RESULT 778  
ID ACD82073 standard; cDNA; 2749 BP.  
DE cDNA encoding human PRO846 polypeptide.  
PN US2003017981-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
Query Match:  
RESULT 779  
ID ADA45904 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003022328-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Conservative: 25  
Mismatch: 72  
Indels: 100  
Query Match:  
RESULT 780  
ID ADA76335 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.

```
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 30.08%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 781
ID ADA18985 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 782
ID ADA61608 standard; cDNA; 2749 BP.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 783
ID ADB19393 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 784
ID ADB27934 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 785
ID ADA86413 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 786
ID ADB15977 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 787
ID ADA38027 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO846.
PN US200308297-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 788
ID ADA47763 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003073215-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 789
ID ADA21713 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO846.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 790
ID ADA10500 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003059831-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 791
ID ADA67558 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 792
ID ADB30565 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 793
ID ADA85861 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 794
ID ADA18044 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO846 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 795
ID ADA97073 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 796
ID ADA79377 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 797
ID ADA47763 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003073215-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
```

```
Query Match: 6.78% Indels: 100
RESULT 797
ID ADA87516 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 798
ID ADB16718 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 799
ID ADA28152 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO846.
PN US2003054359-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 800
ID ADA91810 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 801
ID ADB14873 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 802
ID ADA24754 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 803
ID ADB18834 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 804
ID ADA94049 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 805
ID ADA82268 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
```

---

```
ID ADB19945 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 806
ID ADB13257 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 807
ID ACD98616 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 808
ID ACD29787 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 809
ID ADA12415 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO846.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 810
ID ADA94732 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO846.
PN US2003059832-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 811
ID ADA74511 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 812
ID ADB24744 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide SEQ ID NO 385.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 813
ID ADA82268 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
```

PN US2003082701-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 30.08%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 814  
ID ADA75231 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003073216-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 815  
ID ADA85309 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003082695-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 816  
ID ADA84757 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003082708-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 817  
ID ADB330013 standard; cDNA; 2749 BP.  
DE cDNA encoding human PRO polypeptide #193.  
PN US2003073214-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 818  
ID ADA80541 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003082761-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 819  
ID ADA75783 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003082703-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 820  
ID ADA38957 standard; cDNA; 2749 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO846.  
PN US2003059780-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 821  
ID ADA47008 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003073210-A1.  
PD 17-APR-2003.

PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 822  
ID ADB25304 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide SEQ ID NO 385.  
PN US2003077715-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 823  
ID ADA93480 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003077721-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 824  
ID ADB26830 standard; cDNA; 2749 BP.  
DE cDNA encoding human PRO polypeptide #193.  
PN US2003092147-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 825  
ID ADB31117 standard; cDNA; 2749 BP.  
DE cDNA encoding human PRO polypeptide #193.  
PN US2003096386-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 826  
ID ADA93078 standard; cDNA; 2749 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO846.  
PN US2003060407-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 827  
ID ADA61045 standard; cDNA; 2749 BP.  
DE Homo sapiens.  
PN US2003049817-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 828  
ID ADB24192 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide SEQ ID NO 385.  
PN US2003077714-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatches: 72  
Indels: 100  
RESULT 829  
ID ADA96521 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003082690-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Query Match: 6.78%  
Conservative: 25

Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 830  
 ID ADA81093 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003082702-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match: 6.78%  
 RESULT 831  
 ID ADA95969 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003082759-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match: 6.78%  
 RESULT 832  
 ID ADB26278 standard; cDNA; 2749 BP.  
 DE cDNA encoding human PRO polypeptide #193.  
 PN US2003082760-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match: 6.78%  
 RESULT 833  
 ID ADB21763 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003082765-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match: 6.78%  
 RESULT 834  
 ID ACD29202 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane polypeptide cDNA #46.  
 PN US2003049633-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match: 6.78%  
 RESULT 835  
 ID ADA77542 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003068797-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match: 6.78%  
 RESULT 836  
 ID ADB18282 standard; cDNA; 2749 BP.  
 DE cDNA encoding human PRO polypeptide #193.  
 PN US2003077710-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match: 6.78%  
 RESULT 837  
 ID ADA86965 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003082709-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match: 6.78%  
 RESULT 838  
 ID ADA88068 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003082700-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match: 6.78%  
 RESULT 839  
 ID ADA64656 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003054516-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match: 6.78%  
 RESULT 840  
 ID ADB28486 standard; cDNA; 2749 BP.  
 DE cDNA encoding human PRO polypeptide #193.  
 PN US2003082699-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match: 6.78%  
 RESULT 841  
 ID ADB29038 standard; cDNA; 2749 BP.  
 DE cDNA encoding human PRO polypeptide #193.  
 PN US2003082706-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match: 6.78%  
 RESULT 842  
 ID ACH65634 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein PRO846.  
 PN US2003044806-A1.  
 PD 06-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match: 6.78%  
 RESULT 843  
 ID ADA76990 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003059909-A1.  
 PD 27-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match: 6.78%  
 RESULT 844  
 ID ADA22639 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane polypeptide PRO846.  
 PN US2003040473-A1.  
 PD 27-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match: 6.78%  
 RESULT 845  
 ID ADA88620 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003073213-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match: 6.78%  
 RESULT 846  
 ID ADA97625 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.

```

PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 847
ID ADB27382 standard; cDNA; 2749 BP.
DE CDNA encoding human PRO polypeptide #193.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 848
ID ADB22315 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 849
ID ACD39624 standard; DNA; 2749 BP.
DE Human PRO 846 PCR primer #1.
PN US2003017982-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 850
ID ADA6805 standard; cDNA; 2749 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #147.
PN US2003049638-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 851
ID ADA39498 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO846.
PN US2003059782-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 852
ID ADA67006 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 853
ID ADB22867 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 854
ID ADB23640 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide SEQ ID NO 385.
PN US200307712-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 855
ID ADA92362 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 856
ID ADB15425 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 857
ID ADB38677 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 858
ID ADB96524 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #147.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 859
ID ADB38125 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 860
ID ADB66597 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 861
ID ADB89677 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 862
ID ADB90409 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatches: 72
Indels: 100
RESULT 863
ID ADB39510 standard; cDNA; 2749 BP.

```

DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003082764-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match:  
 RESULT 864  
 ID ADB73721 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide sequence #46.  
 PN US2003045462-A1.  
 PD 06-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match:  
 RESULT 865  
 ID ADB73721 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003082687-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match:  
 RESULT 866  
 ID ADB86740 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003082697-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match:  
 RESULT 867  
 ID ADB76437 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide sequence #46.  
 PN US2003083248-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match:  
 RESULT 868  
 ID ADB77345 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003082696-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match:  
 RESULT 869  
 ID ADB34502 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide SEQ ID NO 385.  
 PN US2003077717-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match:  
 RESULT 870  
 ID ADB35606 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide SEQ ID NO 385.  
 PN US2003077719-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match:  
 RESULT 871  
 ID ADB33950 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide SEQ ID NO 385.

PN US2003077716-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match:  
 RESULT 872  
 ID ADB35054 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide SEQ ID NO 385.  
 PN US2003077718-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match:  
 RESULT 873  
 ID ADB36158 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide SEQ ID NO 385.  
 PN US2003077720-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match:  
 RESULT 874  
 ID ADB46553 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003082692-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match:  
 RESULT 875  
 ID ADC43863 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003054986-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match:  
 RESULT 876  
 ID ADC57996 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #147.  
 PN US2003027754-A1.  
 PD 06-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match:  
 RESULT 877  
 ID ADC55360 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #147.  
 PN US2003045463-A1.  
 PD 06-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match:  
 RESULT 878  
 ID ADC12227 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein PRO846.  
 PN US2003049681-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 72  
 Indels: 100  
 Query Match:  
 RESULT 879  
 ID ADC61623 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003049684-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%



Best Local Similarity: 19.92% Mismatches: 72  
Query Match: 6.78% Indels: 100  
RESULT 880  
ID ADC63587 standard; cDNA; 2749 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
PN US2003054405-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08% Conservative: 25  
Best Local Similarity: 19.92% Mismatches: 72  
Query Match: 6.78% Indels: 100  
RESULT 881  
ID ADC66687 standard; cDNA; 2749 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
PN US2003060406-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08% Conservative: 25  
Best Local Similarity: 19.92% Mismatches: 72  
Query Match: 6.78% Indels: 100  
RESULT 882  
ID ADC56649 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #147.  
PN US2003064375-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08% Conservative: 25  
Best Local Similarity: 19.92% Mismatches: 72  
Query Match: 6.78% Indels: 100  
RESULT 883  
ID ADC68811 standard; cDNA; 2749 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
PN US2003064407-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08% Conservative: 25  
Best Local Similarity: 19.92% Mismatches: 72  
Query Match: 6.78% Indels: 100  
RESULT 884  
ID ADC62871 standard; cDNA; 2749 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
PN US2003068648-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08% Conservative: 25  
Best Local Similarity: 19.92% Mismatches: 72  
Query Match: 6.78% Indels: 100  
RESULT 885  
ID ADC67936 standard; cDNA; 2749 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
PN US2003069178-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08% Conservative: 25  
Best Local Similarity: 19.92% Mismatches: 72  
Query Match: 6.78% Indels: 100  
RESULT 886  
ID ADC11694 standard; cDNA; 2749 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO846.  
PN US2003069403-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08% Conservative: 25  
Best Local Similarity: 19.92% Mismatches: 72  
Query Match: 6.78% Indels: 100  
RESULT 887  
ID ADC41256 standard; cDNA; 2749 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
PN US2003072745-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08% Conservative: 25  
Best Local Similarity: 19.92% Mismatches: 72  
Query Match: 6.78% Indels: 100  
RESULT 888

ID ADC67311 standard; cDNA; 2749 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
PN US2003073131-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08% Conservative: 25  
Best Local Similarity: 19.92% Mismatches: 72  
Query Match: 6.78% Indels: 100  
RESULT 889  
ID ADC62247 standard; cDNA; 2749 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
PN US2003073624-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08% Conservative: 25  
Best Local Similarity: 19.92% Mismatches: 72  
Query Match: 6.78% Indels: 100  
RESULT 890  
ID ADC41880 standard; cDNA; 2749 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
PN US2003104998-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08% Conservative: 25  
Best Local Similarity: 19.92% Mismatches: 72  
Query Match: 6.78% Indels: 100  
RESULT 891  
ID ADC50426 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003092106-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08% Conservative: 25  
Best Local Similarity: 19.92% Mismatches: 72  
Query Match: 6.78% Indels: 100  
RESULT 892  
ID ADC71973 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003092107-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08% Conservative: 25  
Best Local Similarity: 19.92% Mismatches: 72  
Query Match: 6.78% Indels: 100  
RESULT 893  
ID ADC59952 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003092109-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08% Conservative: 25  
Best Local Similarity: 19.92% Mismatches: 72  
Query Match: 6.78% Indels: 100  
RESULT 894  
ID ADC52959 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID385.  
PN US2003087365-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08% Conservative: 25  
Best Local Similarity: 19.92% Mismatches: 72  
Query Match: 6.78% Indels: 100  
RESULT 895  
ID ADC57313 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID385.  
PN US2003087366-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08% Conservative: 25  
Best Local Similarity: 19.92% Mismatches: 72  
Query Match: 6.78% Indels: 100  
RESULT 896  
ID ADC60504 standard; cDNA; 2749 BP.

DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003087367-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 25  
 Indels: 72  
 Indels: 100  
 Query Match:  
 RESULT 897  
 ID ADC50979 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003087361-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 25  
 Indels: 72  
 Indels: 100  
 Query Match:  
 RESULT 898  
 ID ADC65506 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003087362-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 25  
 Indels: 72  
 Indels: 100  
 Query Match:  
 RESULT 899  
 ID ADC54604 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein cDNA Seq ID385.  
 PN US2003087363-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 25  
 Indels: 72  
 Indels: 100  
 Query Match:  
 RESULT 900  
 ID ADC53565 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein cDNA Seq ID385.  
 PN US2003087364-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 25  
 Indels: 72  
 Indels: 100  
 Query Match:  
 RESULT 901  
 ID ADC59088 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein cDNA Seq ID385.  
 PN US2003087359-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 25  
 Indels: 72  
 Indels: 100  
 Query Match:  
 RESULT 902  
 ID ADC55965 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein cDNA Seq ID385.  
 PN US2003087360-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 25  
 Indels: 72  
 Indels: 100  
 Query Match:  
 RESULT 903  
 ID ADC58536 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein cDNA Seq ID385.  
 PN US2003087346-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 25  
 Indels: 72  
 Indels: 100  
 Query Match:  
 RESULT 904  
 ID ADC14816 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.

PN US2003082546-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 25  
 Indels: 72  
 Indels: 100  
 Query Match:  
 RESULT 905  
 ID ADD08348 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US200308623-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 25  
 Indels: 72  
 Indels: 100  
 Query Match:  
 RESULT 906  
 ID ADD03210 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003092104-A1.  
 PD 15-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 25  
 Indels: 72  
 Indels: 100  
 Query Match:  
 RESULT 907  
 ID ADC90202 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003087348-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 25  
 Indels: 72  
 Indels: 100  
 Query Match:  
 RESULT 908  
 ID ADC82173 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #147.  
 PN US2003083461-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 25  
 Indels: 72  
 Indels: 100  
 Query Match:  
 RESULT 909  
 ID ADC69621 standard; cDNA; 2749 BP.  
 DE cDNA encoding human PRO polypeptide #193.  
 PN US2003194770-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 25  
 Indels: 72  
 Indels: 100  
 Query Match:  
 RESULT 910  
 ID ADC48510 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003194773-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 25  
 Indels: 72  
 Indels: 100  
 Query Match:  
 RESULT 911  
 ID ADD10039 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003194776-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 25  
 Indels: 72  
 Indels: 100  
 Query Match:  
 RESULT 912  
 ID ADD07815 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2002193299-A1.  
 PD 19-DEC-2002.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Mismatches: 25  
 Indels: 72  
 Indels: 100  
 Query Match:  
 RESULT 913  
 ID ADC14816 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.

Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 913  
 ID ADD04614 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003087354-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 914  
 ID ADC82706 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #147.  
 PN US2003059833-A1.  
 PD 27-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 915  
 ID ADC80570 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003092103-A1.  
 PD 15-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 916  
 ID ADD11077 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003194774-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 917  
 ID ADD10348 standard; cDNA; 2749 BP.  
 DE Human secreted/transmembrane PRO polypeptide cDNA #30.  
 PN US2003105011-A1.  
 PD 05-JUN-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 918  
 ID ADC47958 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003194771-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 919  
 ID ADD08886 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003073090-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 920  
 ID ADC80018 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003087358-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 921

ID ADD07135 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2002193300-A1.  
 PD 19-DEC-2002.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 922  
 ID ADD11308 standard; cDNA; 2749 BP.  
 DE Human secreted/transmembrane PRO polypeptide cDNA #30.  
 PN US2003105013-A1.  
 PD 05-JUN-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 923  
 ID ADD09487 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003194775-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 924  
 ID ADC83382 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #147.  
 PN US2003059783-A1.  
 PD 27-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 925  
 ID ADD41200 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003203438-A1.  
 PD 30-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 926  
 ID ADD52339 standard; cDNA; 2749 BP.  
 DE CDNA encoding human PRO polypeptide #193.  
 PN US2003194769-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 927  
 ID ADD53079 standard; cDNA; 2749 BP.  
 DE CDNA encoding human PRO polypeptide #193.  
 PN US2003194792-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 928  
 ID ADD51631 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003203437-A1.  
 PD 30-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08% Conservative: 25  
 Best Local Similarity: 19.92% Mismatches: 72  
 Query Match: 6.78% Indels: 100  
 RESULT 929  
 ID ADD55489 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #147.



RESULT 946  
 ID ADE35303 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003203434-A1.  
 PD 30-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72

RESULT 947  
 ID ADE16417 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003203435-A1.  
 PD 30-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72

RESULT 948  
 ID ADD73032 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003203436-A1.  
 PD 30-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72

RESULT 949  
 ID ADE42018 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003194772-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72

RESULT 950  
 ID ADE17835 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003199023-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72

RESULT 951  
 ID ADD91967 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003199053-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72

RESULT 952  
 ID ADE33430 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003194767-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72

RESULT 953  
 ID ADE33982 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003194791-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72

RESULT 954  
 ID ADD78928 standard; cDNA; 2749 BP.

IND ADD80034 standard; cDNA; 2749 BP.  
 DE cDNA encoding human PRO polypeptide #193.  
 PN US2003207417-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72

RESULT 955  
 ID ADD93071 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003194768-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72

RESULT 956  
 ID ADD72390 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003194781-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72

RESULT 957  
 ID ADE19491 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003199025-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72

RESULT 958  
 ID ADE18939 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003199026-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72

RESULT 959  
 ID ADE43135 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003199033-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72

RESULT 960  
 ID ADD95924 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003199059-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72

RESULT 961  
 ID ADE22810 standard; cDNA; 2749 BP.  
 DE cDNA encoding human PRO polypeptide #193.  
 PN US2003199064-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72

RESULT 962  
 ID ADD78928 standard; cDNA; 2749 BP.



PA (GETH ) GENENTECH INC.					
Percent Similarity:	30.08%				
Best Local Similarity:	19.92%	Conservative:	25		
Query Match:	6.78%	Mismatches:	72		
Indels:		Indels:	100		
RESULT 979					
ID ADG60132 standard; cDNA; 2749 BP.					
DE Human cDNA encoding secreted/transmembrane protein, PRO846.					
PN US2003206915-A1.					
PD 06-NOV-2003.					
PA (GETH ) GENENTECH INC.					
Percent Similarity:	30.08%	Conservative:	25		
Best Local Similarity:	19.92%	Mismatches:	72		
Query Match:	6.78%	Indels:	100		
RESULT 980					
ID ADG80023 standard; cDNA; 2749 BP.					
DE Human PRO polynucleotide #193.					
PN US2003207372-A1.					
PD 06-NOV-2003.					
PA (GETH ) GENENTECH INC.					
Percent Similarity:	30.08%	Conservative:	25		
Best Local Similarity:	19.92%	Mismatches:	72		
Query Match:	6.78%	Indels:	100		
RESULT 981					
ID ADH55315 standard; cDNA; 2749 BP.					
DE Novel human secreted and transmembrane protein PRO846 cDNA.					
PN US2003207381-A1.					
PD 06-NOV-2003.					
PA (GETH ) GENENTECH INC.					
Percent Similarity:	30.08%	Conservative:	25		
Best Local Similarity:	19.92%	Mismatches:	72		
Query Match:	6.78%	Indels:	100		
RESULT 982					
ID ADH55867 standard; cDNA; 2749 BP.					
DE Novel human secreted and transmembrane protein PRO846 cDNA.					
PN US2003207379-A1.					
PD 06-NOV-2003.					
PA (GETH ) GENENTECH INC.					
Percent Similarity:	30.08%	Conservative:	25		
Best Local Similarity:	19.92%	Mismatches:	72		
Query Match:	6.78%	Indels:	100		
RESULT 983					
ID ADI35697 standard; cDNA; 2749 BP.					
DE Human PRO polynucleotide #147.					
PN US2003050457-A1.					
PD 13-MAR-2003.					
PA (GETH ) GENENTECH INC.					
Percent Similarity:	30.08%	Conservative:	25		
Best Local Similarity:	19.92%	Mismatches:	72		
Query Match:	6.78%	Indels:	100		
RESULT 984					
ID ADI60892 standard; cDNA; 2749 BP.					
DE Human cDNA encoding secreted/transmembrane protein, PRO846.					
PN US2003077000-A1.					
PD 24-APR-2003.					
PA (GETH ) GENENTECH INC.					
Percent Similarity:	30.08%	Conservative:	25		
Best Local Similarity:	19.92%	Mismatches:	72		
Query Match:	6.78%	Indels:	100		
RESULT 985					
ID ADI64086 standard; cDNA; 2749 BP.					
DE Novel human secreted and transmembrane protein PRO846 cDNA.					
PN US2003207385-A1.					
PD 06-NOV-2003.					
PA (GETH ) GENENTECH INC.					
Percent Similarity:	30.08%	Conservative:	25		
Best Local Similarity:	19.92%	Mismatches:	72		
Query Match:	6.78%	Indels:	100		
RESULT 986					
ID ADI65035 standard; cDNA; 2749 BP.					
DE Novel human secreted and transmembrane protein PRO846 cDNA.					
PN US2003207386-A1.					
PD 06-NOV-2003.					
PA (GETH ) GENENTECH INC.					
Percent Similarity:	30.08%	Conservative:	25		
Best Local Similarity:	19.92%	Mismatches:	72		
Query Match:	6.78%	Indels:	100		
RESULT 987					
ID ADH81948 standard; cDNA; 2749 BP.					
DE Novel human secreted and transmembrane protein PRO846 cDNA.					
PN US2003207388-A1.					
PD 06-NOV-2003.					
PA (GETH ) GENENTECH INC.					
Percent Similarity:	30.08%	Conservative:	25		
Best Local Similarity:	19.92%	Mismatches:	72		
Query Match:	6.78%	Indels:	100		
RESULT 988					
ID ADI00190 standard; cDNA; 2749 BP.					
DE Novel human secreted and transmembrane protein PRO846 cDNA.					
PN US2003049682-A1.					
PD 13-MAR-2003.					
PA (GETH ) GENENTECH INC.					
Percent Similarity:	30.08%	Conservative:	25		
Best Local Similarity:	19.92%	Mismatches:	72		
Query Match:	6.78%	Indels:	100		
RESULT 989					
ID ADH81396 standard; cDNA; 2749 BP.					
DE Novel human secreted and transmembrane protein PRO846 cDNA.					
PN US2003207377-A1.					
PD 06-NOV-2003.					
PA (GETH ) GENENTECH INC.					
Percent Similarity:	30.08%	Conservative:	25		
Best Local Similarity:	19.92%	Mismatches:	72		
Query Match:	6.78%	Indels:	100		
RESULT 990					
ID ABX78063 standard; cDNA; 2749 BP.					
DE Human PRO polynucleotide #147.					
PN US2003027163-A1.					
PD 06-FEB-2003.					
PA (GETH ) GENENTECH INC.					
Percent Similarity:	30.08%	Conservative:	25		
Best Local Similarity:	19.92%	Mismatches:	72		
Query Match:	6.78%	Indels:	100		
RESULT 991					
ID ABX80475 standard; cDNA; 2749 BP.					
DE Human secreted or transmembrane protein related PCR primer #149.					
PN US2002132252-A1.					
PD 19-SEP-2002.					
PA (GETH ) GENENTECH INC.					
Percent Similarity:	30.08%	Conservative:	25		
Best Local Similarity:	19.92%	Mismatches:	72		
Query Match:	6.78%	Indels:	100		
RESULT 992					
ID ACA69381 standard; cDNA; 2749 BP.					
DE Human cDNA encoding secreted/transmembrane protein PRO846.					
PN US2003032023-A1.					
PD 13-FEB-2003.					
PA (GETH ) GENENTECH INC.					
Percent Similarity:	30.08%	Conservative:	25		
Best Local Similarity:	19.92%	Mismatches:	72		
Query Match:	6.78%	Indels:	100		
RESULT 993					
ID ACD24045 standard; cDNA; 2749 BP.					
DE Novel human secreted and transmembrane protein PRO846 cDNA.					
PN US2003032156-A1.					
PD 13-FEB-2003.					
PA (GETH ) GENENTECH INC.					
Percent Similarity:	30.08%	Conservative:	25		
Best Local Similarity:	19.92%	Mismatches:	72		
Query Match:	6.78%	Indels:	100		
RESULT 994					
ID ABX90452 standard; cDNA; 2749 BP.					
DE Human secreted/transmembrane protein cDNA, #183.					
PN US2002160384-A1.					
PD 31-OCT-2002.					
PA (GETH ) GENENTECH INC.					
Percent Similarity:	30.08%	Conservative:	25		
Best Local Similarity:	19.92%	Mismatches:	72		
Query Match:	6.78%	Indels:	100		
RESULT 995					
ID ACD42606 standard; cDNA; 2749 BP.					



```

DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 996
ID ABX64298 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO846 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH ) GENENTECH LTD.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 997
ID ACA67186 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 998
ID ADM62565 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 999
ID ADN15964 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 1000
ID ADN16593 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 1001
ID ADN15412 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 1002
ID ADN14860 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 1003
ID AD163534 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003092108-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 1004
ID ADC81122 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 1005
ID ADD76570 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 1006
ID ADD87934 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 1007
ID ADD86338 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 1008
ID ADE75786 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 1009
ID ADE48549 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 1010
ID ADE41309 standard; cDNA; 2749 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #30.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indels: 100
RESULT 1011
ID ADE23362 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003092108-A1.

```

```

PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 30.08%
Conservative: 25
Mismatches: 72
Indels: 100
Query Match: 6.78%
RESULT 1012
ID ADE23914 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Conservative: 25
Best Local Similarity: 19.92%
Mismatches: 72
Indels: 100
Query Match: 6.78%
RESULT 1013
ID ADE24557 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Conservative: 25
Best Local Similarity: 19.92%
Mismatches: 72
Indels: 100
Query Match: 6.78%
RESULT 1014
ID ADE87382 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Conservative: 25
Best Local Similarity: 19.92%
Mismatches: 72
Indels: 100
Query Match: 6.78%
RESULT 1015
ID ADE89248 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Conservative: 25
Best Local Similarity: 19.92%
Mismatches: 72
Indels: 100
Query Match: 6.78%
RESULT 1016
ID ADE18387 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Conservative: 25
Best Local Similarity: 19.92%
Mismatches: 72
Indels: 100
Query Match: 6.78%
RESULT 1017
ID ADE88696 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Conservative: 25
Best Local Similarity: 19.92%
Mismatches: 72
Indels: 100
Query Match: 6.78%
RESULT 1018
ID ADE89650 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUNA/) TUNAS D.
PA (WOOD/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Percent Similarity: 30.08%
Conservative: 25
Best Local Similarity: 19.92%
Mismatches: 72
Indels: 100
Query Match: 6.78%
RESULT 1019
ID ADF61290 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Conservative: 25
Best Local Similarity: 19.92%
Mismatches: 72
Indels: 100
Query Match: 6.78%
RESULT 1020
ID ADE39982 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Conservative: 25
Best Local Similarity: 19.92%
Mismatches: 72
Indels: 100
Query Match: 6.78%
RESULT 1021
ID ADF45778 standard; cDNA; 2749 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO846.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Conservative: 25
Best Local Similarity: 19.92%
Mismatches: 72
Indels: 100
Query Match: 6.78%
RESULT 1022
ID ADE94716 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO polypeptide #193.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Conservative: 25
Best Local Similarity: 19.92%
Mismatches: 72
Indels: 100
Query Match: 6.78%
RESULT 1023
ID ADE91127 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Conservative: 25
Best Local Similarity: 19.92%
Mismatches: 72
Indels: 100
Query Match: 6.78%
RESULT 1024
ID ADF35642 standard; cDNA; 2749 BP.
DE cDNA encoding human PRO846 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Conservative: 25
Best Local Similarity: 19.92%
Mismatches: 72
Indels: 100
Query Match: 6.78%

```

Query Match: 6.78% Indels: 100  
 RESULT 1025  
 ID ADE95268 standard; cDNA; 2749 BP.  
 DE cDNA encoding human PRO polypeptide #193.  
 PN US2003199052-A1.  
 PD 23-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72  
 Indels: 100

RESULT 1026  
 ID ADE93378 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003199060-A1.  
 PD 23-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72  
 Indels: 100

RESULT 1027  
 ID ADE93378 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003199060-A1.  
 PD 23-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72  
 Indels: 100

RESULT 1028  
 ID ADF40606 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003204055-A1.  
 PD 30-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72  
 Indels: 100

RESULT 1029  
 ID ADF23550 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003203402-A1.  
 PD 30-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72  
 Indels: 100

RESULT 1030  
 ID ADF33533 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003194780-A1.  
 PD 16-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72  
 Indels: 100

RESULT 1031  
 ID ADF34959 standard; cDNA; 2749 BP.  
 DE cDNA encoding human PRO polypeptide #193.  
 PN US2003199029-A1.  
 PD 23-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72  
 Indels: 100

RESULT 1032  
 ID ADF27000 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003199436-A1.  
 PD 23-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72  
 Indels: 100

RESULT 1033  
 ID ADF27636 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003199437-A1.  
 PD 23-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72  
 Indels: 100

RESULT 1034  
 ID ADE92274 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003199051-A1.  
 PD 23-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72  
 Indels: 100

RESULT 1035  
 ID ADE90575 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003199063-A1.  
 PD 23-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72  
 Indels: 100

RESULT 1036  
 ID ADF41230 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003199435-A1.  
 PD 23-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72  
 Indels: 100

RESULT 1037  
 ID ADF32909 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003211091-A1.  
 PD 13-NOV-2003.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72  
 Indels: 100

RESULT 1038  
 ID ADF25275 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003211092-A1.  
 PD 13-NOV-2003.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72  
 Indels: 100

RESULT 1039  
 ID ADF26376 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003199674-A1.  
 PD 23-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72  
 Indels: 100

RESULT 1040  
 ID ADF34165 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003194410-A1.  
 PD 16-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72  
 Indels: 100

RESULT 1041  
 ID ADF34165 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003199436-A1.  
 PD 23-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 Conservative: 25  
 Mismatches: 72  
 Indels: 100

ID ADF46402 standard; cDNA; 2749 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
PN US2003195344-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indel: 100  
RESULT 1042  
ID ADE91722 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003199058-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indel: 100  
RESULT 1043  
ID ADG11892 standard; cDNA; 2749 BP.  
DE cDNA encoding human PRO846 polypeptide.  
PN US2003228655-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indel: 100  
RESULT 1044  
ID ADG02301 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003207352-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indel: 100  
RESULT 1045  
ID ADG22087 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003207360-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indel: 100  
RESULT 1046  
ID ADG20157 standard; cDNA; 2749 BP.  
DE cDNA encoding human PRO polypeptide #193.  
PN US2003207376-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indel: 100  
RESULT 1047  
ID ADF98063 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003207422-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indel: 100  
RESULT 1048  
ID ADG24280 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003207426-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indel: 100  
RESULT 1049  
ID ADF98634 standard; cDNA; 2749 BP.

DE Human PRO polynucleotide #193.  
PN US2003208055-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indel: 100  
RESULT 1050  
ID ADG03465 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003207351-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indel: 100  
RESULT 1051  
ID ADF99186 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003207353-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indel: 100  
RESULT 1052  
ID ADG16771 standard; cDNA; 2749 BP.  
DE cDNA encoding human PRO polypeptide #193.  
PN US2003207359-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indel: 100  
RESULT 1053  
ID ADG05230 standard; cDNA; 2749 BP.  
DE Human PRO polynucleotide #193.  
PN US2003207375-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indel: 100  
RESULT 1054  
ID ADG19497 standard; cDNA; 2749 BP.  
DE cDNA encoding human PRO polypeptide #193.  
PN US2003207425-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indel: 100  
RESULT 1055  
ID ADG13334 standard; cDNA; 2749 BP.  
DE cDNA encoding human PRO polypeptide #193.  
PN US2003207357-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indel: 100  
RESULT 1056  
ID ADG08391 standard; cDNA; 2749 BP.  
DE Novel human secreted and transmembrane protein PRO846 cDNA.  
PN US2003207424-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Percent Similarity: 30.08%  
Best Local Similarity: 19.92%  
Query Match: 6.78%  
Conservative: 25  
Mismatch: 72  
Indel: 100  
RESULT 1057  
ID ADG15561 standard; cDNA; 2749 BP.  
DE cDNA encoding human PRO polypeptide #193.

```

PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 1058
ID ADF6959 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 1059
ID ADG06144 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 1060
ID ADG23728 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 1061
ID ADG04017 standard; cDNA; 2749 BP.
DE Human PRO polynucleotide #193.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 1062
ID ADG24918 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 1063
ID ADG07215 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 1064
ID ADG07767 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 1065
ID ADG55262 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003194778-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 1066
ID ADG55814 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 1067
ID ADG58574 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 1068
ID ADG62030 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 1069
ID ADG57470 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 1070
ID ADG56918 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 1071
ID ADG55814 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 1072
ID ADG58574 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100
RESULT 1073
ID ADG70940 standard; cDNA; 2749 BP.
DE Novel human secreted and transmembrane protein PRO846 cDNA.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 30.08%
Best Local Similarity: 19.92%
Query Match: 6.78%
Conservative: 25
Mismatch: 72
Indel: 100

```

Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 1082			
ID	ADG49764 standard; cDNA; 2749 BP.		
DE	Human cDNA encoding secreted/transmembrane protein, PRO846.		
PN	US2003215905-A1.		
PD	20-NOV-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 1083			
ID	ADG51636 standard; cDNA; 2749 BP.		
DE	Human cDNA encoding secreted/transmembrane protein, PRO846.		
PN	US2003215908-A1.		
PD	20-NOV-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 1084			
ID	ADG52430 standard; cDNA; 2749 BP.		
DE	Novel human secreted and transmembrane protein PRO846 cDNA.		
PN	US2003207414-A1.		
PD	06-NOV-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 1085			
ID	ADG54158 standard; cDNA; 2749 BP.		
DE	Novel human secreted and transmembrane protein PRO846 cDNA.		
PN	US2003207416-A1.		
PD	06-NOV-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 1086			
ID	ADG49140 standard; cDNA; 2749 BP.		
DE	Human cDNA encoding secreted/transmembrane protein, PRO846.		
PN	US2003216305-A1.		
PD	20-NOV-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 1087			
ID	ADG81127 standard; cDNA; 2749 BP.		
DE	Human PRO polynucleotide #193.		
PN	US2003194793-A1.		
PD	16-OCT-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 1088			
ID	ADG56366 standard; cDNA; 2749 BP.		
DE	Novel human secreted and transmembrane protein PRO846 cDNA.		
PN	US2003207366-A1.		
PD	06-NOV-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 1089			
ID	ADH12632 standard; cDNA; 2749 BP.		
DE	Novel human secreted and transmembrane protein PRO846 cDNA.		
PN	US2003207378-A1.		
PD	06-NOV-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100
RESULT 1090			
ID	ADH12632 standard; cDNA; 2749 BP.		
DE	Novel human secreted and transmembrane protein PRO846 cDNA.		
PN	US2003207378-A1.		
PD	06-NOV-2003.		
PA	(GETH ) GENENTECH INC.		
Percent Similarity:	30.08%	Conservative:	25
Best Local Similarity:	19.92%	Mismatches:	72
Query Match:	6.78%	Indels:	100

Query Match: 6.78% Indels: 100  
 RESULT 1090  
 ID ADG48516 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2003216560-A1.  
 PD 20-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 RESULT 1091  
 ID ADH21255 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein PRO846.  
 PN US2003224358-A1.  
 PD 04-DEC-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 RESULT 1092  
 ID ADG61478 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003207429-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 RESULT 1093  
 ID ADH20295 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein PRO846.  
 PN US2003219856-A1.  
 PD 27-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 RESULT 1094  
 ID ADH28565 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2003022331-A1.  
 PD 30-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 RESULT 1095  
 ID ADG54710 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003207367-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 RESULT 1096  
 ID ADG59750 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003207369-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 RESULT 1097  
 ID ADG51012 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2004005312-A1.  
 PD 08-JAN-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 RESULT 1098  
 ID ADG59750 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2004005312-A1.  
 PD 08-JAN-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 RESULT 1099  
 ID ADH34392 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #30.  
 PN US2003224984-A1.  
 PD 04-DEC-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 RESULT 1100  
 ID ADG58956 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2004005657-A1.  
 PD 08-JAN-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 RESULT 1101  
 ID ADI81174 standard; cDNA; 2749 BP.  
 DE cDNA encoding human PRO polypeptide #193.  
 PN US2003207361-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 RESULT 1102  
 ID ADH25437 standard; cDNA; 2749 BP.  
 DE Human neurotrophin homologue related nucleotide sequence SEQ ID NO:215.  
 PN EP1386931-A1.  
 PD 04-FEB-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 RESULT 1103  
 ID ADG09917 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2004005548-A1.  
 PD 15-JAN-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 RESULT 1104  
 ID ADI15388 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003207382-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 RESULT 1105  
 ID ADG09265 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2004005947-A1.  
 PD 15-JAN-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 Indels: 100  
 RESULT 1106  
 ID ADI14720 standard; cDNA; 2749 BP.



DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003207383-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 1107  
 ID ADI18315 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003207349-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 1108  
 ID ADJ63596 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2004039164-A1.  
 PD 26-FEB-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 1109  
 ID ADJ77491 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #193.  
 PN US2004038336-A1.  
 PD 26-FEB-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 1110  
 ID ADK82837 standard; cDNA; 2749 BP.  
 DE Human PRO polynucleotide #30.  
 PN US2004043927-A1.  
 PD 04-MAR-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 1111  
 ID ADJ65613 standard; cDNA; 2749 BP.  
 DE cDNA encoding human PRO polypeptide #193.  
 PN US2004038335-A1.  
 PD 26-FEB-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 1112  
 ID ADM27749 standard; cDNA; 2749 BP.  
 DE cDNA encoding human PRO polypeptide #193.  
 PN US2004048333-A1.  
 PD 11-MAR-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 1113  
 ID ADM17214 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.  
 PN US2004048332-A1.  
 PD 11-MAR-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 1114  
 ID ADL07048 standard; cDNA; 2749 BP.  
 DE Human cDNA encoding secreted/transmembrane protein, PRO846.

PN US2004063921-A1.  
 PD 01-APR-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 1115  
 ID ADM24273 standard; cDNA; 2749 BP.  
 DE cDNA encoding human PRO polypeptide #193.  
 PN US2004058424-A1.  
 PD 25-MAR-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 1116  
 ID ADM28335 standard; cDNA; 2749 BP.  
 DE cDNA encoding human PRO polypeptide #193.  
 PN US2004077064-A1.  
 PD 22-APR-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 1117  
 ID ADI95817 standard; cDNA; 2749 BP.  
 DE cDNA encoding human PRO polypeptide #193.  
 PN US2003077659-A1.  
 PD 24-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 1118  
 ID ADI96369 standard; cDNA; 2749 BP.  
 DE Novel human secreted and transmembrane protein PRO846 cDNA.  
 PN US2003207354-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 30.08%  
 Best Local Similarity: 19.92%  
 Query Match: 6.78%  
 RESULT 1119  
 ID ACC77620 standard; DNA; 3026 BP.  
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
 PN WO2003025332-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 39.31%  
 Best Local Similarity: 24.83%  
 Query Match: 6.78%  
 RESULT 1120  
 ID ACC77632 standard; DNA; 3026 BP.  
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
 PN WO2003025332-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 39.31%  
 Best Local Similarity: 24.83%  
 Query Match: 6.78%  
 RESULT 1121  
 ID ADS55878 standard; cDNA; 3459 BP.  
 DE Bacterial polynucleotide #7865.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Percent Similarity: 36.92%  
 Best Local Similarity: 27.31%  
 Query Match: 6.78%

RESULT 1122  
Percent Similarity: 37.84% Conservative: 16  
Best Local Similarity: 29.19% Mismatches: 83  
Query Match: 6.74% Indels: 32

RESULT 1123  
Percent Similarity: 37.84% Conservative: 16  
Best Local Similarity: 29.19% Mismatches: 83  
Query Match: 6.78% Indels: 32

RESULT 1124  
Percent Similarity: 37.84% Conservative: 16  
Best Local Similarity: 29.19% Mismatches: 83  
Query Match: 6.78% Indels: 32

RESULT 1125  
Percent Similarity: 37.84% Conservative: 16  
Best Local Similarity: 29.19% Mismatches: 83  
Query Match: 6.78% Indels: 32

RESULT 1126  
Percent Similarity: 37.84% Conservative: 16  
Best Local Similarity: 29.19% Mismatches: 83  
Query Match: 6.78% Indels: 32

ID ADJ40534 standard; cDNA; 1611 BP.  
DE Plant cDNA #1534.  
PN US2004016025-A1.  
PD 22-JAN-2004.  
PA (BUDW/) BUDWORTH P.  
PA (MOUG/) MOUGHAMER T.  
PA (BRIG/) BRIGGS S P.  
PA (COOP/) COOPER B.  
PA (GLAZ/) GLAZEBROOK J.  
PA (GOFF/) GOFF S A.  
PA (KATA/) KATAGIRI F.  
PA (KREP/) KREPS J.  
PA (PROV/) PROVANT N.  
PA (RICK/) RICKS D.  
PA (ZHUT/) ZHU T.  
Percent Similarity: 38.91% Conservative: 24  
Best Local Similarity: 28.87% Mismatches: 87  
Query Match: 6.74% Indels: 60

RESULT 1127  
Percent Similarity: 38.91% Conservative: 24  
Best Local Similarity: 28.87% Mismatches: 87  
Query Match: 6.74% Indels: 60

ID ADO57711 standard; DNA; 1950 BP.  
DE Actinobacillus actinomycetemcomitans immunogenic polypeptide gene #81.  
PN WO2004045499-A2.  
PD 03-JUN-2004.  
PA (UYFL ) UNIV FLORIDA.  
Percent Similarity: 37.25% Conservative: 35  
Best Local Similarity: 23.08% Mismatches: 127  
Query Match: 6.74% Indels: 28

RESULT 1128  
Percent Similarity: 37.25% Conservative: 35  
Best Local Similarity: 23.08% Mismatches: 127  
Query Match: 6.74% Indels: 28

ID ABD14922 standard; DNA; 2496 BP.  
DE Pseudomonas aeruginosa polynucleotide #13526.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 35.91% Conservative: 25  
Best Local Similarity: 26.25% Mismatches: 90  
Query Match: 6.74% Indels: 77

RESULT 1129  
Percent Similarity: 35.91% Conservative: 25  
Best Local Similarity: 26.25% Mismatches: 90  
Query Match: 6.74% Indels: 77

ID AD192549 standard; DNA; 2526 BP.  
DE Synthetic 5' nuclease DNA SEQ ID 102.  
PN WO200190337-A2.  
PD 29-NOV-2001.  
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
Percent Similarity: 36.30% Conservative: 33  
Best Local Similarity: 25.00% Mismatches: 114  
Query Match: 6.74% Indels: 74

RESULT 1130  
Percent Similarity: 36.30% Conservative: 33  
Best Local Similarity: 25.00% Mismatches: 114  
Query Match: 6.74% Indels: 74

ID ABD15329 standard; DNA; 2622 BP.  
DE Pseudomonas aeruginosa polynucleotide #13933.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 35.91% Conservative: 25  
Best Local Similarity: 26.25% Mismatches: 90  
Query Match: 6.74% Indels: 77

RESULT 1131  
Percent Similarity: 35.91% Conservative: 25  
Best Local Similarity: 26.25% Mismatches: 90  
Query Match: 6.74% Indels: 77

ID ABD15222 standard; DNA; 2685 BP.

DE Pseudomonas aeruginosa polynucleotide #13826.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 35.91% Conservative: 25  
Best Local Similarity: 26.25% Mismatches: 90  
Query Match: 6.74% Indels: 77

RESULT 1132  
Percent Similarity: 35.91% Conservative: 25  
Best Local Similarity: 26.25% Mismatches: 90  
Query Match: 6.74% Indels: 77

ID AAV02312 standard; cDNA; 3065 BP.  
DE C16N gene for promoting neuron survival and type 1 collagen production.  
PN WO9740150-A1.  
PD 30-OCT-1997.  
PA (SUMU ) SUMITOMO PHARM CO LTD.  
Percent Similarity: 30.84% Conservative: 30  
Best Local Similarity: 22.19% Mismatches: 95  
Query Match: 6.74% Indels: 146

RESULT 1133  
Percent Similarity: 30.84% Conservative: 30  
Best Local Similarity: 22.19% Mismatches: 95  
Query Match: 6.74% Indels: 146

ID ACC77988 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64% Conservative: 33  
Best Local Similarity: 25.34% Mismatches: 113  
Query Match: 6.74% Indels: 74

RESULT 1134  
Percent Similarity: 36.64% Conservative: 33  
Best Local Similarity: 25.34% Mismatches: 113  
Query Match: 6.74% Indels: 74

ID ACC77981 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64% Conservative: 33  
Best Local Similarity: 25.34% Mismatches: 113  
Query Match: 6.74% Indels: 74

RESULT 1135  
Percent Similarity: 36.64% Conservative: 33  
Best Local Similarity: 25.34% Mismatches: 113  
Query Match: 6.74% Indels: 74

ID ACC78005 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64% Conservative: 33  
Best Local Similarity: 25.34% Mismatches: 113  
Query Match: 6.74% Indels: 74

RESULT 1136  
Percent Similarity: 36.64% Conservative: 33  
Best Local Similarity: 25.34% Mismatches: 113  
Query Match: 6.74% Indels: 74

ID ACC77997 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64% Conservative: 33  
Best Local Similarity: 25.34% Mismatches: 113  
Query Match: 6.74% Indels: 74

RESULT 1137  
Percent Similarity: 36.64% Conservative: 33  
Best Local Similarity: 25.34% Mismatches: 113  
Query Match: 6.74% Indels: 74

ID AAZ40178 standard; cDNA; 3337 BP.  
DE Mouse C16N-2 coding sequence.  
PN JP11308995-A.  
PD 09-NOV-1999.  
PA (SUMU ) SUMITOMO SEIYAKU KK.  
Percent Similarity: 30.84% Conservative: 30  
Best Local Similarity: 22.19% Mismatches: 95  
Query Match: 6.74% Indels: 146

RESULT 1138  
Percent Similarity: 30.84% Conservative: 30  
Best Local Similarity: 22.19% Mismatches: 95  
Query Match: 6.74% Indels: 146

ID AAZ44729 standard; cDNA; 3337 BP.  
DE Murine C16N-2 cDNA.  
PN WO200001405-A1.  
PD 13-JAN-2000.  
PA (SUMU ) SUMITOMO PHARM CO LTD.  
Percent Similarity: 30.84% Conservative: 30  
Best Local Similarity: 22.19% Mismatches: 95  
Query Match: 6.74% Indels: 146

RESULT 1139  
Percent Similarity: 30.84% Conservative: 30  
Best Local Similarity: 22.19% Mismatches: 95  
Query Match: 6.74% Indels: 146

ID AAZ40177 standard; cDNA; 3674 BP.  
DE Mouse C16N-1 coding sequence.

PN JP11308995-A.  
 PD 09-NOV-1999.  
 PA (SUMU ) SUMITOMO SEIYAKU KK.  
 Percent Similarity: 30.84%  
 Best Local Similarity: 22.19%  
 Query Match: 6.74%  
 RESULT 1140  
 ID AAZ44728 standard; cDNA; 3674 BP.  
 DE Murine C16N-1 cDNA.  
 PN WO200001405-A1.  
 PD 13-JAN-2000.  
 PA (SUMU ) SUMITOMO PHARM CO LTD.  
 Percent Similarity: 30.84%  
 Best Local Similarity: 22.19%  
 Query Match: 6.74%  
 RESULT 1141  
 ID AAD07024 standard; DNA; 5054 BP.  
 DE Pseudomonas putida PHA synthase DNA.  
 PN WO200123596-A2.  
 PD 05-APR-2001.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
 Percent Similarity: 39.16%  
 Best Local Similarity: 25.86%  
 Query Match: 6.74%  
 RESULT 1142  
 ID ABA17139 standard; DNA; 32179 BP.  
 DE Human nervous system related polynucleotide SEQ ID NO 9470.  
 PN WO200159063-A2.  
 PD 16-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 32.89%  
 Best Local Similarity: 22.59%  
 Query Match: 6.74%  
 RESULT 1143  
 ID ABX34289 standard; DNA; 135638 BP.  
 DE S. atroolivaceus leinamycin biosynthesis gene cluster.  
 PN WO200277179-A2.  
 PD 03-OCT-2002.  
 PA (REGC ) UNIV CALIFORNIA.  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 Percent Similarity: 41.04%  
 Best Local Similarity: 25.47%  
 Query Match: 6.74%  
 RESULT 1145  
 ID AAH64966 standard; DNA; 349980 BP.  
 DE C glutamicum coding sequence fragment SEQ ID NO: 1.  
 PN EPI108790-A2.  
 PD 20-JUN-2001.  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 Percent Similarity: 39.29%  
 Best Local Similarity: 25.00%  
 Query Match: 6.74%  
 RESULT 1146  
 ID ACD93801 standard; cDNA; 536 BP.  
 DE Human colon cancer cell expressed cDNA #2213.  
 PN US2002155438-A1.  
 PD 24-OCT-2002.  
 PA (SIMP/) SIMPSON A J G.  
 PA (NETO/) NETO E D.  
 PA (BREN/) BRENTANI R R.  
 Percent Similarity: 34.64%  
 Best Local Similarity: 28.49%  
 Query Match: 6.70%  
 RESULT 1147  
 ID ADM94403 standard; cDNA; 1069 BP.  
 DE Wheat MRP4 ABC transporter cDNA #2.  
 PN US6677502-B1.  
 PD 13-JAN-2004.

PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Percent Similarity: 37.59%  
 Best Local Similarity: 23.78%  
 Query Match: 6.70%  
 RESULT 1148  
 ID ADT47090 standard; cDNA; 1338 BP.  
 DE Bacterial polynucleotide #21841.  
 PN US200323675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Percent Similarity: 37.35%  
 Best Local Similarity: 25.29%  
 Query Match: 6.70%  
 RESULT 1149  
 ID ADJ79603 standard; DNA; 1521 BP.  
 DE Glyphosphate resistant corn EPSPS DNA with corn codon usage ID10.  
 PN WO2004009761-A2.  
 PD 29-JAN-2004.  
 PA (MONS ) MONSANTO TECHNOLOGY LLC.  
 Percent Similarity: 36.79%  
 Best Local Similarity: 25.42%  
 Query Match: 6.70%  
 RESULT 1150  
 ID ADH76897 standard; cDNA; 1670 BP.  
 DE Human SOX18 cDNA.  
 PN US2002142415-A1.  
 PD 03-OCT-2002.  
 PA (KOOP/) KOOPMAN P A.  
 PA (MUSC/) MUSCAT G B O.  
 Percent Similarity: 34.28%  
 Best Local Similarity: 23.67%  
 Query Match: 6.70%  
 RESULT 1151  
 ID ABD08413 standard; DNA; 1929 BP.  
 DE Pseudomonas aeruginosa polynucleotide #7017.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 36.75%  
 Best Local Similarity: 28.21%  
 Query Match: 6.70%  
 RESULT 1152  
 ID ABD08507 standard; DNA; 1947 BP.  
 DE Pseudomonas aeruginosa polynucleotide #7111.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 36.75%  
 Best Local Similarity: 28.21%  
 Query Match: 6.70%  
 RESULT 1153  
 ID ADA69772 standard; DNA; 2016 BP.  
 DE Rice gene, SEQ ID 3095.  
 PN WO200300898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 Percent Similarity: 32.14%  
 Best Local Similarity: 23.93%  
 Query Match: 6.70%  
 RESULT 1154  
 ID ADB84163 standard; DNA; 2160 BP.  
 DE Gene expression estimation method-related DNA sequence #23.  
 PN WO200304227-A1.  
 PD 30-MAY-2003.  
 PA (NAG-) NAT INST AGROBIOLOGICAL SCI.  
 Percent Similarity: 32.14%  
 Best Local Similarity: 23.93%  
 Query Match: 6.70%

```

RESULT 1155
ID AAV62155 standard; DNA; 2341 BP.
DE HSV-2 strain SBS Contig ID 11 DNA sequence.
PN WO9820016-A1.
PD 14-MAY-1998.
PA (SMIK ) SMITHKLINE BEECHAM CORP.
Percent Similarity: 34.46%
Best Local Similarity: 27.03%
Query Match: 6.70%
Conservative: 22
Mismatch: 109
Indels: 86
RESULT 1156
ID ABK14883 standard; DNA; 2499 BP.
DE DNA encoding Tag DNA polymerase cold-sensitive mutant Cs#3.
PN US6333159-B1.
PD 25-DEC-2001.
PA (UNIW ) UNIV WASHINGTON.
Percent Similarity: 41.79%
Best Local Similarity: 26.07%
Query Match: 6.70%
Conservative: 44
Mismatch: 107
Indels: 57
RESULT 1157
ID ABA97303 standard; DNA; 2499 BP.
DE Cold sensitive mutant DNA polymerase DNA #3.
PN US6316202-B1.
PD 13-NOV-2001.
PA (UNIW ) UNIV WASHINGTON.
Percent Similarity: 41.79%
Best Local Similarity: 26.07%
Query Match: 6.70%
Conservative: 44
Mismatch: 107
Indels: 57
RESULT 1158
ID AAV62145 standard; DNA; 2694 BP.
DE HSV-2 strain SBS Contig ID 90 DNA sequence.
PN WO9820016-A1.
PD 14-MAY-1998.
PA (SMIK ) SMITHKLINE BEECHAM CORP.
Percent Similarity: 34.46%
Best Local Similarity: 27.03%
Query Match: 6.70%
Conservative: 22
Mismatch: 109
Indels: 86
RESULT 1159
ID ACC78004 standard; DNA; 3221 BP.
DE Thermus thermophilus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVT-) INVITROGEN CORP.
Percent Similarity: 36.64%
Best Local Similarity: 25.34%
Query Match: 6.70%
Conservative: 33
Mismatch: 113
Indels: 74
RESULT 1160
ID AAK90702 standard; DNA; 3281 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 4278.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 34.23%
Best Local Similarity: 28.08%
Query Match: 6.70%
Conservative: 16
Mismatch: 101
Indels: 70
RESULT 1161
ID AAK90701 standard; DNA; 3704 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 4277.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 34.23%
Best Local Similarity: 28.08%
Query Match: 6.70%
Conservative: 16
Mismatch: 101
Indels: 70
RESULT 1162
ID AAL44297 standard; DNA; 8651 BP.
DE Agropyron medolanus Y1 operon (C50 carotenoid producing operon).
PN WO200241833-A2.
PD 30-MAY-2002.
PA (CRGI ) CARGILL INC.
Percent Similarity: 34.55%
Best Local Similarity: 26.02%
Query Match: 6.70%
Conservative: 21
Mismatch: 87
Indels: 74
RESULT 1163
ID AAV62155 standard; DNA; 2341 BP.
DE HSV-2 strain SBS Contig ID 11 DNA sequence.
PN WO9820016-A1.
PD 14-MAY-1998.
PA (SMIK ) SMITHKLINE BEECHAM CORP.
Percent Similarity: 34.46%
Best Local Similarity: 27.03%
Query Match: 6.70%
Conservative: 22
Mismatch: 109
Indels: 86
RESULT 1164
ID AAZ23904 standard; DNA; 49999 BP.
DE Human LOBO homologue genomic DNA fragment 6.
PN WO9950284-A2.
PD 07-OCT-1999.
PA (ROSE/) ROSENTHAL A.
Percent Similarity: 36.11%
Best Local Similarity: 25.93%
Query Match: 6.70%
Conservative: 22
Mismatch: 80
Indels: 58
RESULT 1165
ID AAZ23904 standard; DNA; 49999 BP.
DE Human LOBO homologue genomic DNA fragment 6.
PN WO9950284-A2.
PD 07-OCT-1999.
PA (ROSE/) ROSENTHAL A.
Percent Similarity: 36.11%
Best Local Similarity: 25.93%
Query Match: 6.70%
Conservative: 22
Mismatch: 80
Indels: 58
RESULT 1166
ID AAZ23904 standard; DNA; 49999 BP.
DE Human LOBO homologue genomic DNA fragment 6.
PN WO9950284-A2.
PD 07-OCT-1999.
PA (ROSE/) ROSENTHAL A.
Percent Similarity: 36.11%
Best Local Similarity: 25.93%
Query Match: 6.70%
Conservative: 22
Mismatch: 80
Indels: 58
RESULT 1167
ID AAZ23904 standard; DNA; 49999 BP.
DE Human LOBO homologue genomic DNA fragment 6.
PN WO9950284-A2.
PD 07-OCT-1999.
PA (ROSE/) ROSENTHAL A.
Percent Similarity: 36.11%
Best Local Similarity: 25.93%
Query Match: 6.70%
Conservative: 22
Mismatch: 80
Indels: 58
RESULT 1168
ID AAZ23904 standard; DNA; 49999 BP.
DE Human LOBO homologue genomic DNA fragment 6.
PN WO9950284-A2.
PD 07-OCT-1999.
PA (ROSE/) ROSENTHAL A.
Percent Similarity: 36.11%
Best Local Similarity: 25.93%
Query Match: 6.70%
Conservative: 22
Mismatch: 80
Indels: 58
RESULT 1169
ID AAZ23904 standard; DNA; 49999 BP.
DE Human LOBO homologue genomic DNA fragment 6.
PN WO9950284-A2.
PD 07-OCT-1999.
PA (ROSE/) ROSENTHAL A.
Percent Similarity: 36.11%
Best Local Similarity: 25.93%
Query Match: 6.70%
Conservative: 22
Mismatch: 80
Indels: 58
RESULT 1170
ID AAZ23904 standard; DNA; 49999 BP.
DE Human LOBO homologue genomic DNA fragment 6.
PN WO9950284-A2.
PD 07-OCT-1999.
PA (ROSE/) ROSENTHAL A.
Percent Similarity: 36.11%
Best Local Similarity: 25.93%
Query Match: 6.70%
Conservative: 22
Mismatch: 80
Indels: 58
RESULT 1171
ID AAZ23904 standard; DNA; 49999 BP.
DE Human LOBO homologue genomic DNA fragment 6.
PN WO9950284-A2.
PD 07-OCT-1999.
PA (ROSE/) ROSENTHAL A.
Percent Similarity: 36.11%
Best Local Similarity: 25.93%
Query Match: 6.70%
Conservative: 22
Mismatch: 80
Indels: 58
RESULT 1172
ID AAZ23904 standard; DNA; 49999 BP.
DE Human LOBO homologue genomic DNA fragment 6.
PN WO9950284-A2.
PD 07-OCT-1999.
PA (ROSE/) ROSENTHAL A.
Percent Similarity: 36.11%
Best Local Similarity: 25.93%
Query Match: 6.70%
Conservative: 22
Mismatch: 80
Indels: 58
RESULT 1173
ID AAZ23904 standard; DNA; 49999 BP.
DE Human LOBO homologue genomic DNA fragment 6.
PN WO9950284-A2.
PD 07-OCT-1999.
PA (ROSE/) ROSENTHAL A.
Percent Similarity: 36.11%
Best Local Similarity: 25.93%
Query Match: 6.70%
Conservative: 22
Mismatch: 80
Indels: 58
RESULT 1174
ID AAZ23904 standard; DNA; 49999 BP.
DE Human LOBO homologue genomic DNA fragment 6.
PN WO9950284-A2.
PD 07-OCT-1999.
PA (ROSE/) ROSENTHAL A.
Percent Similarity: 36.11%
Best Local Similarity: 25.93%
Query Match: 6.70%
Conservative: 22
Mismatch: 80
Indels: 58
RESULT 1175
ID AAZ23904 standard; DNA; 49999 BP.
DE Human LOBO homologue genomic DNA fragment 6.
PN WO9950284-A2.
PD 07-OCT-1999.
PA (ROSE/) ROSENTHAL A.
Percent Similarity: 36.11%
Best Local Similarity: 25.93%
Query Match: 6.70%
Conservative: 22
Mismatch: 80
Indels: 58

```

ID ABD14888 standard; DNA; 1359 BP.  
 DE Pseudomonas aeruginosa polynucleotide #13492.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 32.39%  
 Best Local Similarity: 22.33%  
 Query Match: 6.66%  
 RESULT 1176  
 ID ABD05006 standard; DNA; 1605 BP.  
 DE Pseudomonas aeruginosa polynucleotide #3610.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 33.77%  
 Best Local Similarity: 25.97%  
 Query Match: 6.66%  
 RESULT 1177  
 ID ADT42143 standard; cDNA; 2418 BP.  
 DE Bacterial polynucleotide #16894.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Percent Similarity: 34.40%  
 Best Local Similarity: 23.40%  
 Query Match: 6.66%  
 RESULT 1178  
 ID ACC77989 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.64%  
 Best Local Similarity: 25.34%  
 Query Match: 6.66%  
 RESULT 1179  
 ID ABD05159 standard; DNA; 3270 BP.  
 DE Pseudomonas aeruginosa polynucleotide #3763.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 33.77%  
 Best Local Similarity: 25.97%  
 Query Match: 6.66%  
 RESULT 1180  
 ID AAF90037 standard; DNA; 6462 BP.  
 DE Nucleotide sequence of a type I polyketide synthase.  
 PN WO200140497-A2.  
 PD 07-JUN-2001.  
 PA (AVET ) AVENTIS PHARMA SA.  
 Percent Similarity: 36.63%  
 Best Local Similarity: 23.43%  
 Query Match: 6.66%  
 RESULT 1181  
 ID AAS32623 standard; DNA; 10646 BP.  
 DE Human genomic DNA for novel endocrine antigen, SEQ ID No 577.  
 PN WO200155319-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 39.23%  
 Best Local Similarity: 30.14%  
 Query Match: 6.66%  
 RESULT 1182  
 ID AAA81519 standard; DNA; 16677 BP.  
 DE N. meningitidis partial DNA sequence gnm\_66 SEQ ID NO:66.  
 PN WO200022430-A2.  
 PD 20-APR-2000.  
 PA (CHIR ) CHIRON CORP.  
 Percent Similarity: 37.80%  
 Best Local Similarity: 24.39%  
 Query Match: 6.66%  
 RESULT 1183  
 ID AAF90033 standard; DNA; 34071 BP.  
 DE Nucleotide sequence of cosmid a26g1 (coding strand).  
 PN WO200140497-A2.  
 PD 07-JUN-2001.  
 PA (AVET ) AVENTIS PHARMA SA.  
 Percent Similarity: 36.63%  
 Best Local Similarity: 23.43%  
 Query Match: 6.66%  
 RESULT 1184  
 ID AAF90032 standard; DNA; 42717 BP.  
 DE Nucleotide sequence of cosmid a26g1 (non-coding strand).  
 PN WO200140497-A2.  
 PD 07-JUN-2001.  
 PA (AVET ) AVENTIS PHARMA SA.  
 Percent Similarity: 36.63%  
 Best Local Similarity: 23.43%  
 Query Match: 6.66%  
 RESULT 1185  
 ID AAC55087 standard; DNA; 540 BP.  
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 80072.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 PA (GENO-) INST GENOMIC RES.  
 Percent Similarity: 37.80%  
 Best Local Similarity: 24.39%  
 Query Match: 6.66%  
 RESULT 1187  
 ID AAC55087 standard; DNA; 540 BP.  
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 80072.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 PA (CHIR ) CHIRON CORP.  
 Percent Similarity: 37.80%  
 Best Local Similarity: 24.39%  
 Query Match: 6.66%  
 RESULT 1188  
 ID ACF06134 standard; DNA; 1254 BP.  
 DE Bacterial P450 enzyme encoding DNA SEQ ID NO:51.  
 PN WO2003052050-A2.  
 PD 26-JUN-2003.  
 PA (DIVE-) DIVERSA CORP.  
 Percent Similarity: 33.44%  
 Best Local Similarity: 25.08%  
 Query Match: 6.63%  
 RESULT 1189  
 ID ACA38073 standard; DNA; 1374 BP.  
 DE Prokaryotic essential gene #19730.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 40.00%  
 Best Local Similarity: 32.31%  
 Query Match: 6.63%  
 RESULT 1190  
 ID ABX34196 standard; cDNA; 1568 BP.  
 DE Human FBX031-3 (F-Box only protein 31 alternate form 3) cDNA #2.  
 PN WO200281514-A2.  
 PD 17-OCT-2002.  
 PA (ISIS-) ISIS INNOVATION LTD.  
 Percent Similarity: 32.26%  
 Best Local Similarity: 25.81%  
 Query Match: 6.63%  
 RESULT 1191  
 ID ABX34198 standard; cDNA; 1602 BP.  
 DE Human FBX031-4 (F-Box only protein 31 alternate form 4) cDNA #2.  
 PN WO200281514-A2.

PD 17-OCT-2002.  
 PA (ISIS-) ISIS INNOVATION LTD.  
 Percent Similarity: 32.26%  
 Best Local Similarity: 25.81%  
 Query Match: 6.63%  
 RESULT 1192  
 ID AAN90395 standard; DNA; 1905 BP.  
 DE Genomic/cDNA composite DNA of Bovine Mullerian inhibiting substance.  
 PN WO8906695-A.  
 PD 27-JUL-1989.  
 PA (BIOJ) BIOGEN INC.  
 Percent Similarity: 35.28%  
 Best Local Similarity: 25.57%  
 Query Match: 6.63%  
 RESULT 1193  
 ID ACC77602 standard; DNA; 3026 BP.  
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 39.31%  
 Best Local Similarity: 24.83%  
 Query Match: 6.63%  
 RESULT 1194  
 ID ACC77583 standard; DNA; 3026 BP.  
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 42.09%  
 Best Local Similarity: 26.62%  
 Query Match: 6.63%  
 RESULT 1195  
 ID ACN37398 standard; cDNA; 3705 BP.  
 DE Tumour-associated antigenic target (TAT) cDNA DNA323852, SEQ ID NO:254.  
 PN WO2004030615-A2.  
 PD 15-APR-2004.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 35.19%  
 Best Local Similarity: 25.93%  
 Query Match: 6.63%  
 RESULT 1196  
 ID ABL27024 standard; DNA; 4706 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 32545.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Percent Similarity: 35.80%  
 Best Local Similarity: 28.40%  
 Query Match: 6.63%  
 RESULT 1197  
 ID ADP21336 standard; DNA; 8374 BP.  
 DE Gene CACNAIC for screening for cardiac therapeutic preparation.  
 PN WO2004050894-A2.  
 PD 17-JUN-2004.  
 PA (ARTE-) ARTESIAN THERAPEUTICS INC.  
 Percent Similarity: 32.52%  
 Best Local Similarity: 23.40%  
 Query Match: 6.63%  
 RESULT 1198  
 ID ADG75175 standard; DNA; 9369 BP.  
 DE Human herpesvirus 2 strain HG52 UL36 DNA - SEQ ID 247.  
 PN WO2003086308-A2.  
 PD 23-OCT-2003.  
 PA (CORI-) CORIXA CORP.  
 Percent Similarity: 34.46%  
 Best Local Similarity: 27.03%  
 Query Match: 6.63%  
 RESULT 1199  
 ID ADG75118 standard; DNA; 9369 BP.  
 DE Human herpesvirus 2 UL36 ORF DNA - SEQ ID 190.  
 PN WO2003086308-A2.  
 PD 23-OCT-2003.

PA (CORI-) CORIXA CORP.  
 Percent Similarity: 34.46%  
 Best Local Similarity: 27.03%  
 Query Match: 6.63%  
 RESULT 1200  
 ID ABD10349 standard; DNA; 1008 BP.  
 DE Pseudomonas aeruginosa polynucleotide #8953.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 34.52%  
 Best Local Similarity: 26.90%  
 Query Match: 6.59%  
 RESULT 1201  
 ID ABD10349 standard; DNA; 1008 BP.  
 DE Pseudomonas aeruginosa polynucleotide #8953.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 34.52%  
 Best Local Similarity: 26.90%  
 Query Match: 6.59%  
 RESULT 1202  
 ID AAS54191 standard; DNA; 1014 BP.  
 DE Pseudomonas aeruginosa DNA for cellular proliferation protein #322.  
 PN WO200170955-A2.  
 PD 27-SEP-2001.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 34.63%  
 Best Local Similarity: 25.11%  
 Query Match: 6.59%  
 RESULT 1203  
 ID ACA2441 standard; DNA; 1014 BP.  
 DE Prokaryotic essential gene #24098.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 34.63%  
 Best Local Similarity: 25.11%  
 Query Match: 6.59%  
 RESULT 1204  
 ID ABD01581 standard; DNA; 1035 BP.  
 DE Pseudomonas aeruginosa polynucleotide #185.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 34.63%  
 Best Local Similarity: 25.11%  
 Query Match: 6.59%  
 RESULT 1205  
 ID ABD01558 standard; DNA; 1074 BP.  
 DE Pseudomonas aeruginosa polynucleotide #162.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 34.63%  
 Best Local Similarity: 25.11%  
 Query Match: 6.59%  
 RESULT 1206  
 ID ACA23686 standard; DNA; 1263 BP.  
 DE Prokaryotic essential gene #5343.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 39.19%  
 Query Match: 6.59%  
 RESULT 1207  
 ID ABD01558 standard; DNA; 1074 BP.  
 DE Pseudomonas aeruginosa polynucleotide #162.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 34.63%  
 Best Local Similarity: 25.11%  
 Query Match: 6.59%  
 RESULT 1208  
 ID ACA23686 standard; DNA; 1263 BP.  
 DE Prokaryotic essential gene #5343.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 39.19%  
 Query Match: 6.59%  
 RESULT 1209  
 ID ABD01558 standard; DNA; 1074 BP.  
 DE Pseudomonas aeruginosa polynucleotide #162.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 34.63%  
 Best Local Similarity: 25.11%  
 Query Match: 6.59%  
 RESULT 1210  
 ID ACA23686 standard; DNA; 1263 BP.  
 DE Prokaryotic essential gene #5343.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 39.19%  
 Query Match: 6.59%

Best Local Similarity: 22.52% Mismatches: 82  
 Query Match: 6.59% Indels: 54  
 RESULT 1209  
 ID ABD13880 standard; DNA; 1293 BP.  
 DE Pseudomonas aeruginosa polynucleotide #12484.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 31.03% Conservative: 23  
 Best Local Similarity: 23.82% Mismatches: 88  
 Query Match: 6.59% Indels: 132  
 RESULT 1210  
 ID ABD14385 standard; DNA; 1422 BP.  
 DE Pseudomonas aeruginosa polynucleotide #12989.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 31.03% Conservative: 23  
 Best Local Similarity: 23.82% Mismatches: 88  
 Query Match: 6.59% Indels: 132  
 RESULT 1211  
 ID ADS56274 standard; cDNA; 1437 BP.  
 DE Bacterial polynucleotide #8261.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Percent Similarity: 38.28% Conservative: 29  
 Best Local Similarity: 24.40% Mismatches: 92  
 Query Match: 6.59% Indels: 37  
 RESULT 1212  
 ID ABD01554 standard; DNA; 1455 BP.  
 DE Pseudomonas aeruginosa polynucleotide #158.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 34.63% Conservative: 22  
 Best Local Similarity: 25.11% Mismatches: 85  
 Query Match: 6.59% Indels: 66  
 RESULT 1213  
 ID ABX70924 standard; cDNA; 1696 BP.  
 DE Novel human cDNA sequence #149.  
 PN WO200281731-A2.  
 PD 17-OCT-2002.  
 PA (HYSE-) HYSEQ INC.  
 PA (GOOD/) GOODRICH R W.  
 Percent Similarity: 34.53% Conservative: 23  
 Best Local Similarity: 26.18% Mismatches: 81  
 Query Match: 6.59% Indels: 100  
 RESULT 1214  
 ID AAN70309 standard; cDNA; 1814 BP.  
 DE Sequence of bovine mullerian inhibiting substance (MIS) cDNA.  
 PN EP221761-A.  
 PD 13-MAY-1987.  
 PA (BIOJ/) BIOGEN NV.  
 PA (GEOH) GEN HOSPITAL CORP.  
 Percent Similarity: 32.03% Conservative: 22  
 Best Local Similarity: 24.84% Mismatches: 99  
 Query Match: 6.59% Indels: 109  
 RESULT 1215  
 ID AAS87226 standard; cDNA; 2327 BP.  
 DE DNA encoding novel human diagnostic protein #23030.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 32.92% Conservative: 18  
 Best Local Similarity: 25.51% Mismatches: 101  
 Query Match: 6.59% Indels: 63  
 RESULT 1216  
 ID ACN40432 standard; cDNA; 2327 BP.

DE Tumour-associated antigenic target (TAT) cDNA DNA326544, SEQ ID NO:5208.  
 PN WO2004030615-A2.  
 PD 15-APR-2004.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 32.92% Conservative: 18  
 Best Local Similarity: 25.51% Mismatches: 101  
 Query Match: 6.59% Indels: 63  
 RESULT 1217  
 ID AAX87254 standard; cDNA; 2413 BP.  
 DE cDNA clone encoding human PRO201, amplified in tumour cells.  
 PN WO9935170-A2.  
 PD 15-JUL-1999.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 32.92% Conservative: 18  
 Best Local Similarity: 25.51% Mismatches: 101  
 Query Match: 6.59% Indels: 63  
 RESULT 1218  
 ID AAZ32137 standard; cDNA; 2413 BP.  
 DE Human PRO201 (Nsp1) protein encoding cDNA clone DNA30676.  
 PN WO954467-A1.  
 PD 28-OCT-1999.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 32.92% Conservative: 18  
 Best Local Similarity: 25.51% Mismatches: 101  
 Query Match: 6.59% Indels: 63  
 RESULT 1219  
 ID AAZ89573 standard; cDNA; 2413 BP.  
 DE Human PRO201 cDNA.  
 PN US6051403-A.  
 PD 18-APR-2000.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 32.92% Conservative: 18  
 Best Local Similarity: 25.51% Mismatches: 101  
 Query Match: 6.59% Indels: 63  
 RESULT 1220  
 ID AAZ89585 standard; cDNA; 2413 BP.  
 DE Human PRO201 cDNA.  
 PN US6051690-A.  
 PD 18-APR-2000.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 32.92% Conservative: 18  
 Best Local Similarity: 25.51% Mismatches: 101  
 Query Match: 6.59% Indels: 63  
 RESULT 1221  
 ID AAA46900 standard; cDNA; 2413 BP.  
 DE cDNA encoding novel polypeptide PRO201.  
 PN WO200037640-A2.  
 PD 29-JUN-2000.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 32.92% Conservative: 18  
 Best Local Similarity: 25.51% Mismatches: 101  
 Query Match: 6.59% Indels: 63  
 RESULT 1222  
 ID ADJ58630 standard; cDNA; 2413 BP.  
 DE Human DNA30676 cDNA encoding PRO201 (Nsp1) protein.  
 PN US2003191283-A1.  
 PD 09-OCT-2003.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 32.92% Conservative: 18  
 Best Local Similarity: 25.51% Mismatches: 101  
 Query Match: 6.59% Indels: 63  
 RESULT 1223  
 ID ACN92210 standard; DNA; 2454 BP.  
 DE Breast cancer related marker, seq id 13360.  
 PN US200309974-A1.  
 PD 29-MAY-2003.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Percent Similarity: 32.92% Conservative: 18  
 Best Local Similarity: 25.51% Mismatches: 101  
 Query Match: 6.59% Indels: 63  
 RESULT 1224  
 ID AAV63400 standard; DNA; 2507 BP.  
 DE DNA sequence encoding a DNA polymerase enzyme.



PN US5837450-A.  
PD 17-NOV-1998.  
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
Percent Similarity: 40.43%  
Best Local Similarity: 25.99%  
Query Match: 6.59%  
Indels: 52  
RESULT 1225  
ID ABD10528 standard; DNA; 2511 BP.  
DE Pseudomonas aeruginosa polynucleotide #9132.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 34.52%  
Best Local Similarity: 26.90%  
Query Match: 6.59%  
Indels: 46  
RESULT 1226  
ID ADD69661 standard; cDNA; 2846 BP.  
DE Human REMAP cDNA - SEQ ID 90.  
PN WO2003048305-A2.  
PD 12-JUN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Percent Similarity: 37.83%  
Best Local Similarity: 24.78%  
Query Match: 6.59%  
Indels: 74  
RESULT 1227  
ID AAA38444 standard; DNA; 2893 BP.  
DE Human desmin gene 5' flanking region, including the promoter region.  
PN EP999278-A1.  
PD 10-MAY-2000.  
PA (UYPA-) UNIV PARIS VII.  
Percent Similarity: 33.33%  
Best Local Similarity: 21.02%  
Query Match: 6.59%  
Indels: 116  
RESULT 1228  
ID ADRO7302 standard; cDNA; 3024 BP.  
DE Full length human cDNA useful for treating neurological disease Seq 808.  
PN EP1447413-A2.  
PD 18-AUG-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Percent Similarity: 32.78%  
Best Local Similarity: 24.50%  
Query Match: 6.59%  
Indels: 118  
RESULT 1229  
ID ADQ85143 standard; cDNA; 3152 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1957.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH-) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 37.83%  
Best Local Similarity: 24.78%  
Query Match: 6.59%  
Indels: 74  
RESULT 1230  
ID ADQ84395 standard; cDNA; 3152 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1209.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH-) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 37.83%  
Best Local Similarity: 24.78%  
Query Match: 6.59%  
Indels: 74  
RESULT 1231  
ID ADQ86325 standard; cDNA; 3152 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3197.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH-) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 37.83%  
Indels: 30

Best Local Similarity: 24.78%  
Query Match: 6.59%  
Indels: 74  
RESULT 1232  
ID ADQ83912 standard; cDNA; 3152 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #726.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH-) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 37.83%  
Best Local Similarity: 24.78%  
Query Match: 6.59%  
Indels: 74  
RESULT 1233  
ID ADQ83232 standard; cDNA; 3152 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #46.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH-) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 37.83%  
Best Local Similarity: 24.78%  
Query Match: 6.59%  
Indels: 74  
RESULT 1234  
ID ACN37500 standard; cDNA; 3152 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA194600, SEQ ID NO:428.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH-) GENENTECH INC.  
Percent Similarity: 37.83%  
Best Local Similarity: 24.78%  
Query Match: 6.59%  
Indels: 74  
RESULT 1235  
ID ACC77986 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64%  
Best Local Similarity: 25.34%  
Query Match: 6.59%  
Indels: 74  
RESULT 1236  
ID ACC77953 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64%  
Best Local Similarity: 25.00%  
Query Match: 6.59%  
Indels: 74  
RESULT 1237  
ID ACC77950 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64%  
Best Local Similarity: 25.00%  
Query Match: 6.59%  
Indels: 74  
RESULT 1238  
ID ACC77982 standard; DNA; 3221 BP.  
DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 36.64%  
Best Local Similarity: 25.34%  
Query Match: 6.59%  
Indels: 74  
RESULT 1239  
ID ADQ23554 standard; DNA; 3289 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6374.  
PN WO2004048938-A2.

PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Percent Similarity: 32.78% Conservative: 25  
 Best Local Similarity: 24.50% Mismatches: 85  
 Query Match: 6.59% Indels: 118  
 RESULT 1240  
 ID ABK94417 standard; cDNA; 3633 BP.  
 DE Human cDNA differentially expressed in granulocytic cells #988.  
 PN WO200228999-A2.  
 PD 11-APR-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 38.80% Conservative: 39  
 Best Local Similarity: 23.20% Mismatches: 97  
 Query Match: 6.59% Indels: 57  
 RESULT 1241  
 ID ABL30051 standard; DNA; 4567 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 41626.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Percent Similarity: 39.64% Conservative: 27  
 Best Local Similarity: 27.48% Mismatches: 77  
 Query Match: 6.59% Indels: 57  
 RESULT 1242  
 ID ADNA1761 standard; DNA; 22459 BP.  
 DE Novel human secreted protein polynucleotide seqid 883.  
 PN US2004044191-A1.  
 PD 04-MAR-2004.  
 PA (FISC/) FISCHER C L.  
 PA (ROSE/) ROSEN C A.  
 PA (SOPP/) SOPPET D R.  
 PA (RUBE/) RUBEN S M.  
 PA (KYAW/) KYAW H.  
 PA (LIYI/) LI Y.  
 PA (ZENG/) ZENG Z.  
 PA (LAFI/) LAFLEUR D W.  
 PA (MOOR/) MOORE P A.  
 PA (SHIY/) SHI Y.  
 PA (OLSE/) OLSEN H.  
 PA (EBNE/) EBNER R.  
 PA (BIRS/) BIRSE C E.  
 Percent Similarity: 39.73% Conservative: 15  
 Best Local Similarity: 29.45% Mismatches: 60  
 Query Match: 6.59% Indels: 28  
 RESULT 1243  
 ID ABV99730 standard; cDNA; 30350 BP.  
 DE Human Ras-like protein encoding cDNA.  
 Percent Similarity: 36.03% Conservative: 21  
 Best Local Similarity: 28.31% Mismatches: 93  
 Query Match: 6.59% Indels: 82  
 RESULT 1244  
 ID ABZ66810 standard; DNA; 37116 BP.  
 DE Orthosomycin biosynthetic gene cluster SEQ ID NO 279.  
 PN WO200279505-A2.  
 PD 10-OCT-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Percent Similarity: 33.58% Conservative: 14  
 Best Local Similarity: 28.30% Mismatches: 96  
 Query Match: 6.59% Indels: 81  
 RESULT 1245  
 ID AAA11992 standard; DNA; 37856 BP.  
 DE S. cellulosum DNA encoding polyketide and hereropolyketide enzymes.  
 PN DE19846493-A1.  
 PD 13-APR-2000.  
 PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
 Percent Similarity: 37.27% Conservative: 31  
 Best Local Similarity: 25.83% Mismatches: 87  
 Query Match: 6.59% Indels: 83  
 RESULT 1246  
 ID ADM45913 standard; DNA; 84428 BP.  
 DE Streptomyces mycarofaciens midcamycin polyketide synthetase DNA.  
 PN JP2004049100-A.  
 PD 19-FEB-2004.

PA (MEIJ ) MEIJI SEIKA KAISHA LTD.  
 Percent Similarity: 33.33% Conservative: 24  
 Best Local Similarity: 25.17% Mismatches: 100  
 Query Match: 6.59% Indels: 96  
 RESULT 1247  
 ID AAS08693 standard; DNA; 109519 BP.  
 DE Micromonospora DNA encoding biosynthetic enzymes for Everninomycin.  
 PN WO200228999-A2.  
 PD 11-APR-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 38.80% Conservative: 39  
 Best Local Similarity: 23.20% Mismatches: 97  
 Query Match: 6.59% Indels: 57  
 RESULT 1241  
 ID ABL30051 standard; DNA; 4567 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 41626.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Percent Similarity: 39.64% Conservative: 27  
 Best Local Similarity: 27.48% Mismatches: 77  
 Query Match: 6.59% Indels: 57  
 RESULT 1242  
 ID ADNA1761 standard; DNA; 22459 BP.  
 DE Novel human secreted protein polynucleotide seqid 883.  
 PN US2004044191-A1.  
 PD 04-MAR-2004.  
 PA (FISC/) FISCHER C L.  
 PA (ROSE/) ROSEN C A.  
 PA (SOPP/) SOPPET D R.  
 PA (RUBE/) RUBEN S M.  
 PA (KYAW/) KYAW H.  
 PA (LIYI/) LI Y.  
 PA (ZENG/) ZENG Z.  
 PA (LAFI/) LAFLEUR D W.  
 PA (MOOR/) MOORE P A.  
 PA (SHIY/) SHI Y.  
 PA (OLSE/) OLSEN H.  
 PA (EBNE/) EBNER R.  
 PA (BIRS/) BIRSE C E.  
 Percent Similarity: 39.73% Conservative: 15  
 Best Local Similarity: 29.45% Mismatches: 60  
 Query Match: 6.59% Indels: 28  
 RESULT 1243  
 ID ABV99730 standard; cDNA; 30350 BP.  
 DE Human Ras-like protein encoding cDNA.  
 Percent Similarity: 36.03% Conservative: 21  
 Best Local Similarity: 28.31% Mismatches: 93  
 Query Match: 6.59% Indels: 82  
 RESULT 1244  
 ID ABZ66810 standard; DNA; 37116 BP.  
 DE Orthosomycin biosynthetic gene cluster SEQ ID NO 279.  
 PN WO200279505-A2.  
 PD 10-OCT-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Percent Similarity: 33.58% Conservative: 14  
 Best Local Similarity: 28.30% Mismatches: 96  
 Query Match: 6.59% Indels: 81  
 RESULT 1245  
 ID AAA11992 standard; DNA; 37856 BP.  
 DE S. cellulosum DNA encoding polyketide and hereropolyketide enzymes.  
 PN DE19846493-A1.  
 PD 13-APR-2000.  
 PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
 Percent Similarity: 37.27% Conservative: 31  
 Best Local Similarity: 25.83% Mismatches: 87  
 Query Match: 6.59% Indels: 83  
 RESULT 1246  
 ID ADM45913 standard; DNA; 84428 BP.  
 DE Streptomyces mycarofaciens midcamycin polyketide synthetase DNA.  
 PN JP2004049100-A.  
 PD 19-FEB-2004.

RESULT 1259  
 ID ADT46061 standard; cDNA; 1281 BP.  
 DE Bacterial polynucleotide #20812.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Percent Similarity: 35.79%  
 Best Local Similarity: 24.35%  
 Query Match: 6.55%  
 RESULT 1260  
 ID ADS56330 standard; cDNA; 2402 BP.  
 DE Bacterial polynucleotide #8317.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Percent Similarity: 32.73%  
 Best Local Similarity: 24.02%  
 Query Match: 6.55%  
 RESULT 1261  
 ID ACA45126 standard; DNA; 2487 BP.  
 DE Prokaryotic essential gene #26783.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 35.86%  
 Best Local Similarity: 23.03%  
 Query Match: 6.55%  
 RESULT 1262  
 ID ADI92574 standard; DNA; 2517 BP.  
 DE Synthetic 5' nuclease DNA SEQ ID 127.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 42.09%  
 Best Local Similarity: 23.62%  
 Query Match: 6.55%  
 RESULT 1263  
 ID ABK62569 standard; cDNA; 3730 BP.  
 DE Rat sequence differentially expressed in response to a hepatotoxin #476.  
 PN WO200210453-A2.  
 PD 07-FEB-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 33.83%  
 Best Local Similarity: 23.74%  
 Query Match: 6.55%  
 RESULT 1264  
 ID ADS58760 standard; DNA; 3730 BP.  
 DE Toxicity-related gene, SEQ ID 3786.  
 PN WO2003064624-A2.  
 PD 07-AUG-2003.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 33.83%  
 Best Local Similarity: 23.74%  
 Query Match: 6.55%  
 RESULT 1265  
 ID ADP71852 standard; DNA; 3730 BP.  
 DE Renal toxin progression gene marker #441.  
 PN WO2004048598-A2.  
 PD 10-JUN-2004.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 33.83%  
 Best Local Similarity: 23.74%  
 Query Match: 6.55%  
 RESULT 1266  
 ID ADD40759 standard; cDNA; 3885 BP.  
 DE Renal toxin progression gene marker #441.  
 PN WO2004048598-A2.  
 PD 10-JUN-2004.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 33.83%  
 Best Local Similarity: 23.74%  
 Query Match: 6.55%  
 RESULT 1267  
 ID ADT46061 standard; cDNA; 1281 BP.  
 DE Bacterial polynucleotide #20812.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Percent Similarity: 35.79%  
 Best Local Similarity: 24.35%  
 Query Match: 6.55%  
 RESULT 1268  
 ID ADS56330 standard; cDNA; 2402 BP.  
 DE Bacterial polynucleotide #8317.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Percent Similarity: 32.73%  
 Best Local Similarity: 24.02%  
 Query Match: 6.55%  
 RESULT 1269  
 ID ACA45126 standard; DNA; 2487 BP.  
 DE Prokaryotic essential gene #26783.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 35.86%  
 Best Local Similarity: 23.03%  
 Query Match: 6.55%  
 RESULT 1270  
 ID ADI92574 standard; DNA; 2517 BP.  
 DE Synthetic 5' nuclease DNA SEQ ID 127.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 42.09%  
 Best Local Similarity: 23.62%  
 Query Match: 6.55%  
 RESULT 1271  
 ID ABK62569 standard; cDNA; 3730 BP.  
 DE Rat sequence differentially expressed in response to a hepatotoxin #476.  
 PN WO200210453-A2.  
 PD 07-FEB-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 33.83%  
 Best Local Similarity: 23.74%  
 Query Match: 6.55%  
 RESULT 1272  
 ID ADS58760 standard; DNA; 3730 BP.  
 DE Toxicity-related gene, SEQ ID 3786.  
 PN WO2003064624-A2.  
 PD 07-AUG-2003.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 33.83%  
 Best Local Similarity: 23.74%  
 Query Match: 6.55%  
 RESULT 1273  
 ID ADP71852 standard; DNA; 3730 BP.  
 DE Renal toxin progression gene marker #441.  
 PN WO2004048598-A2.  
 PD 10-JUN-2004.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 33.83%  
 Best Local Similarity: 23.74%  
 Query Match: 6.55%  
 RESULT 1274  
 ID ADD40759 standard; cDNA; 3885 BP.  
 DE Renal toxin progression gene marker #441.  
 PN WO2004048598-A2.  
 PD 10-JUN-2004.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 33.83%  
 Best Local Similarity: 23.74%  
 Query Match: 6.55%

DE Human tenascin-W coding sequence.  
 PN WO2003080663-A2.  
 PD 02-OCT-2003.  
 PA (NOVS ) NOVARTIS FORSCHUNGSSTIFTUNG ZWEIGNIEDERL.  
 Percent Similarity: 35.88%  
 Best Local Similarity: 27.57%  
 Query Match: 6.55%  
 RESULT 1267  
 ID ACN45195 standard; cDNA; 3885 BP.  
 DE Human mRNA sequence hCT15314.  
 PN WO2003073826-A2.  
 PD 12-SEP-2003.  
 PA (SAGR-) SAGRES DISCOVERY.  
 Percent Similarity: 35.88%  
 Best Local Similarity: 27.57%  
 Query Match: 6.55%  
 RESULT 1268  
 ID ADQ19282 standard; DNA; 4750 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2101.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Percent Similarity: 35.88%  
 Best Local Similarity: 27.57%  
 Query Match: 6.55%  
 RESULT 1269  
 ID ADR89531 standard; DNA; 4750 BP.  
 DE Apoptosis-inducing protein coding sequence, SEQ ID 55.  
 PN WO2004078112-A2.  
 PD 16-SEP-2004.  
 PA (ASAH-) ASAH KASEI PHARMA CORP.  
 Percent Similarity: 35.88%  
 Best Local Similarity: 27.57%  
 Query Match: 6.55%  
 RESULT 1270  
 ID ABK84242 standard; cDNA; 43599 BP.  
 DE Human cDNA differentially expressed in granulocytic cells #813.  
 PN WO200228999-A2.  
 PD 11-APR-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 35.61%  
 Best Local Similarity: 24.62%  
 Query Match: 6.55%  
 RESULT 1271  
 ID ADE86070 standard; DNA; 47988 BP.  
 DE Streptomyces hygrosopicus non-ribosomal peptide synthetase complex DNA.  
 PN WO2003082909-A1.  
 PD 09-OCT-2003.  
 PA (AMHP ) WYETH.  
 Percent Similarity: 38.10%  
 Best Local Similarity: 28.57%  
 Query Match: 6.55%  
 RESULT 1272  
 ID ABD02013 standard; DNA; 849 BP.  
 DE Pseudomonas aeruginosa polynucleotide #617.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 35.29%  
 Best Local Similarity: 26.80%  
 Query Match: 6.52%  
 RESULT 1273  
 ID ADS14773 standard; DNA; 933 BP.  
 DE Pseudomonas aeruginosa quorum sensing controlled gene PA2339, SEQ ID 328.  
 PN WO2004083385-A2.  
 PD 30-SEP-2004.  
 PA (IOWA ) UNIV IOWA RES FOUND.  
 Percent Similarity: 34.52%  
 Best Local Similarity: 26.90%  
 Query Match: 6.52%  
 RESULT 1274  
 ID AAD11173 standard; DNA; 1053 BP.  
 DE Pseudomonas stutzeri open reading frame-P (ORF-P) DNA.

PN WO200153309-A1.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 Percent Similarity: 37.80% Conservative: 17  
 Best Local Similarity: 29.67% Mismatches: 73  
 Query Match: 6.52% Indels: 57  
 RESULT 1282  
 ID ABD02082 standard; DNA; 2379 BP.  
 DE Pseudomonas aeruginosa polynucleotide #686.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 34.24% Conservative: 32  
 Best Local Similarity: 23.39% Mismatches: 87  
 Query Match: 6.52% Indels: 107  
 RESULT 1283  
 ID ABD02092 standard; DNA; 2499 BP.  
 DE Pseudomonas aeruginosa polynucleotide #696.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 34.24% Conservative: 32  
 Best Local Similarity: 23.39% Mismatches: 87  
 Query Match: 6.52% Indels: 107  
 RESULT 1284  
 ID ADI92882 standard; DNA; 2508 BP.  
 DE Construct TthAKK H641A DNA SEQ ID 435.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.33% Conservative: 33  
 Best Local Similarity: 24.91% Mismatches: 112  
 Query Match: 6.52% Indels: 74  
 RESULT 1285  
 ID ADI92548 standard; DNA; 2526 BP.  
 DE Synthetic 5' nuclease DNA SEQ ID 101.  
 PN WO200190337-A2.  
 PD 29-NOV-2001.  
 PA (THIR-) THIRD WAVE TECHNOLOGIES INC.  
 Percent Similarity: 36.30% Conservative: 32  
 Best Local Similarity: 25.34% Mismatches: 114  
 Query Match: 6.52% Indels: 74  
 RESULT 1286  
 ID ADI21750 standard; cDNA; 3212 BP.  
 DE Novel human protein cDNA #9.  
 PN WO2003025148-A2.  
 PD 27-MAR-2003.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 34.92% Conservative: 21  
 Best Local Similarity: 26.59% Mismatches: 83  
 Query Match: 6.52% Indels: 82  
 RESULT 1287  
 ID AA157998 standard; cDNA; 4071 BP.  
 DE Human polynucleotide SEQ ID NO 201.  
 PN WO200153312-A1.  
 PD 26-JUL-2001.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 38.63% Conservative: 26  
 Best Local Similarity: 27.47% Mismatches: 70  
 Query Match: 6.52% Indels: 74  
 RESULT 1288  
 ID AD807615 standard; DNA; 4989 BP.  
 DE Novel coding sequence (useful for identifying genetic disorders) #681.  
 PN WO2003054152-A2.  
 PD 03-JUL-2003.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 49.30% Conservative: 8  
 Best Local Similarity: 38.03% Mismatches: 24  
 Query Match: 6.52% Indels: 12  
 RESULT 1289  
 ID AB11939 standard; cDNA; 7335 BP.  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 30299.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.

PN WO200153309-A1.  
 PA (IDAH-) IDAHO RES FOUND INC.  
 Percent Similarity: 38.24% Conservative: 21  
 Best Local Similarity: 29.41% Mismatches: 88  
 Query Match: 6.52% Indels: 60  
 RESULT 1275  
 ID ADS14581 standard; DNA; 1377 BP.  
 DE Pseudomonas aeruginosa quorum sensing controlled gene PA2180, SEQ ID 136.  
 PN WO2004083385-A2.  
 PD 30-SEP-2004.  
 PA (IOWA) UNIV IOWA RES FOUND.  
 Percent Similarity: 35.91% Conservative: 30  
 Best Local Similarity: 25.84% Mismatches: 87  
 Query Match: 6.52% Indels: 104  
 RESULT 1276  
 ID ADH76980 standard; DNA; 1402 BP.  
 DE Human SOX18 related DNA.  
 PN US2002142415-A1.  
 PD 03-OCT-2002.  
 PA (KOOP/) KOOPMAN P A.  
 Percent Similarity: 35.76% Conservative: 37  
 Best Local Similarity: 22.92% Mismatches: 109  
 Query Match: 6.52% Indels: 78  
 RESULT 1277  
 ID ABD04496 standard; DNA; 1575 BP.  
 DE Pseudomonas aeruginosa polynucleotide #3100.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 40.00% Conservative: 23  
 Best Local Similarity: 29.55% Mismatches: 90  
 Query Match: 6.52% Indels: 42  
 RESULT 1278  
 ID ADS48122 standard; cDNA; 1803 BP.  
 DE Bacterial polynucleotide #2865.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Percent Similarity: 35.18% Conservative: 32  
 Best Local Similarity: 22.53% Mismatches: 81  
 Query Match: 6.52% Indels: 83  
 RESULT 1279  
 ID ABD17609 standard; DNA; 1866 BP.  
 DE Pseudomonas aeruginosa polynucleotide #16213.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 37.37% Conservative: 35  
 Best Local Similarity: 25.28% Mismatches: 80  
 Query Match: 6.52% Indels: 102  
 RESULT 1280  
 ID ABD04585 standard; DNA; 1956 BP.  
 DE Pseudomonas aeruginosa polynucleotide #3189.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 40.00% Conservative: 23  
 Best Local Similarity: 29.55% Mismatches: 90  
 Query Match: 6.52% Indels: 42  
 RESULT 1281  
 ID ADB63152 standard; cDNA; 2082 BP.  
 DE Human cDNA encoding clone SPLEN20043460.  
 PN EPI308459-A2.  
 PD 07-MAY-2003.  
 PA (HELI-) HELIX RES INST.

Percent Similarity: 34.27% Conservative: 34  
 Best Local Similarity: 22.38% Mismatches: 83  
 Query Match: 6.52% Indels: 106  
 RESULT 1290  
 ID AAH98395 standard; cDNA; 8836 BP.  
 DE Human EST-derived coding sequence SEQ ID NO: 252.  
 PN WO200154477-A2.  
 PD 02-AUG-2001.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 32.74% Conservative: 27  
 Best Local Similarity: 24.78% Mismatches: 90  
 Query Match: 6.52% Indels: 138  
 RESULT 1291  
 ID AAS36759 standard; DNA; 9745 BP.  
 DE Human cardiovascular system antigen genomic DNA SEQ ID NO 2259.  
 PN WO200155321-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 34.82% Conservative: 20  
 Best Local Similarity: 25.89% Mismatches: 74  
 Query Match: 6.52% Indels: 72  
 RESULT 1292  
 ID ADE47453 standard; DNA; 9745 BP.  
 DE Human cardiovascular system related genomic DNA #1019.  
 PN US2003059908-A1.  
 PD 27-MAR-2003.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 34.82% Conservative: 20  
 Best Local Similarity: 25.89% Mismatches: 74  
 Query Match: 6.52% Indels: 72  
 RESULT 1293  
 ID ADJ08871 standard; DNA; 9745 BP.  
 DE Human cardiovascular system associated polypeptide-related DNA SeqID2259.  
 PN US2004005575-A1.  
 PD 08-JAN-2004.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 34.82% Conservative: 20  
 Best Local Similarity: 25.89% Mismatches: 74  
 Query Match: 6.52% Indels: 72  
 RESULT 1294  
 ID ABL11938 standard; cDNA; 10026 BP.  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 30296.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Percent Similarity: 34.27% Conservative: 34  
 Best Local Similarity: 22.38% Mismatches: 83  
 Query Match: 6.52% Indels: 106  
 RESULT 1295  
 ID AAS36758 standard; DNA; 12149 BP.  
 DE Human cardiovascular system antigen genomic DNA SEQ ID NO 2258.  
 PN WO200155321-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 34.82% Conservative: 20  
 Best Local Similarity: 25.89% Mismatches: 74  
 Query Match: 6.52% Indels: 72  
 RESULT 1296  
 ID ADE47452 standard; DNA; 12149 BP.  
 DE Human cardiovascular system related genomic DNA #1018.  
 PN US2003059908-A1.  
 PD 27-MAR-2003.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 34.82% Conservative: 20  
 Best Local Similarity: 25.89% Mismatches: 74  
 Query Match: 6.52% Indels: 72  
 RESULT 1297  
 ID ADJ08870 standard; DNA; 12149 BP.  
 DE Human cardiovascular system associated polypeptide-related DNA SeqID2258.  
 PN US2004005575-A1.  
 PD 08-JAN-2004.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 34.82% Conservative: 20

Best Local Similarity: 25.89% Mismatches: 74  
 Query Match: 6.52% Indels: 72  
 RESULT 1298  
 ID ABZ74518 standard; DNA; 13361 BP.  
 DE Secreted protein gene 330 genomic fragment HTLCX82, SEQ ID NO:1665.  
 PN WO200277013-A2.  
 PD 03-OCT-2002.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 35.06% Conservative: 15  
 Best Local Similarity: 26.44% Mismatches: 60  
 Query Match: 6.52% Indels: 53  
 RESULT 1299  
 ID ADC20950 standard; DNA; 13361 BP.  
 DE Human secreted protein-related DNA sequence #368.  
 PN WO200292787-A2.  
 PD 21-NOV-2002.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 35.06% Conservative: 15  
 Best Local Similarity: 26.44% Mismatches: 60  
 Query Match: 6.52% Indels: 53  
 RESULT 1300  
 ID ADC26981 standard; DNA; 20922 BP.  
 DE Sorangium cellulosum tmbA gene cluster tmbB DNA.  
 PN US2003054547-A1.  
 PD 20-MAR-2003.  
 PA (JULI/) JULIEN B.  
 Percent Similarity: 34.55% Conservative: 25  
 Best Local Similarity: 25.45% Mismatches: 116  
 Query Match: 6.52% Indels: 65  
 RESULT 1301  
 ID ADQ97295 standard; DNA; 21293 BP.  
 DE Human cancer associated sequence HD08-027, SEQ ID 272.  
 PN WO2004060304-A2.  
 PD 22-JUL-2004.  
 PA (SAGR-) SAGRES DISCOVERY INC.  
 Percent Similarity: 35.06% Conservative: 15  
 Best Local Similarity: 26.44% Mismatches: 60  
 Query Match: 6.52% Indels: 53  
 RESULT 1302  
 ID AAD11177 standard; DNA; 25801 BP.  
 DE Pseudomonas stutzeri cosmid pT31 DNA.  
 PN WO200153309-A1.  
 PD 26-JUL-2001.  
 PA (IDAH-) IDAHO RES FOUND INC.  
 PA (PASZ/) PASZCZYNSKI A.  
 Percent Similarity: 38.24% Conservative: 21  
 Best Local Similarity: 29.41% Mismatches: 88  
 Query Match: 6.52% Indels: 60  
 RESULT 1303  
 ID ACN44790 standard; DNA; 98546 BP.  
 DE Human genomic sequence hCG23145.  
 PN WO2003073826-A2.  
 PD 12-SEP-2003.  
 PA (SAGR-) SAGRES DISCOVERY.  
 Percent Similarity: 33.45% Conservative: 24  
 Best Local Similarity: 24.91% Mismatches: 104  
 Query Match: 6.52% Indels: 83  
 RESULT 1304  
 Percent Similarity: 35.22% Conservative: 21  
 Best Local Similarity: 22.01% Mismatches: 48  
 Query Match: 6.52% Indels: 55  
 RESULT 1305  
 Percent Similarity: 35.22% Conservative: 21  
 Best Local Similarity: 22.01% Mismatches: 48  
 Query Match: 6.52% Indels: 55  
 RESULT 1306  
 Percent Similarity: 35.22% Conservative: 21  
 Best Local Similarity: 22.01% Mismatches: 48  
 Query Match: 6.52% Indels: 55  
 RESULT 1307  
 Percent Similarity: 35.22% Conservative: 21  
 Best Local Similarity: 22.01% Mismatches: 48

Query Match: 6.52% Indels: 55  
 RESULT 1308  
 Percent Similarity: 35.22% Conservative: 21  
 Best Local Similarity: 22.01% Mismatches: 48  
 Query Match: 6.52% Indels: 55  
 RESULT 1309  
 Percent Similarity: 35.22% Conservative: 21  
 Best Local Similarity: 22.01% Mismatches: 48  
 Query Match: 6.52% Indels: 55  
 RESULT 1310  
 Percent Similarity: 37.10% Conservative: 28  
 Best Local Similarity: 25.81% Mismatches: 112  
 Query Match: 6.52% Indels: 44  
 RESULT 1311  
 Percent Similarity: 37.10% Conservative: 28  
 Best Local Similarity: 25.81% Mismatches: 112  
 Query Match: 6.52% Indels: 44  
 RESULT 1312  
 Percent Similarity: 37.10% Conservative: 28  
 Best Local Similarity: 25.81% Mismatches: 112  
 Query Match: 6.52% Indels: 44  
 RESULT 1313  
 Percent Similarity: 37.10% Conservative: 28  
 Best Local Similarity: 25.81% Mismatches: 112  
 Query Match: 6.52% Indels: 44  
 RESULT 1314  
 Percent Similarity: 37.10% Conservative: 28  
 Best Local Similarity: 25.81% Mismatches: 112  
 Query Match: 6.52% Indels: 44  
 RESULT 1315  
 Percent Similarity: 37.10% Conservative: 28  
 Best Local Similarity: 25.81% Mismatches: 112  
 Query Match: 6.52% Indels: 44  
 RESULT 1316  
 Percent Similarity: 37.10% Conservative: 28  
 Best Local Similarity: 25.81% Mismatches: 112  
 Query Match: 6.52% Indels: 44  
 RESULT 1317  
 Percent Similarity: 37.10% Conservative: 28  
 Best Local Similarity: 25.81% Mismatches: 112  
 Query Match: 6.52% Indels: 44  
 RESULT 1318  
 Percent Similarity: 37.10% Conservative: 28  
 Best Local Similarity: 25.81% Mismatches: 112  
 Query Match: 6.52% Indels: 44  
 RESULT 1319  
 Percent Similarity: 35.22% Conservative: 21  
 Best Local Similarity: 22.01% Mismatches: 48  
 Query Match: 6.52% Indels: 55  
 RESULT 1320  
 Percent Similarity: 35.22% Conservative: 21  
 Best Local Similarity: 22.01% Mismatches: 48  
 Query Match: 6.52% Indels: 55  
 RESULT 1321  
 ID ADL13684 standard; DNA; 247509 BP.  
 DE Osteoarthritis-associated polymorphic nucleotide #216.  
 PN WO2003054166-A2.  
 PD 03-JUL-2003.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Percent Similarity: 34.82% Conservative: 20  
 Best Local Similarity: 25.89% Mismatches: 74  
 Query Match: 6.52% Indels: 72  
 RESULT 1322  
 ID ADS61562 standard; cDNA; 660 BP.  
 DE Bacterial polynucleotide #13549.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Percent Similarity: 42.68% Conservative: 28

Best Local Similarity: 25.61% Mismatches: 54  
 Query Match: 6.48% Indels: 40  
 RESULT 1323  
 ID ABD08014 standard; DNA; 930 BP.  
 DE Pseudomonas aeruginosa polynucleotide #6618.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 35.53% Conservative: 19  
 Best Local Similarity: 27.19% Mismatches: 106  
 Query Match: 6.48% Indels: 41  
 RESULT 1324  
 ID ACA36198 standard; DNA; 1027 BP.  
 DE Prokaryotic essential gene #17855.  
 PN WO20027183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 37.32% Conservative: 34  
 Best Local Similarity: 25.35% Mismatches: 105  
 Query Match: 6.48% Indels: 73  
 RESULT 1325  
 ID AAZ91271 standard; DNA; 1074 BP.  
 DE Nucleotide sequence fccr SEQ ID NO:36.  
 PN WO200004158-A2.  
 PD 27-JAN-2000.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Percent Similarity: 37.76% Conservative: 39  
 Best Local Similarity: 24.13% Mismatches: 101  
 Query Match: 6.48% Indels: 79  
 RESULT 1326  
 ID ABD15610 standard; DNA; 1158 BP.  
 DE Pseudomonas aeruginosa polynucleotide #14214.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 35.65% Conservative: 22  
 Best Local Similarity: 26.09% Mismatches: 91  
 Query Match: 6.48% Indels: 58  
 RESULT 1327  
 ID ABD08045 standard; DNA; 1308 BP.  
 DE Pseudomonas aeruginosa polynucleotide #6649.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 35.53% Conservative: 19  
 Best Local Similarity: 27.19% Mismatches: 106  
 Query Match: 6.48% Indels: 41  
 RESULT 1328  
 ID AAZ91259 standard; DNA; 1377 BP.  
 DE CoA ligase fccf nucleotide sequence SEQ ID NO:12.  
 PN WO200004158-A2.  
 PD 27-JAN-2000.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Percent Similarity: 37.76% Conservative: 39  
 Best Local Similarity: 24.13% Mismatches: 101  
 Query Match: 6.48% Indels: 79  
 RESULT 1329  
 ID AAT74890 standard; DNA; 1535 BP.  
 DE Human neurogenic differentiation protein (NeuroD2) DNA clone 14B1.  
 PN WO9716548-A1.  
 PD 09-MAY-1997.  
 PA (WEIN/) HUTCHINSON CANCER RES CENT FRED.  
 PA (WEIN/) WEINTRAUB N.  
 Percent Similarity: 38.71% Conservative: 11  
 Best Local Similarity: 31.61% Mismatches: 59  
 Query Match: 6.48% Indels: 36  
 RESULT 1330  
 ID AAV42931 standard; DNA; 1535 BP.  
 DE DNA encoding human neuroD2 protein, which is a bHLH protein.  
 PN US5795723-A.  
 PD 18-AUG-1998.  
 PA (HUTC-) HUTCHINSON CANCER RES CENT FRED.  
 Percent Similarity: 38.71% Conservative: 11

Best Local Similarity: 31.61% Mismatches: 59  
 Query Match: 6.48% Indels: 36  
 RESULT 1331  
 ID ABS56389 standard; DNA; 1535 BP.  
 DE Human BHLH family neuroD2 genomic DNA, clone 14B1.  
 PN US6444463-B1.  
 PD 03-SEP-2002.  
 PA (HUTC-) HUTCHINSON CANCER RES CENT FRED.  
 Percent Similarity: 38.71% Conservative: 11  
 Best Local Similarity: 31.61% Mismatches: 59  
 Query Match: 6.48% Indels: 36  
 RESULT 1332  
 ID ADP72550 standard; DNA; 1580 BP.  
 DE Renal toxin progression gene marker #1139.  
 PN WO2004048598-A2.  
 PD 10-JUN-2004.  
 PA (GENE-) GENE LOGIC INC.  
 Percent Similarity: 34.11% Conservative: 31  
 Best Local Similarity: 22.09% Mismatches: 79  
 Query Match: 6.48% Indels: 91  
 RESULT 1333  
 ID ABZ11712 standard; cDNA; 1625 BP.  
 DE Human polynucleotide SEQ ID NO 594.  
 PN WO200270539-A2.  
 PD 12-SEP-2002.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 41.10% Conservative: 39  
 Best Local Similarity: 24.58% Mismatches: 84  
 Query Match: 6.48% Indels: 55  
 RESULT 1334  
 ID ADM44230 standard; cDNA; 1625 BP.  
 DE Novel human arginine-rich protein cDNA #594.  
 PN US2004053250-A1.  
 PD 18-MAR-2004.  
 PA (TANG/) TANG Y T.  
 PA (XUE/) XUE A.  
 PA (DRNA/) DRMANAC R T.  
 Percent Similarity: 41.10% Conservative: 39  
 Best Local Similarity: 24.58% Mismatches: 84  
 Query Match: 6.48% Indels: 55  
 RESULT 1335  
 ID ABD11546 standard; DNA; 1650 BP.  
 DE Pseudomonas aeruginosa polynucleotide #10150.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 33.91% Conservative: 29  
 Best Local Similarity: 23.88% Mismatches: 83  
 Query Match: 6.48% Indels: 108  
 RESULT 1336  
 ID ABD11322 standard; DNA; 1725 BP.  
 DE Pseudomonas aeruginosa polynucleotide #9926.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 33.91% Conservative: 29  
 Best Local Similarity: 23.88% Mismatches: 83  
 Query Match: 6.48% Indels: 108  
 RESULT 1337  
 ID ABD14631 standard; DNA; 2145 BP.  
 DE Pseudomonas aeruginosa polynucleotide #13235.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 32.99% Conservative: 24  
 Best Local Similarity: 24.83% Mismatches: 112  
 Query Match: 6.48% Indels: 85  
 RESULT 1338  
 ID ADA52692 standard; cDNA; 2198 BP.  
 DE Human coding sequence, SEQ ID 260.  
 PN EP1293569-A2.  
 PD 19-MAR-2003.  
 PA (HELI-) HELIX RES INST.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 Percent Similarity: 37.44% Conservative: 20  
 Best Local Similarity: 27.59% Mismatches: 49  
 Query Match: 6.48% Indels: 78  
 RESULT 1339  
 ID ABL24533 standard; DNA; 2244 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 25072.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Percent Similarity: 41.61% Conservative: 22  
 Best Local Similarity: 26.85% Mismatches: 58  
 Query Match: 6.48% Indels: 29  
 RESULT 1340  
 ID ABA97188 standard; DNA; 2326 BP.  
 DE Goat lactoferrin-associated DNA #2.  
 PN KR98043944-A.  
 PD 05-SEP-1998.  
 PA (KOAD) KOREA ADV INST SCI & TECHNOLOGY.  
 Percent Similarity: 34.95% Conservative: 27  
 Best Local Similarity: 25.61% Mismatches: 97  
 Query Match: 6.48% Indels: 91  
 RESULT 1341  
 ID ACC77593 standard; DNA; 3026 BP.  
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 39.38% Conservative: 37  
 Best Local Similarity: 26.71% Mismatches: 97  
 Query Match: 6.48% Indels: 81  
 RESULT 1342  
 ID ACC77767 standard; DNA; 3026 BP.  
 DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 38.14% Conservative: 38  
 Best Local Similarity: 25.09% Mismatches: 102  
 Query Match: 6.48% Indels: 79  
 RESULT 1343  
 ID AAH02112 standard; DNA; 3297 BP.  
 DE Mycobacterium tuberculosis nucleotide sequence SEQ ID NO:2105.  
 PN WO200123604-A2.  
 PD 05-APR-2001.  
 PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.  
 Percent Similarity: 36.73% Conservative: 24  
 Best Local Similarity: 26.94% Mismatches: 100  
 Query Match: 6.48% Indels: 56  
 RESULT 1344  
 ID AAH52090 standard; DNA; 3297 BP.  
 DE Mycobacterium tuberculosis potential drug target gene SEQ ID 144.  
 PN WO200135317-A1.  
 PD 17-MAY-2001.  
 PA (REGC) UNIV CALIFORNIA.  
 Percent Similarity: 36.73% Conservative: 24  
 Best Local Similarity: 26.94% Mismatches: 100  
 Query Match: 6.48% Indels: 56  
 RESULT 1345  
 ID ACH97234 standard; DNA; 3390 BP.  
 DE Klebsiella pneumoniae polynucleotide seqid 3029.  
 PN US6610836-B1.  
 PD 26-AUG-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 26.88% Conservative: 26  
 Best Local Similarity: 20.58% Mismatches: 101  
 Query Match: 6.48% Indels: 201  
 RESULT 1346  
 ID ABD07965 standard; DNA; 3741 BP.  
 DE Pseudomonas aeruginosa polynucleotide #6569.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.



Percent Similarity: 35.53% Conservative: 19  
 Best Local Similarity: 27.19% Mismatches: 106  
 Query Match: 6.48% Indels: 41  
 RESULT 1347  
 ID AAI59784 standard; cDNA; 3913 BP.  
 DE Human polynucleotide SEQ ID NO 3773.  
 PN WO20015312-A1.  
 PD 26-JUL-2001.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 38.57% Conservative: 25  
 Best Local Similarity: 27.35% Mismatches: 64  
 Query Match: 6.48% Indels: 74  
 RESULT 1348  
 ID ABD14252 standard; DNA; 4431 BP.  
 DE Pseudomonas aeruginosa polynucleotide #12856.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 30.34% Conservative: 16  
 Best Local Similarity: 24.34% Mismatches: 79  
 Query Match: 6.48% Indels: 109  
 RESULT 1349  
 ID ABL24532 standard; DNA; 4649 BP.  
 DE Drophiella melanogaster genomic polynucleotide SEQ ID NO 25069.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PERE-) PE CORP NY.  
 Percent Similarity: 41.61% Conservative: 22  
 Best Local Similarity: 26.85% Mismatches: 58  
 Query Match: 6.48% Indels: 29  
 RESULT 1350  
 ID AAS59642 standard; DNA; 5870 BP.  
 DE Propionibacterium acnes immunogenic protein encoding DNA #137.  
 PN WO200181581-A2.  
 PD 01-NOV-2001.  
 PA (CORI-) CORIXA CORP.  
 Percent Similarity: 36.22% Conservative: 25  
 Best Local Similarity: 26.38% Mismatches: 87  
 Query Match: 6.48% Indels: 75  
 RESULT 1351  
 ID ACF64571 standard; DNA; 5870 BP.  
 DE Propionibacterium acnes DNA contig sequence #137.  
 PN WO2003033515-A1.  
 PD 24-APR-2003.  
 PA (CORI-) CORIXA CORP.  
 Percent Similarity: 36.22% Conservative: 25  
 Best Local Similarity: 26.38% Mismatches: 87  
 Query Match: 6.48% Indels: 75  
 RESULT 1352  
 ID ADP55748 standard; cDNA; 5908 BP.  
 DE Human PRO cDNA sequence SEQ ID NO:1724.  
 PN WO2004039956-A2.  
 PD 13-MAY-2004.  
 PA (GETH) GENENTECH INC.  
 Percent Similarity: 34.44% Conservative: 22  
 Best Local Similarity: 25.31% Mismatches: 95  
 Query Match: 6.48% Indels: 64  
 RESULT 1353  
 ID ADH13157 standard; DNA; 6131 BP.  
 DE Human malignant neoplasia-related gene SeqID6.  
 PN EP1365034-A2.  
 PD 26-NOV-2003.  
 PA (FARB) BAYER AG.  
 Percent Similarity: 38.71% Conservative: 11  
 Best Local Similarity: 31.61% Mismatches: 59  
 Query Match: 6.48% Indels: 36  
 RESULT 1354  
 ID ACA26658 standard; DNA; 7802 BP.  
 DE Prokaryotic essential gene #8315.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 33.33% Conservative: 23

Best Local Similarity: 24.21% Mismatches: 90  
 Query Match: 6.48% Indels: 78  
 RESULT 1355  
 ID AAV58938 standard; DNA; 10095 BP.  
 DE Mycobacterium tuberculosis embCAB operon.  
 PN WO9841533-A1.  
 PD 24-SEP-1998.  
 PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.  
 Percent Similarity: 36.73% Conservative: 24  
 Best Local Similarity: 26.94% Mismatches: 100  
 Query Match: 6.48% Indels: 56  
 RESULT 1356  
 ID ADN36912 standard; DNA; 20640 BP.  
 DE X. albilineans XALB1 gene cluster DNA encoding protein AlBI.  
 PN WO2004035760-A2.  
 PD 29-APR-2004.  
 PA (UYFL) UNIV FLORIDA.  
 Percent Similarity: 38.13% Conservative: 32  
 Best Local Similarity: 25.68% Mismatches: 116  
 Query Match: 6.48% Indels: 44  
 RESULT 1357  
 ID AAZ91253 standard; DNA; 24494 BP.  
 DE Bacterium 2412.1 fumonisin-catabolising gene cluster.  
 PN WO200004158-A2.  
 PD 27-JAN-2000.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Percent Similarity: 37.76% Conservative: 39  
 Best Local Similarity: 24.13% Mismatches: 101  
 Query Match: 6.48% Indels: 79  
 RESULT 1358  
 ID ADN36893 standard; DNA; 55839 BP.  
 DE X. albilineans XALB1 gene cluster DNA.  
 PN WO2004035760-A2.  
 PD 29-APR-2004.  
 PA (UYFL) UNIV FLORIDA.  
 Percent Similarity: 38.13% Conservative: 32  
 Best Local Similarity: 25.68% Mismatches: 116  
 Query Match: 6.48% Indels: 44  
 RESULT 1359  
 ID ADC26995 standard; DNA; 67251 BP.  
 DE Sorangium cellulosum tmbA gene cluster.  
 PN US2003054547-A1.  
 PD 20-MAR-2003.  
 PA (JULI/) JULIEN B.  
 Percent Similarity: 40.59% Conservative: 28  
 Best Local Similarity: 26.73% Mismatches: 71  
 Query Match: 6.48% Indels: 50  
 RESULT 1360  
 Percent Similarity: 37.03% Conservative: 43  
 Best Local Similarity: 23.42% Mismatches: 107  
 Query Match: 6.48% Indels: 93  
 RESULT 1361  
 Percent Similarity: 36.73% Conservative: 24  
 Best Local Similarity: 26.94% Mismatches: 100  
 Query Match: 6.48% Indels: 56  
 RESULT 1362  
 Percent Similarity: 37.03% Conservative: 43  
 Best Local Similarity: 23.42% Mismatches: 107  
 Query Match: 6.48% Indels: 93  
 RESULT 1363  
 Percent Similarity: 36.73% Conservative: 24  
 Best Local Similarity: 26.94% Mismatches: 100  
 Query Match: 6.48% Indels: 56  
 RESULT 1364  
 Percent Similarity: 49.53% Conservative: 23  
 Best Local Similarity: 28.04% Mismatches: 36  
 Query Match: 6.48% Indels: 18  
 RESULT 1365  
 ID ABZ38468 standard; DNA; 507 BP.  
 DE N. gonorrhoeae nucleotide sequence SEQ ID 1525.  
 PN WO200279243-A2.

PD 10-OCT-2002.  
 PA (CHIR-) CHIRON SPA. Conservative: 26  
 Percent Similarity: 43.4%  
 Best Local Similarity: 27.9%  
 Query Match: 6.44%  
 Indels: 31  
 RESULT 1366  
 ID AC339058 standard; DNA; 855 BP.  
 DE Prokaryotic essential gene #20715.  
 PN WO20027183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC. Conservative: 20  
 Percent Similarity: 44.2%  
 Best Local Similarity: 27.8%  
 Query Match: 6.44%  
 Indels: 15  
 RESULT 1367  
 ID ADL03828 standard; DNA; 888 BP.  
 DE DNA encoding a M. catarrhalis protein #1514.  
 PN US6673910-B1.  
 PD 06-JAN-2004.  
 PA (GENO-) GENOME THERAPEUTICS CORP. Conservative: 20  
 Percent Similarity: 44.2%  
 Best Local Similarity: 27.8%  
 Query Match: 6.44%  
 Indels: 15  
 RESULT 1368  
 ID AAH65144 standard; DNA; 921 BP.  
 DE C glutamicum coding sequence fragment SEQ ID NO: 179.  
 PN EP1108790-A2.  
 PD 20-JUN-2001.  
 PA (KYOM) KYOMA HAKKO KOGYO KK. Conservative: 31  
 Percent Similarity: 35.7%  
 Best Local Similarity: 23.2%  
 Query Match: 6.44%  
 Indels: 68  
 RESULT 1369  
 ID ABD12950 standard; DNA; 1086 BP.  
 DE Pseudomonas aeruginosa polynucleotide #11554.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP. Conservative: 16  
 Percent Similarity: 39.1%  
 Best Local Similarity: 31.6%  
 Query Match: 6.44%  
 Indels: 40  
 RESULT 1370  
 ID ABD05166 standard; DNA; 1251 BP.  
 DE Pseudomonas aeruginosa polynucleotide #3770.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP. Conservative: 20  
 Percent Similarity: 39.7%  
 Best Local Similarity: 28.0%  
 Query Match: 6.44%  
 Indels: 35  
 RESULT 1371  
 ID ABD07415 standard; DNA; 1425 BP.  
 DE Pseudomonas aeruginosa polynucleotide #6019.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP. Conservative: 34  
 Percent Similarity: 35.9%  
 Best Local Similarity: 24.2%  
 Query Match: 6.44%  
 Indels: 89  
 RESULT 1372  
 ID ADJ48292 standard; DNA; 1428 BP.  
 DE Maize oil-associated gene #110.  
 PN US2004025202-A1.  
 PD 05-FEB-2004.  
 PA (LAUR/) LAURIE C C. Conservative: 27  
 PA (RAVA/) RAVANELLO M. Mismatches: 78  
 PA (SAVA/) SAVAGE T. Indels: 97  
 PA (LEDE/) LEDEAUX J R.  
 PA (ROGE/) ROGERS J A.  
 Percent Similarity: 36.8%  
 Best Local Similarity: 27.0%  
 Query Match: 6.44%  
 Indels: 97  
 RESULT 1373

ID AAF59130 standard; DNA; 1546 BP.  
 DE Streptomyces sp. SK glucose isomerase nucleotide sequence SEQ ID NO:1.  
 PN JP2000333684-A.  
 PD 05-DEC-2000.  
 PA (NOVO) NOVO NORDISK AS. Conservative: 28  
 Percent Similarity: 36.7%  
 Best Local Similarity: 26.5%  
 Query Match: 6.44%  
 Indels: 98  
 RESULT 1374  
 ID AAS71366 standard; cDNA; 1588 BP.  
 DE DNA encoding novel human diagnostic protein #7170.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC. Conservative: 8  
 Percent Similarity: 43.4%  
 Best Local Similarity: 35.8%  
 Query Match: 6.44%  
 Indels: 31  
 RESULT 1375  
 ID ABT18484 standard; DNA; 1666 BP.  
 DE Aspergillus fumigatus essential gene #842.  
 PN WO200286090-A2.  
 PD 31-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC. Conservative: 29  
 Percent Similarity: 33.7%  
 Best Local Similarity: 22.4%  
 Query Match: 6.44%  
 Indels: 81  
 RESULT 1376  
 ID ACH96895 standard; DNA; 1707 BP.  
 DE Klebsiella pneumoniae polynucleotide seqid 2690.  
 PN US6610836-B1.  
 PD 26-AUG-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP. Conservative: 24  
 Percent Similarity: 37.8%  
 Best Local Similarity: 28.5%  
 Query Match: 6.44%  
 Indels: 68  
 RESULT 1377  
 ID ABD07686 standard; DNA; 1989 BP.  
 DE Pseudomonas aeruginosa polynucleotide #6290.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP. Conservative: 34  
 Percent Similarity: 35.9%  
 Best Local Similarity: 24.2%  
 Query Match: 6.44%  
 Indels: 89  
 RESULT 1378  
 ID ADQ23026 standard; DNA; 1990 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5846.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC. Conservative: 20  
 Percent Similarity: 33.9%  
 Best Local Similarity: 25.4%  
 Query Match: 6.44%  
 Indels: 75  
 RESULT 1379  
 ID ADM47721 standard; DNA; 2005 BP.  
 DE Polynucleotide sequence #139 useful in producing transgenic plants.  
 PN US2003233670-A1.  
 PD 18-DEC-2003.  
 PA (EDGE/) EDGERTON M D. Conservative: 23  
 PA (CHOM/) CHOMET P S. Mismatches: 81  
 PA (LACC/) LACCETTI L B. Indels: 76  
 Percent Similarity: 35.3%  
 Best Local Similarity: 25.9%  
 Query Match: 6.44%  
 Indels: 76  
 RESULT 1380  
 ID ADB6264 standard; cDNA; 2165 BP.  
 DE Human cDNA encoding clone CTONG20189000.  
 PN EP1308459-A2.  
 PD 07-MAY-2003.  
 PA (HELI-) HELIX RES INST. Conservative: 21  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY. Mismatches: 84  
 Percent Similarity: 38.8%  
 Best Local Similarity: 28.6%  
 Query Match: 6.44%  
 Indels: 84  
 RESULT 1381

Query Match: 6.44% Indels: 43  
 RESULT 1381  
 ID ABD02122 standard; DNA; 2367 BP.  
 DE Pseudomonas aeruginosa polynucleotide #726.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 38.89% Conservative: 28  
 Best Local Similarity: 25.93% Mismatches: 65  
 Query Match: 6.44% Indels: 67  
 RESULT 1382  
 ID ABA00886 standard; DNA; 2502 BP.  
 DE Novel TepJ51 DNA polymerase coding sequence.  
 PN WO2003004632-A2.  
 PD 16-JAN-2003.  
 PA (AMSH ) AMERSHAM BIOSCIENCES CORP.  
 Percent Similarity: 34.44% Conservative: 22  
 Best Local Similarity: 26.30% Mismatches: 94  
 Query Match: 6.44% Indels: 83  
 RESULT 1383  
 ID AAS22249 standard; cDNA; 2740 BP.  
 DE cDNA sequence #36 encoding novel human secreted protein.  
 PN WO200177291-A2.  
 PD 18-OCT-2001.  
 PA (GEMY ) GENETICS INST INC.  
 Percent Similarity: 37.44% Conservative: 24  
 Best Local Similarity: 26.07% Mismatches: 92  
 Query Match: 6.44% Indels: 40  
 RESULT 1384  
 ID ACN37277 standard; cDNA; 2779 BP.  
 DE Tumour-associated antigenic target (TAT) cDNA DNA323744, SEQ ID NO:55.  
 PN WO2004030615-A2.  
 PD 15-APR-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 38.83% Conservative: 21  
 Best Local Similarity: 28.64% Mismatches: 84  
 Query Match: 6.44% Indels: 43  
 RESULT 1385  
 ID AAR32326 standard; DNA; 3049 BP.  
 DE Thermus flavus DNA polymerase I coding sequence.  
 PN WO9614417-A1.  
 PD 17-MAY-1996.  
 PA (MOLE-) MOLECULAR BIOLOGY RESOURCES INC.  
 Percent Similarity: 36.86% Conservative: 32  
 Best Local Similarity: 25.94% Mismatches: 112  
 Query Match: 6.44% Indels: 75  
 RESULT 1386  
 ID AAD29059 standard; cDNA; 3075 BP.  
 DE Human guanine nucleotide exchange factor (GEF) 32529 cDNA.  
 PN WO200206325-A2.  
 PD 24-JAN-2002.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Percent Similarity: 38.83% Conservative: 21  
 Best Local Similarity: 28.64% Mismatches: 84  
 Query Match: 6.44% Indels: 43  
 RESULT 1387  
 ID ADQ85401 standard; cDNA; 3148 BP.  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #2215.  
 PN WO2004060270-A2.  
 PD 22-JUL-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 41.70% Conservative: 24  
 Best Local Similarity: 30.94% Mismatches: 75  
 Query Match: 6.44% Indels: 57  
 RESULT 1388  
 ID ACN39921 standard; cDNA; 3148 BP.  
 DE Tumour-associated antigenic target (TAT) cDNA DNA326094, SEQ ID NO:4368.  
 PN WO2004030615-A2.  
 PD 15-APR-2004.  
 PA (GETH ) GENENTECH INC.  
 Percent Similarity: 41.70% Conservative: 24

Best Local Similarity: 30.94% Mismatches: 75  
 Query Match: 6.44% Indels: 57  
 RESULT 1389  
 ID ADI81640 standard; DNA; 3213 BP.  
 DE Malaria mosquito DNA encoding protein ebiP7471.  
 PN US2004009537-A1.  
 PD 15-JAN-2004.  
 PA (ROOS/) ROOS J.  
 PA (STAU/) STAUDERMAN K.  
 PA (VELI/) VELICELEBI G.  
 Percent Similarity: 41.97% Conservative: 34  
 Best Local Similarity: 29.56% Mismatches: 90  
 Query Match: 6.44% Indels: 69  
 RESULT 1390  
 ID ACC77949 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.30% Conservative: 33  
 Best Local Similarity: 25.00% Mismatches: 114  
 Query Match: 6.44% Indels: 74  
 RESULT 1391  
 ID ACC77952 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.30% Conservative: 33  
 Best Local Similarity: 25.00% Mismatches: 114  
 Query Match: 6.44% Indels: 74  
 RESULT 1392  
 ID ACC77959 standard; DNA; 3221 BP.  
 DE Thermus thermophilus mutant DNA polymerase encoding DNA.  
 PN WO2003025132-A2.  
 PD 27-MAR-2003.  
 PA (INVI-) INVITROGEN CORP.  
 Percent Similarity: 36.30% Conservative: 33  
 Best Local Similarity: 25.00% Mismatches: 114  
 Query Match: 6.44% Indels: 74  
 RESULT 1393  
 ID ABT17890 standard; DNA; 3666 BP.  
 DE Aspergillus fumigatus essential gene #248.  
 PN WO200286090-A2.  
 PD 31-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 33.72% Conservative: 29  
 Best Local Similarity: 22.48% Mismatches: 90  
 Query Match: 6.44% Indels: 81  
 RESULT 1394  
 ID ADC10041 standard; DNA; 3721 BP.  
 DE Human NOVX polypeptide coding sequence SEQ ID NO: 61.  
 PN WO200300842-A2.  
 PD 03-JAN-2003.  
 PA (CURA-) CURAGEN CORP.  
 Percent Similarity: 41.70% Conservative: 24  
 Best Local Similarity: 30.94% Mismatches: 75  
 Query Match: 6.44% Indels: 57  
 RESULT 1395  
 ID ABD05211 standard; DNA; 3825 BP.  
 DE Pseudomonas aeruginosa polynucleotide #3815.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 39.77% Conservative: 20  
 Best Local Similarity: 28.07% Mismatches: 68  
 Query Match: 6.44% Indels: 35  
 RESULT 1396  
 ID ABD05091 standard; DNA; 4506 BP.  
 DE Pseudomonas aeruginosa polynucleotide #3695.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.

Percent Similarity: 39.77% Conservative: 20  
 Best Local Similarity: 28.07% Mismatches: 68  
 Query Match: 6.44% Indels: 35  
 RESULT 1397  
 ID AAC86156 standard; cDNA; 4815 BP.  
 DE FCTR4 nucleic acid.  
 PN WO200146231-A2.  
 PD 28-JUN-2001.  
 PA (CURA-) CURAGEN CORP.  
 Percent Similarity: 38.83% Conservative: 21  
 Best Local Similarity: 28.64% Mismatches: 84  
 Query Match: 6.44% Indels: 43  
 RESULT 1398  
 ID ADR24186 standard; DNA; 5285 BP.  
 DE Breast cancer prognosis marker #47.  
 PN WO2004065545-A2.  
 PD 05-AUG-2004.  
 PA (ROSE-) ROSETTA INPHARMATICS LLC.  
 PA (NECA-) NETHERLANDS CANCER INST.  
 Percent Similarity: 37.44% Conservative: 24  
 Best Local Similarity: 26.07% Mismatches: 92  
 Query Match: 6.44% Indels: 40  
 RESULT 1399  
 ID AAD27271 standard; cDNA; 5540 BP.  
 DE Human transporter and ion channel-18 (TRICH-18) cDNA.  
 PN WO200192304-A2.  
 PD 06-DEC-2001.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Percent Similarity: 37.44% Conservative: 24  
 Best Local Similarity: 26.07% Mismatches: 92  
 Query Match: 6.44% Indels: 40  
 RESULT 1400  
 ID AAD54236 standard; DNA; 6297 BP.  
 DE Streptomyces amphibiosporus lactimidomycin ORF6 DNA.  
 PN WO200288176-A2.  
 PD 07-NOV-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Percent Similarity: 39.06% Conservative: 30  
 Best Local Similarity: 26.18% Mismatches: 90  
 Query Match: 6.44% Indels: 55  
 RESULT 1401  
 ID AAT06768 standard; DNA; 7000 BP.  
 DE Pseudomonas fluorescens pyrrolnitrin gene cluster.  
 PN WO9533818-A2.  
 PD 14-DEC-1995.  
 PA (CIBA ) CIBA GEIGY AG.  
 Percent Similarity: 30.22% Conservative: 18  
 Best Local Similarity: 23.74% Mismatches: 76  
 Query Match: 6.44% Indels: 118  
 RESULT 1402  
 ID AAT89955 standard; DNA; 7001 BP.  
 DE Pseudomonas fluorescens pyrrolnitrin gene cluster genomic DNA.  
 PN US5662898-A.  
 PD 02-SEP-1997.  
 PA (CIBA ) CIBA GEIGY CORP.  
 Percent Similarity: 30.22% Conservative: 18  
 Best Local Similarity: 23.74% Mismatches: 76  
 Query Match: 6.44% Indels: 118  
 RESULT 1403  
 ID AAV58730 standard; DNA; 7001 BP.  
 DE Pyrrolnitrin gene region.  
 PN US5817502-A.  
 PD 06-OCT-1998.  
 PA (NOVS ) NOVARTIS FINANCE CORP.  
 Percent Similarity: 30.22% Conservative: 18  
 Best Local Similarity: 23.74% Mismatches: 76  
 Query Match: 6.44% Indels: 118  
 RESULT 1404  
 ID AAV39840 standard; DNA; 7001 BP.  
 DE Pseudomonas fluorescens pyrrolnitrin gene cluster.  
 PN WO9824919-A1.  
 PD 11-JUN-1998.  
 PA (NOVS ) NOVARTIS AG.

Percent Similarity: 30.22% Conservative: 18  
 Best Local Similarity: 23.74% Mismatches: 76  
 Query Match: 6.44% Indels: 118  
 RESULT 1405  
 ID AAX9371 standard; DNA; 7001 BP.  
 DE P. fluorescens pyrrolnitrin gene cluster sequence.  
 PN US955348-A.  
 PD 21-SEP-1999.  
 PA (NOVS ) NOVARTIS AG.  
 Percent Similarity: 30.22% Conservative: 18  
 Best Local Similarity: 23.74% Mismatches: 76  
 Query Match: 6.44% Indels: 118  
 RESULT 1406  
 ID AAAV5298 standard; DNA; 7001 BP.  
 DE DNA sequence of Pseudomonas fluorescens pyrrolnitrin gene region.  
 PN US6117670-A.  
 PD 12-SEP-2000.  
 PA (NOVS ) NOVARTIS FINANCE CORP.  
 Percent Similarity: 30.22% Conservative: 18  
 Best Local Similarity: 23.74% Mismatches: 76  
 Query Match: 6.44% Indels: 118  
 RESULT 1407  
 ID AAD36299 standard; cDNA; 7610 BP.  
 DE Human transporter and ion channel (TRICH) 2 cDNA.  
 PN WO200222684-A2.  
 PD 21-MAR-2002.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Percent Similarity: 37.44% Conservative: 24  
 Best Local Similarity: 26.07% Mismatches: 92  
 Query Match: 6.44% Indels: 40  
 RESULT 1408  
 ID ACD28255 standard; DNA; 7697 BP.  
 DE Mouse soluble guanylyl cyclase sGC associated DNA #2.  
 PN US2003096240-A1.  
 PD 22-MAY-2003.  
 PA (MURA/) MURAD F.  
 PA (SHAR/) SHARINA I G.  
 PA (KRUM/) KRUMENACKER J S.  
 PA (MART/) MARTIN E.  
 Percent Similarity: 41.73% Conservative: 19  
 Best Local Similarity: 28.06% Mismatches: 53  
 Query Match: 6.44% Indels: 28  
 RESULT 1409  
 ID ADL33384 standard; DNA; 7706 BP.  
 DE Human transporter and ion channel (TRICH) gene #29.  
 PN WO2003083085-A2.  
 PD 09-OCT-2003.  
 PA (INCY-) INCYTE CORP.  
 Percent Similarity: 37.44% Conservative: 24  
 Best Local Similarity: 26.07% Mismatches: 92  
 Query Match: 6.44% Indels: 40  
 RESULT 1410  
 ID ABX70982 standard; cDNA; 8037 BP.  
 DE Novel human cDNA sequence #207.  
 PN WO200281731-A2.  
 PD 17-OCT-2002.  
 PA (HYSE-) HYSEQ INC.  
 PA (GOOD/) GOODRICH R W.  
 Percent Similarity: 37.44% Conservative: 24  
 Best Local Similarity: 26.07% Mismatches: 92  
 Query Match: 6.44% Indels: 40  
 RESULT 1411  
 ID AAF57452 standard; cDNA; 8040 BP.  
 DE Human ABCA2 transporter protein encoding cDNA.  
 PN WO200121798-A2.  
 PD 29-MAR-2001.  
 PA (FOXC-) FOX CHASE CANCER CENT.  
 Percent Similarity: 37.44% Conservative: 24  
 Best Local Similarity: 26.07% Mismatches: 92  
 Query Match: 6.44% Indels: 40  
 RESULT 1412  
 ID ABV74350 standard; DNA; 8056 BP.  
 DE Human ABC transporter ABCA2 encoding polynucleotide SEQ ID NO 3.

PN WO200264781-A2.  
PD 22-AUG-2002.  
PA (ACTI-) ACTIVE PASS PHARM INC.  
Percent Similarity: 37.44% Conservative: 24  
Best Local Similarity: 26.07% Mismatches: 92  
Query Match: 6.44% Indels: 40  
RESULT 1413  
ID AAH75187 standard; cDNA; 8195 BP.  
DE Nucleotide sequence of a human 17114 transporter polypeptide.  
PN WO200164875-A2.  
PD 07-SEP-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Percent Similarity: 37.44% Conservative: 24  
Best Local Similarity: 26.07% Mismatches: 92  
Query Match: 6.44% Indels: 40  
RESULT 1414  
ID ABL53009 standard; DNA; 8269 BP.  
DE Human ATP binding cassette transporter protein, ABCA2, coding sequence.  
PN WO200208424-A1.  
PD 31-JAN-2002.  
PA (BANY) BANYU PHARM CO LTD.  
Percent Similarity: 37.44% Conservative: 24  
Best Local Similarity: 26.07% Mismatches: 92  
Query Match: 6.44% Indels: 40  
RESULT 1415  
ID AAK68713 standard; DNA; 11477 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23525.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 33.33% Conservative: 30  
Best Local Similarity: 22.92% Mismatches: 101  
Query Match: 6.44% Indels: 92  
RESULT 1416  
ID AAK71247 standard; DNA; 11477 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26059.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 33.33% Conservative: 30  
Best Local Similarity: 22.92% Mismatches: 101  
Query Match: 6.44% Indels: 92  
RESULT 1417  
ID AAK68712 standard; DNA; 11482 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23524.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 33.33% Conservative: 30  
Best Local Similarity: 22.92% Mismatches: 101  
Query Match: 6.44% Indels: 92  
RESULT 1418  
ID AAK71246 standard; DNA; 11482 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26058.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 33.33% Conservative: 30  
Best Local Similarity: 22.92% Mismatches: 101  
Query Match: 6.44% Indels: 92  
RESULT 1419  
ID AAS59566 standard; DNA; 34088 BP.  
DE Propionibacterium acnes immunogenic protein encoding DNA #61.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 41.06% Conservative: 42  
Best Local Similarity: 25.10% Mismatches: 80  
Query Match: 6.44% Indels: 75  
RESULT 1420  
ID ACF64495 standard; DNA; 34088 BP.  
DE Propionibacterium acnes DNA contig sequence #61.

PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Percent Similarity: 41.06% Conservative: 42  
Best Local Similarity: 25.10% Mismatches: 80  
Query Match: 6.44% Indels: 75  
RESULT 1421  
ID ADH48030 standard; DNA; 37507 BP.  
DE Clone PS3-135 DNA sequence SEQ ID NO:2.  
PN EP1386966-A1.  
PD 04-FEB-2004.  
PA (LIBR-) LIBRAGEN.  
Percent Similarity: 40.00% Conservative: 14  
Best Local Similarity: 31.25% Mismatches: 61  
Query Match: 6.44% Indels: 35  
RESULT 1422  
ID AAD54230 standard; DNA; 50543 BP.  
DE Streptomyces amphibiosporus lactimidomycin DNA.  
PN WO200288176-A2.  
PD 07-NOV-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Percent Similarity: 39.06% Conservative: 30  
Best Local Similarity: 26.18% Mismatches: 90  
Query Match: 6.44% Indels: 55  
RESULT 1423  
ID AAC55842 standard; DNA; 53500 BP.  
DE Complete nucleotide sequence of the mitomycin biosynthetic genes.  
PN WO200053737-A2.  
PD 14-SEP-2000.  
PA (MINU) UNIV MINNESOTA.  
Percent Similarity: 34.74% Conservative: 25  
Best Local Similarity: 25.96% Mismatches: 121  
Query Match: 6.44% Indels: 65  
RESULT 1424  
ID ADE10261 standard; DNA; 53500 BP.  
DE S. lavendulae mitomycin biosynthetic genes complete sequence.  
PN US2003134398-A1.  
PD 17-JUL-2003.  
PA (SHER/) SHERMAN D H.  
Percent Similarity: 34.74% Conservative: 25  
Best Local Similarity: 25.96% Mismatches: 121  
Query Match: 6.44% Indels: 65  
RESULT 1425  
ID AAF28545 standard; DNA; 62909 BP.  
DE Genomic fragment #32.  
PN WO200078968-A2.  
PD 28-DEC-2000.  
PA (INGY-) INCYTE GENOMICS INC.  
Percent Similarity: 44.26% Conservative: 20  
Best Local Similarity: 27.87% Mismatches: 53  
Query Match: 6.44% Indels: 15  
RESULT 1426  
ID ACC45150 standard; DNA; 96649 BP.  
DE Human NAC nucleotide sequence SEQ ID NO:10.  
PN WO2003024988-A1.  
PD 27-MAR-2003.  
PA (ISIS-) ISIS PHARM INC.  
Percent Similarity: 33.33% Conservative: 30  
Best Local Similarity: 22.92% Mismatches: 101  
Query Match: 6.44% Indels: 92  
RESULT 1427  
Percent Similarity: 32.86% Conservative: 42  
Best Local Similarity: 20.86% Mismatches: 106  
Query Match: 6.44% Indels: 129

RESULT 1428  
 Percent Similarity: 32.86%  
 Best Local Similarity: 20.86%  
 Query Match: 6.44%  
 Indels: 129  
 Conservative: 42  
 Mismatches: 106

DE US2004016025-A1.  
 PD 22-JAN-2004.  
 PA (BUDW/) BUDWORTH P.  
 PA (MOUG/) MOUGHAMER T.  
 PA (BRIG/) BRIGGS S P.  
 PA (COOP/) COOPER B.  
 PA (GLAZ/) GLAZEBROOK J.  
 PA (GOFF/) GOFF S A.  
 PA (KATA/) KATAGIRI F.  
 PA (KREP/) KREPS J.  
 PA (PROV/) PROVART N.  
 PA (RICK/) RICHE D.  
 PA (ZHUT/) ZHU T.  
 Percent Similarity: 35.09%  
 Best Local Similarity: 21.51%  
 Query Match: 6.40%  
 Indels: 100  
 Conservative: 36  
 Mismatches: 72

DE Pseudomonas aeruginosa polynucleotide #22870.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Percent Similarity: 35.09%  
 Best Local Similarity: 21.51%  
 Query Match: 6.40%  
 Indels: 100  
 Conservative: 36  
 Mismatches: 72

DE Pseudomonas aeruginosa polynucleotide #6178.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 36.59%  
 Best Local Similarity: 26.48%  
 Query Match: 6.40%  
 Indels: 78  
 Conservative: 29  
 Mismatches: 105

DE Bacterial polynucleotide #17596.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Percent Similarity: 38.33%  
 Best Local Similarity: 25.42%  
 Query Match: 6.40%  
 Indels: 50  
 Conservative: 31  
 Mismatches: 98

DE Sequence encoding AA sequence (iii) of a polypeptide having human DE haematopoietic cell growth potentiating factor (HCGPF) activity.  
 PN EP232707-A.  
 PD 19-AUG-1987.  
 PA (AJIN ) AJINOMOTO KK.  
 Percent Similarity: 38.58%  
 Best Local Similarity: 27.17%  
 Query Match: 6.40%  
 Indels: 63  
 Conservative: 29  
 Mismatches: 94

DE Bacterial polynucleotide #11927.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Percent Similarity: 36.62%  
 Best Local Similarity: 23.24%  
 Query Match: 6.40%  
 Indels: 78  
 Conservative: 38  
 Mismatches: 102

DE Sorangium cellulosum tmba gene cluster ORF 3 DNA.  
 PN US2003054547-A1.  
 PD 20-MAR-2003.  
 PA (JULI/) JULIEN B.  
 Percent Similarity: 40.50%  
 Best Local Similarity: 27.50%  
 Query Match: 6.40%  
 Indels: 48  
 Conservative: 26  
 Mismatches: 73

DE ADJ39859 standard; cDNA; 1030 BP.  
 ID ADJ39859 standard; cDNA; 1030 BP.

DE Plant cDNA #859.  
 PN US2004016025-A1.  
 PD 22-JAN-2004.  
 PA (BUDW/) BUDWORTH P.  
 PA (MOUG/) MOUGHAMER T.  
 PA (BRIG/) BRIGGS S P.  
 PA (COOP/) COOPER B.  
 PA (GLAZ/) GLAZEBROOK J.  
 PA (GOFF/) GOFF S A.  
 PA (KATA/) KATAGIRI F.  
 PA (KREP/) KREPS J.  
 PA (PROV/) PROVART N.  
 PA (RICK/) RICHE D.  
 PA (ZHUT/) ZHU T.  
 Percent Similarity: 34.15%  
 Best Local Similarity: 24.39%  
 Query Match: 6.40%  
 Indels: 106  
 Conservative: 28  
 Mismatches: 83

DE Human ORF448 polynucleotide sequence SEQ ID NO:895.  
 PN WO200058473-A2.  
 PD 05-OCT-2000.  
 PA (CURA-) CURAGEN CORP.  
 Percent Similarity: 37.75%  
 Best Local Similarity: 26.51%  
 Query Match: 6.40%  
 Indels: 69  
 Conservative: 28  
 Mismatches: 86

DE Pseudomonas aeruginosa polynucleotide #7107.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 36.12%  
 Best Local Similarity: 24.08%  
 Query Match: 6.40%  
 Indels: 90  
 Conservative: 36  
 Mismatches: 101

DE Novel human protein cDNA #174.  
 PN WO2003025148-A2.  
 PD 27-MAR-2003.  
 PA (HYSE-) HYSEQ INC.  
 Percent Similarity: 35.80%  
 Best Local Similarity: 26.46%  
 Query Match: 6.40%  
 Indels: 61  
 Conservative: 24  
 Mismatches: 104

DE Pseudomonas aeruginosa polynucleotide #9231.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 34.20%  
 Best Local Similarity: 26.94%  
 Query Match: 6.40%  
 Indels: 67  
 Conservative: 14  
 Mismatches: 60

DE Aspergillus fumigatus essential gene #1436.  
 PN WO200286090-A2.  
 PD 31-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 33.47%  
 Best Local Similarity: 21.37%  
 Query Match: 6.40%  
 Indels: 82  
 Conservative: 30  
 Mismatches: 83

DE RAQ92784 standard; cDNA; 1906 BP.  
 ID RAQ92784 standard; cDNA; 1906 BP.  
 DE Mullerian inhibiting substance cDNA.  
 PN US5427780-A.  
 PD 27-JUN-1995.  
 PA (BIOJ ) BIOGEN INC.  
 PA (GEO ) GEN HOSPITAL CORP.  
 Percent Similarity: 32.41%  
 Best Local Similarity: 24.69%  
 Query Match: 6.40%  
 Indels: 107  
 Conservative: 25  
 Mismatches: 112

DE ADJ39859 standard; cDNA; 1030 BP.  
 ID ADJ39859 standard; cDNA; 1030 BP.

ID ABD10214 standard; DNA; 2019 BP.  
DE Pseudomonas aeruginosa polynucleotide #8818.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 34.20% Conservative: 14  
Best Local Similarity: 26.94% Mismatches: 60  
Query Match: 6.40% Indels: 67  
RESULT 1443  
ID ABD08834 standard; DNA; 2094 BP.  
DE Pseudomonas aeruginosa polynucleotide #7438.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 36.86% Conservative: 30  
Best Local Similarity: 24.15% Mismatches: 92  
Query Match: 6.40% Indels: 57  
RESULT 1444  
ID ADG91050 standard; DNA; 2120 BP.  
DE Hepatic specific nucleic acid encoding sequence #239.  
PN WO2003066877-A2.  
PD 14-AUG-2003.  
PA (DIAD-) DIADEXUS INC.  
Percent Similarity: 43.74% Conservative: 36  
Best Local Similarity: 29.71% Mismatches: 85  
Query Match: 6.40% Indels: 74  
RESULT 1445  
ID AAI20576 standard; DNA; 2144 BP.  
DE Probe #10509 for gene expression analysis in human cervical cell sample.  
PN WO200157278-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 30.69% Conservative: 12  
Best Local Similarity: 26.35% Mismatches: 87  
Query Match: 6.40% Indels: 105  
RESULT 1446  
ID ABA65620 standard; DNA; 2144 BP.  
DE Human foetal liver single exon nucleic acid probe #13925.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 30.69% Conservative: 12  
Best Local Similarity: 26.35% Mismatches: 87  
Query Match: 6.40% Indels: 105  
RESULT 1447  
ID AAI45786 standard; DNA; 2144 BP.  
DE Probe #14472 used to measure gene expression in human placenta sample.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 30.69% Conservative: 12  
Best Local Similarity: 26.35% Mismatches: 87  
Query Match: 6.40% Indels: 105  
RESULT 1448  
ID ABA47725 standard; DNA; 2144 BP.  
DE Human breast cell single exon nucleic acid probe #6420.  
PN WO200157271-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 30.69% Conservative: 12  
Best Local Similarity: 26.35% Mismatches: 87  
Query Match: 6.40% Indels: 105  
RESULT 1449  
ID ABA32707 standard; DNA; 2144 BP.  
DE Probe #11173 for gene expression analysis in human heart cell sample.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 30.69% Conservative: 12  
Best Local Similarity: 26.35% Mismatches: 87  
Query Match: 6.40% Indels: 105  
RESULT 1450  
ID AAK39770 standard; DNA; 2144 BP.  
DE Human bone marrow expressed single exon probe SEQ ID NO: 14327.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 30.69% Conservative: 12  
Best Local Similarity: 26.35% Mismatches: 87  
Query Match: 6.40% Indels: 105  
RESULT 1451  
ID AAK14023 standard; DNA; 2144 BP.  
DE Human brain expressed single exon probe SEQ ID NO: 14014.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 30.69% Conservative: 12  
Best Local Similarity: 26.35% Mismatches: 87  
Query Match: 6.40% Indels: 105  
RESULT 1452  
ID ABS39357 standard; DNA; 2144 BP.  
DE Human liver single exon probe, SEQ ID NO 14347.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 30.69% Conservative: 12  
Best Local Similarity: 26.35% Mismatches: 87  
Query Match: 6.40% Indels: 105  
RESULT 1453  
ID AAI06275 standard; DNA; 2144 BP.  
DE Probe #6266 used to measure gene expression in human breast sample.  
PN WO200157270-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 30.69% Conservative: 12  
Best Local Similarity: 26.35% Mismatches: 87  
Query Match: 6.40% Indels: 105  
RESULT 1454  
ID ABS13864 standard; DNA; 2144 BP.  
DE Human genome-derived single exon probe ORF from lung SEQ ID NO 13855.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Percent Similarity: 30.69% Conservative: 12  
Best Local Similarity: 26.35% Mismatches: 87  
Query Match: 6.40% Indels: 105  
RESULT 1455  
ID ACN43048 standard; CDNA; 2155 BP.  
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1923.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Percent Similarity: 38.35% Conservative: 27  
Best Local Similarity: 28.67% Mismatches: 95  
Query Match: 6.40% Indels: 78  
RESULT 1456  
ID AAI61256 standard; CDNA; 2174 BP.  
DE Human polynucleotide SEQ ID NO 5245.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 30.69% Conservative: 12  
Best Local Similarity: 26.35% Mismatches: 87  
Query Match: 6.40% Indels: 105  
RESULT 1457  
ID ADG91053 standard; DNA; 2280 BP.  
DE Hepatic specific nucleic acid encoding sequence #242.  
PN WO2003066877-A2.  
PD 14-AUG-2003.  
PA (DIAD-) DIADEXUS INC.  
Percent Similarity: 42.75% Conservative: 36  
Best Local Similarity: 29.71% Mismatches: 85  
Query Match: 6.40% Indels: 74  
RESULT 1458  
ID ADG91055 standard; DNA; 2321 BP.  
DE Hepatic specific nucleic acid encoding sequence #244.



```

PN WO2003066877-A2.
PD 14-AUG-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 42.75%
Best Local Similarity: 29.71%
Mismatches: 85
Indels: 74
Query Match: 6.40%
RESULT 1459
ID ADT47024 standard; cDNA; 2412 BP.
DE Bacterial polynucleotide #21775.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Percent Similarity: 41.11%
Best Local Similarity: 27.41%
Mismatches: 87
Indels: 72
Query Match: 6.40%
RESULT 1460
ID ADG91049 standard; DNA; 2457 BP.
DE Hepatic specific nucleic acid encoding sequence #238.
PN WO2003066877-A2.
PD 14-AUG-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 42.75%
Best Local Similarity: 29.71%
Mismatches: 85
Indels: 74
Query Match: 6.40%
RESULT 1461
ID ACA2329 standard; DNA; 2463 BP.
DE Prokaryotic essential gene #2396.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Percent Similarity: 33.65%
Best Local Similarity: 26.35%
Mismatches: 117
Indels: 94
Query Match: 6.40%
RESULT 1462
ID ADG91048 standard; DNA; 2489 BP.
DE Hepatic specific nucleic acid encoding sequence #237.
PN WO2003066877-A2.
PD 14-AUG-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 42.75%
Best Local Similarity: 29.71%
Mismatches: 85
Indels: 74
Query Match: 6.40%
RESULT 1463
ID ADI2554 standard; DNA; 2517 BP.
DE Synthetic 5' nuclease DNA SEQ ID 107.
PN WO200190337-A2.
PD 29-NOV-2001.
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
Percent Similarity: 38.28%
Best Local Similarity: 24.48%
Mismatches: 102
Indels: 79
Query Match: 6.40%
RESULT 1464
ID ADG91047 standard; DNA; 2520 BP.
DE Hepatic specific nucleic acid encoding sequence #236.
PN WO2003066877-A2.
PD 14-AUG-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 42.75%
Best Local Similarity: 29.71%
Mismatches: 85
Indels: 74
Query Match: 6.40%
RESULT 1465
ID ADG91054 standard; DNA; 2641 BP.
DE Hepatic specific nucleic acid encoding sequence #243.
PN WO2003066877-A2.
PD 14-AUG-2003.
PA (DIAD-) DIADEXUS INC.
Percent Similarity: 42.75%
Best Local Similarity: 29.71%
Mismatches: 85
Indels: 74
Query Match: 6.40%
RESULT 1466
ID ABD17161 standard; DNA; 2814 BP.
DE Pseudomonas aeruginosa polynucleotide #15765.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 33.65%
Best Local Similarity: 26.35%
Mismatches: 117
Indels: 94
Query Match: 6.40%
RESULT 1467
ID ABD08894 standard; DNA; 3012 BP.
DE Pseudomonas aeruginosa polynucleotide #7498.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Percent Similarity: 36.86%
Best Local Similarity: 24.15%
Mismatches: 92
Indels: 57
Query Match: 6.40%
RESULT 1468
ID ACC77568 standard; DNA; 3026 BP.
DE Thermus aquaticus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 39.31%
Best Local Similarity: 24.83%
Mismatches: 99
Indels: 79
Query Match: 6.40%
RESULT 1469
ID ACC77580 standard; DNA; 3026 BP.
DE Thermus aquaticus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 39.31%
Best Local Similarity: 24.83%
Mismatches: 99
Indels: 79
Query Match: 6.40%
RESULT 1470
ID ACC77561 standard; DNA; 3026 BP.
DE Thermus aquaticus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 42.09%
Best Local Similarity: 26.62%
Mismatches: 109
Indels: 53
Query Match: 6.40%
RESULT 1471
ID ACC77598 standard; DNA; 3026 BP.
DE Thermus aquaticus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 38.62%
Best Local Similarity: 24.83%
Mismatches: 101
Indels: 79
Query Match: 6.40%
RESULT 1472
ID ACC77839 standard; DNA; 3026 BP.
DE Thermus aquaticus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 39.31%
Best Local Similarity: 24.48%
Mismatches: 99
Indels: 79
Query Match: 6.40%
RESULT 1473
ID ACC77780 standard; DNA; 3026 BP.
DE Thermus aquaticus mutant DNA polymerase encoding DNA.
PN WO2003025132-A2.
PD 27-MAR-2003.
PA (INVI-) INVITROGEN CORP.
Percent Similarity: 38.62%
Best Local Similarity: 25.17%
Mismatches: 101
Indels: 79
Query Match: 6.40%
RESULT 1474

```

ID ACC77777 standard; DNA; 3026 BP.  
DE Thermus aquaticus mutant DNA polymerase encoding DNA.  
PN WO2003025132-A2.  
PD 27-MAR-2003.  
PA (INVI-) INVITROGEN CORP.  
Percent Similarity: 38.62%  
Best Local Similarity: 25.17%  
Query Match: 6.40%  
Conservative: 39  
Mismatches: 101  
Indels: 79  
RESULT 1475  
ID ABD17264 standard; DNA; 3357 BP.  
DE Pseudomonas aeruginosa polynucleotide #15868.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Percent Similarity: 33.65%  
Best Local Similarity: 26.35%  
Query Match: 6.40%  
Conservative: 23  
Mismatches: 117  
Indels: 94  
RESULT 1476  
ID ADL45191 standard; DNA; 3574 BP.  
DE Human ovarian cancer DNA marker #19081.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Percent Similarity: 36.09%  
Best Local Similarity: 23.91%  
Query Match: 6.40%  
Conservative: 28  
Mismatches: 73  
Indels: 74  
RESULT 1477  
ID AAX87412 standard; cDNA; 3607 BP.  
DE Hepatocellular carcinoma marker gene L4 cDNA.  
PN WO9939200-A1.  
PD 05-AUG-1999.  
PA (UYJE-) UNIV JEFFERSON THOMAS.  
Percent Similarity: 30.69%  
Best Local Similarity: 26.35%  
Query Match: 6.40%  
Conservative: 12  
Mismatches: 87  
Indels: 105  
RESULT 1478  
ID AAI59470 standard; cDNA; 3613 BP.  
DE Human polynucleotide SEQ ID NO 1673.  
PN WO20015312-A1.  
PD 26-JUL-2003.  
PA (HYSE-) HYSEQ INC.  
Percent Similarity: 30.69%  
Best Local Similarity: 26.35%  
Query Match: 6.40%  
Conservative: 12  
Mismatches: 87  
Indels: 105  
RESULT 1479  
ID ADQ86127 standard; cDNA; 4093 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #2999.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Percent Similarity: 30.69%  
Best Local Similarity: 26.35%  
Query Match: 6.40%  
Conservative: 12  
Mismatches: 87  
Indels: 105  
RESULT 1480  
ID ADE83409 standard; DNA; 4134 BP.  
DE Rat gene M73049, SEQ ID NO 11004.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Percent Similarity: 35.62%  
Best Local Similarity: 25.75%  
Query Match: 6.40%  
Conservative: 23  
Mismatches: 94  
Indels: 56  
RESULT 1481  
ID ADH76479 standard; DNA; 11364 BP.  
DE Chimeric pPCR-GalV-1 plasmid DNA sequence.  
PN FR2832424-A1.  
PD 23-MAY-2003.  
PA (GENE-) GENETHON III.  
Percent Similarity: 35.34%  
Best Local Similarity: 24.42%  
Conservative: 33  
Mismatches: 91

Query Match: 6.40%  
Indels: 105  
RESULT 1482  
ID ABA20357 standard; DNA; 11585 BP.  
DE Human nervous system related polynucleotide SEQ ID NO 12688.  
PN WO200159063-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Percent Similarity: 30.69%  
Best Local Similarity: 26.35%  
Query Match: 6.40%  
Conservative: 12  
Mismatches: 87  
Indels: 105  
RESULT 1483  
ID AAH48620 standard; DNA; 16951 BP.  
DE Human fascin DNA fragment SEQ ID 72.  
PN WO200151631-A2.  
PD 19-JUL-2001.  
PA (RESK/) RESKE-KUNZ A.  
PA (ROSS/) ROSS X.  
PA (ROSS/) ROSS R.  
PA (BROS/) BROS M.  
Percent Similarity: 31.43%  
Best Local Similarity: 23.49%  
Query Match: 6.40%  
Conservative: 25  
Mismatches: 98  
Indels: 118  
RESULT 1484  
ID AAH48622 standard; DNA; 16951 BP.  
DE Human fascin DNA fragment #2.  
PN WO200151631-A2.  
PD 19-JUL-2001.  
PA (RESK/) RESKE-KUNZ A.  
PA (ROSS/) ROSS X.  
PA (ROSS/) ROSS R.  
PA (BROS/) BROS M.  
Percent Similarity: 31.43%  
Best Local Similarity: 23.49%  
Query Match: 6.40%  
Conservative: 25  
Mismatches: 98  
Indels: 118  
RESULT 1485  
ID AAF30757 standard; DNA; 47981 BP.  
DE Micromonospora megalomicea megalomicin biosynthetic gene cluster.  
PN WO200056762-A2.  
PD 28-SEP-2000.  
PA (NOVO) NOVO NORDISK BIOTECH INC.  
PA (NOVO) NOVO NORDISK AS.  
Percent Similarity: 34.93%  
Best Local Similarity: 23.92%  
Query Match: 6.40%  
Conservative: 23  
Mismatches: 88  
Indels: 48  
RESULT 1487  
ID AAF14299 standard; cDNA; 637 BP.  
DE Aspergillus oryzae EST SEQ ID NO:6822.  
PN WO200056762-A2.  
PD 28-SEP-2000.  
PA (NOVO) NOVO NORDISK BIOTECH INC.  
PA (NOVO) NOVO NORDISK AS.  
Percent Similarity: 36.49%  
Best Local Similarity: 25.12%  
Query Match: 6.37%  
Conservative: 24  
Mismatches: 59  
Indels: 75  
RESULT 1488  
ID ABZ37810 standard; DNA; 810 BP.  
DE N. gonorrhoeae nucleotide sequence SEQ ID 209.  
PN WO200279243-A2.  
PD 10-OCT-2002.  
PA (CHIR-) CHIRON SPA.  
Percent Similarity: 39.04%  
Best Local Similarity: 27.63%  
Query Match: 6.37%  
Conservative: 26  
Mismatches: 84  
Indels: 56  
RESULT 1489  
ID ABZ40942 standard; DNA; 810 BP.  
DE N. gonorrhoeae nucleotide sequence SEQ ID 6473.  
PN WO200279243-A2.  
PD 10-OCT-2002.  
PA (CHIR-) CHIRON SPA.  
Percent Similarity: 39.04%  
Best Local Similarity: 27.63%  
Query Match: 6.37%  
Conservative: 26  
Mismatches: 84  
Indels: 56  
RESULT 1490

ID ABD14325 standard; DNA; 909 BP.  
 DE Pseudomonas aeruginosa polynucleotide #12929.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 32.30% Conservative: 19  
 Best Local Similarity: 25.77% Mismatches: 97  
 Query Match: 6.37% Indels: 100  
 RESULT 1491  
 ID ABZ80091 standard; cDNA; 930 BP.  
 DE Synecococcus methyltransferase encoding cDNA SEQ ID NO:44.  
 PN WO2003016482-A2.  
 PD 27-FEB-2003.  
 PA (MONS) MONSANTO TECHNOLOGY LLC.  
 Percent Similarity: 35.20% Conservative: 17  
 Best Local Similarity: 26.53% Mismatches: 61  
 Query Match: 6.37% Indels: 66  
 RESULT 1492  
 ID ABZ37722 standard; DNA; 981 BP.  
 DE N. gonorrhoeae nucleotide sequence SEQ ID 33.  
 PN WO200279243-A2.  
 PD 10-OCT-2002.  
 PA (CHIR-) CHIRON SPA.  
 Percent Similarity: 39.04% Conservative: 26  
 Best Local Similarity: 27.63% Mismatches: 84  
 Query Match: 6.37% Indels: 56  
 RESULT 1493  
 ID ABZ41892 standard; DNA; 1023 BP.  
 DE N. gonorrhoeae nucleotide sequence SEQ ID 8373.  
 PN WO200279243-A2.  
 PD 10-OCT-2002.  
 PA (CHIR-) CHIRON SPA.  
 Percent Similarity: 39.04% Conservative: 26  
 Best Local Similarity: 27.63% Mismatches: 84  
 Query Match: 6.37% Indels: 56  
 RESULT 1494  
 ID ACA25487 standard; DNA; 1221 BP.  
 DE Prokaryotic essential gene #7144.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Percent Similarity: 35.58% Conservative: 30  
 Best Local Similarity: 24.34% Mismatches: 78  
 Query Match: 6.37% Indels: 94  
 RESULT 1495  
 ID ABD10094 standard; DNA; 1269 BP.  
 DE Pseudomonas aeruginosa polynucleotide #8698.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 37.59% Conservative: 37  
 Best Local Similarity: 23.68% Mismatches: 97  
 Query Match: 6.37% Indels: 69  
 RESULT 1496  
 ID ABA21155 standard; DNA; 1695 BP.  
 DE Human nervous system related polynucleotide SEQ ID NO 13486.  
 PN WO200159063-A2.  
 PD 16-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 32.98% Conservative: 10  
 Best Local Similarity: 27.66% Mismatches: 92  
 Query Match: 6.37% Indels: 34  
 RESULT 1497  
 ID AAS30164 standard; DNA; 1695 BP.  
 DE Human lung antigen genomic DNA #234.  
 PN WO200155303-A2.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 32.98% Conservative: 10  
 Best Local Similarity: 27.66% Mismatches: 92  
 Query Match: 6.37% Indels: 34  
 RESULT 1498  
 ID ADB33501 standard; DNA; 1695 BP.  
 DE Human novel lung related polypeptide DNA SEQ ID NO 428.  
 PN US2003054368-A1.  
 PD 20-MAR-2003.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Percent Similarity: 32.98% Conservative: 10  
 Best Local Similarity: 27.66% Mismatches: 92  
 Query Match: 6.37% Indels: 34  
 RESULT 1499  
 ID ABD10477 standard; DNA; 1944 BP.  
 DE Pseudomonas aeruginosa polynucleotide #9081.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Percent Similarity: 37.59% Conservative: 37  
 Best Local Similarity: 23.68% Mismatches: 97  
 Query Match: 6.37% Indels: 69  
 RESULT 1500  
 ID ADT45918 standard; cDNA; 1944 BP.  
 DE Bacterial polynucleotide #20669.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Percent Similarity: 39.85% Conservative: 32  
 Best Local Similarity: 27.82% Mismatches: 74  
 Query Match: 6.37% Indels: 87

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 19, 2005, 21:20:51 ; Search time 4655 Seconds

(without alignments)  
2727.232 Million cell updates/sec

Title: US-10-017-407a-306

Perfect score: 1343

Sequence: 1 MTQVPRLSVPRALALGSA.....VRVVISLPLDGLTLAFKI 262

Scoring table:

	BLOSUM62	Xgapop 10.0	Xgapext 0.5
Ygapop 10.0			0.5
Ygapop 6.0			7.0
Delop 6.0			7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/cgn2\_1/USPTO.spool/US10017407/runat\_19042005\_142533\_29467/app\_query.fasta\_1.455  
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0\_1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bites -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1500  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10017407 @CGN 1.1 4200 @runat\_19042005\_142533\_29467 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.\*

1: gb.ba.\*

2: gb.htg.\*

3: gb.in.\*

4: gb.ov.\*

5: gb.pat.\*

6: gb.ph.\*

7: gb.pl.\*

8: gb.pr.\*

9: gb.ro.\*

10: gb.ste.\*

11: gb.sy.\*

12: gb.un.\*

13: gb.vi.\*

14: gb.vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1343	100.0	789	6	CQ721501 Sequence
2	1343	100.0	789	6	AX338456 Sequence
3	1343	100.0	913	9	BC023663 Homo sapi
4	1343	100.0	985	6	BD222712 Human sig

5	1343	100.0	989	6	AX201342 Sequence
6	1343	100.0	989	6	AX697237 Sequence
7	1343	100.0	989	9	AY358476 Homo sapi
8	1343	100.0	1037	6	AX338454 Sequence
9	1343	100.0	1041	9	BC047774 Homo sapi
10	1337	99.6	988	9	AK074421 Homo sapi
11	1156	86.1	946	10	BC049670 Mus muscu
12	1028	76.5	38679	9	AL390034 Human DNA
13	1028	76.5	169612	2	AC027393 Homo sapi
14	870.5	64.8	89888	2	AY294423 3
15	870.5	64.8	161371	10	AC132590 Mus muscu
16	850.5	63.3	228354	2	AC137429 Rattus no
17	850.5	63.3	266634	2	AC123487 Rattus no
18	722	53.8	110000	2	AC105718 3
19	676.5	50.4	237829	2	AC120475
20	520	38.7	237221	1	AP003599
21	507.5	37.8	157428	10	AL606832 Mouse DNA
22	507.5	37.8	209643	10	AC080018 Mus muscu
23	484	36.0	300465	1	AE016962 Cxiella
24	477.5	35.6	110000	1	CR628337 25
25	474.5	35.3	2955	1	AF075724 Legionell
26	474.5	35.3	110000	1	AE017354 25
27	469.5	35.0	110000	1	CR628336 25
28	453	33.7	11171	6	CQ801141 Sequence
29	450.5	33.5	10882	1	AE002493 Neisseria
30	450.5	33.5	349980	6	AX044032 Sequence
31	445.5	33.2	304282	1	AE016910 Chromobac
32	443	33.0	329861	1	NMA522491
33	438.5	32.7	14100	1	MXU24657
34	438	32.6	675	6	CQ801150 Sequence
35	436	32.5	1210	8	AK063541 Oryza sat
36	431.5	32.1	10840	1	AE004550 Pseudomon
37	425.5	31.7	2381	1	ST00MDMC
38	425.5	31.7	2381	1	E06690 DNA encodin
39	424	31.6	663	12	AY657514 Synthetic
40	413	30.8	1218	6	AX146637 Sequence
41	409.5	30.5	69644	1	AY179507 Streptomy
42	408	30.4	1167	8	ZMA242981
43	405.5	30.2	980	6	AR236704 Sequence
44	405	30.2	134199	1	SYCSLRF
45	401	29.9	891	6	AR236694 Sequence
46	398.5	29.7	744	6	CQ760958 Sequence
47	398.5	29.7	744	6	AX259371 Sequence
48	398.5	29.7	966	6	MSU20736
49	398.5	29.7	1906	6	CQ760964 Sequence
50	398	29.6	837	8	AY094008 Arabidops
51	398	29.6	1068	8	EG12228
52	398	29.6	1107	8	AY070483
53	396	29.5	783	6	AX654276 Sequence
54	396	29.5	976	8	AB110168 Oryza sat
55	396	29.5	996	8	AK104326 Oryza sat
56	396	29.5	1052	8	AK065744 Oryza sat
57	396	29.5	1058	6	AR236699 Sequence
58	396	29.5	1096	8	AK104801 Oryza sat
59	396	29.5	1098	8	AK071482 Oryza sat
60	394	29.3	1078	6	AR236714 Sequence
61	394	29.3	1078	8	BT009389 Triticum
62	394	29.3	188267	2	AC137230 Rattus no
63	393	29.3	1006	8	AF046122 Eucalyptu
64	393	29.3	1338	6	AX654529 Sequence
65	392.5	29.2	962	6	AR236705 Sequence
66	392.5	29.2	1023	6	AR236706 Sequence
67	392.5	29.2	1895	8	AK106735 Oryza sat
68	391.5	29.2	780	6	CQ804646 Sequence
69	391.5	29.2	780	6	CQ805684 Sequence
70	391.5	29.2	780	8	AY143979 Arabidops
71	391.5	29.2	815	8	AY081457 Arabidops
72	391.5	29.2	976	8	VVCCOAMT
73	391.5	29.2	999	8	AY062630 Arabidops
74	391.5	29.2	1026	6	AY057554 Arabidops
75	389	29.0	997	6	AR236700 Sequence
76	388.5	28.9	1025	8	AJ224894 Populus b
77	387.5	28.9	939	8	AJ224896 Populus b

78	387.5	28.9	963	8	AY620245	Amni maju	151	353.5	26.3	1152	8	AY279032	Zea mays
79	387.5	28.9	1049	8	PBTAJ4895	AJ224895 Populus b	152	353	26.3	1180	6	AX798857	Sequence
80	387.5	28.9	1258	8	PUMCCOAMT	M69184 Petroselinu	153	351.5	26.2	1466	8	AK065515	Oryza sat
81	387	28.8	953	6	AR236716	Sequence	154	350.5	26.1	1136	8	AY279034	Zea mays
82	387	28.8	953	6	BT009394	Triticum	155	350.5	26.1	1181	6	AX798855	Sequence
83	386.5	28.8	967	6	AR225249	Sequence	156	350.5	26.1	1181	8	AY279005	Zea mays
84	386.5	28.8	1046	6	PTU27116	Populus tre	157	350.5	26.1	1181	8	AY279024	Zea mays
c	85	386	798	6	AX660925	Sequence	158	350.5	26.1	1181	8	AY279026	Zea mays
86	386	28.7	1012	6	BD224370	Materials	159	349.5	26.0	300299	1	AE017288	Leptospi
87	386	28.7	1012	6	AR216420	Sequence	160	348	25.9	77534	1	BP235504	Streptomy
88	386	28.7	1012	6	AR432822	Sequence	161	348	25.9	77536	6	BD235937	Polyretid
89	386	28.7	1026	6	AR066484	Sequence	162	348	25.9	77536	6	AR271638	Sequence
90	386	28.7	1026	6	AR074097	Sequence	163	348	25.9	77536	6	AR564393	Sequence
91	386	28.7	1026	6	AR143609	Sequence	164	347.5	25.9	706	8	PBA130841	Sequence
92	386	28.7	1026	6	BD224282	Sequence	165	346	25.8	1013	8	SLASADEN	L22203 Stellar
93	386	28.7	1026	6	AR216332	Sequence	166	345.5	25.7	10029	1	AE011228	Leptospi
94	386	28.7	1026	6	AR432734	Sequence	167	345	25.7	890	8	AY145521	Mesembrya
95	386	28.7	1026	6	BD005645	Materials	168	345	25.7	1145	8	AY279031	Zea mays
96	386	28.7	1026	6	BD005645	Materials	169	345	25.7	1150	8	AY279012	Zea mays
97	386	28.7	1118	8	AR236712	Sequence	170	345	25.7	1150	8	AY279013	Zea mays
98	386	28.7	1146	6	BT009186	Triticum	171	345	25.7	1150	8	AY279030	Zea mays
99	385.5	28.7	726	8	AR236695	Sequence	172	345	25.7	1150	8	AY279033	Zea mays
100	385.5	28.7	931	6	AF240466	Populus t	173	345	25.7	1150	8	AY279035	Zea mays
101	385	28.7	1136	8	AR236702	Sequence	174	343	25.5	1206	8	AY279008	Zea mays
102	384.5	28.6	1033	8	AY088577	Arabidops	175	343	25.5	1209	8	AY279028	Zea mays
103	384	28.6	783	6	AX654528	Sequence	176	343	25.5	1222	8	AY279029	Zea mays
104	384	28.6	1149	8	AK061757	Oryza sat	177	341	25.4	982	6	AR236709	Sequence
105	383.5	28.6	1016	8	NTCCOAMT	Z56282 N.tabacum m	c	340	25.3	82746	1	AF453501	Actinosyn
106	383.5	28.6	1023	8	AB061268	Solanum t	179	338	25.2	1227	8	NT282982	Nicotina ta
107	383.5	28.6	1057	6	AR236696	Sequence	180	337.5	25.1	1451	8	AY279004	Zea mays
108	382.5	28.5	929	6	AR236703	Sequence	181	337	25.1	1182	8	AY279009	Zea mays
109	381	28.4	1049	6	AR236715	Sequence	182	336.5	25.1	1434	8	AY279014	Zea mays
110	379.5	28.3	845	6	AR225248	Sequence	183	335	24.9	1463	8	AY279016	Zea mays
111	379.5	28.3	1258	6	A22706	CAfreoyl-Co	184	335	24.9	1464	8	AY279015	Zea mays
112	379	28.2	1112	6	AX660732	Sequence	185	333	24.8	1172	8	AY279006	Zea mays
113	377.5	28.1	959	8	AK108479	Oryza sat	186	333	24.8	1172	8	AY279025	Zea mays
114	377	28.1	875	8	AB158406	Triticum	187	333	24.8	1172	8	AY279027	Zea mays
115	377	28.1	1018	8	BT009093	Triticum	188	333	24.8	1442	8	AY279019	Zea mays
116	376	28.0	909	8	BT013139	Lycopersi	189	333	24.8	1444	8	AY279017	Zea mays
117	376	28.0	923	6	AR236697	Sequence	190	333	24.8	1445	8	AY279018	Zea mays
118	373.5	27.8	816	8	AF022775	Nicotiana	191	333	24.8	1445	8	AY279022	Zea mays
119	373.5	27.8	870	6	AR225246	Sequence	192	333	24.8	1445	8	AY279022	Zea mays
120	373.5	27.8	890	8	NTU38612	U38612 Nicotiana t	193	332.5	24.8	591	8	AY607699	Apium Gra
121	373.5	27.8	955	8	NTU62736	U62736 Nicotiana t	194	332.5	24.8	1438	8	AY279021	Zea mays
122	373.5	27.8	1003	8	NTU62735	U62735 Nicotiana t	195	332.5	24.8	1451	8	AY279020	Zea mays
123	373.5	27.8	1014	8	NTU62734	U62734 Nicotiana t	196	331	24.6	908	8	AY500159	Corchorus
124	372.5	27.7	811	6	AR225247	Sequence	197	331	24.6	1298	8	AY323254	Zea mays
125	372.5	27.7	1104	8	AF053553	Mesembrya	198	331	24.6	1298	8	AY323255	Zea mays
126	372.5	27.7	1258	6	AR122016	Sequence	199	331	24.6	1298	8	AY323258	Zea mays
127	372.5	27.7	1258	6	I92681	Sequence 1	200	331	24.6	1298	8	AY323259	Zea mays
128	369	27.5	730	8	AY056313	Arabidops	201	331	24.6	1298	8	AY323260	Zea mays
129	369	27.5	956	8	AF360317	Arabidops	202	331	24.6	1298	8	AY323261	Zea mays
130	369	27.5	1098	8	AY128822	Arabidops	203	331	24.6	1298	8	AY323263	Zea mays
131	369	27.5	1185	8	AY087981	Arabidops	204	331	24.6	1298	8	AY323265	Zea mays
132	369	27.5	1201	8	AY093172	Arabidops	205	331	24.6	1536	8	AY323241	Zea mays
133	369	27.5	1252	6	Q0857676	Sequence	206	331	24.6	1536	8	AY323243	Zea mays
134	368.5	27.4	744	8	AF327458	Populus a	207	331	24.6	1536	8	AY323245	Zea mays
135	368.5	27.4	1013	8	AF168780	AF168780 Eucalyptu	208	331	24.6	1536	8	AY323247	Zea mays
136	368.5	27.4	1018	6	AR236711	Sequence	209	331	24.6	1536	8	AY323248	Zea mays
137	367.5	27.4	835	6	AX660084	Sequence	210	331	24.6	1536	8	AY323250	Zea mays
138	366	27.3	326	6	AX407985	Sequence	211	331	24.6	1537	8	AY323251	Zea mays
139	365	27.2	1232	8	AF036095	Pinus tae	212	330.5	24.6	772	8	FVAJ1447	Fragaria
140	365	27.2	153751	3	AC116551	Dictyoste	213	329.5	24.5	1153	8	AY279010	Zea mays
141	364.5	27.1	918	8	ZEUI3151	U13151 Zinnia eleg	214	327.5	24.5	1314	8	AY323253	Zea mays
142	364.5	27.1	1158	8	AY644637	Oryza sat	215	327.5	24.4	1314	8	AY323268	Zea mays
143	364.5	27.1	137354	8	AP000364	AP000364 Oryza sat	216	327	24.3	1272	8	AY644636	Oryza sat
144	363.5	27.1	1116	8	AY644638	Arabidops	217	327	24.3	105815	8	AP002536	AB023482 Oryza sat
145	362	27.0	917	8	AY087244	Arabidops	218	327	24.3	156054	8	AB023482	Oryza sat
146	360.5	26.8	730	8	AF060180	Nicotiana	219	326	24.3	1311	8	AY323252	Zea mays
147	360	26.8	729	6	AX507705	Sequence	220	326	24.3	1311	8	AY323257	Zea mays
148	354	26.4	912	6	AR236707	Sequence	221	326	24.3	1311	8	AY323264	Zea mays
149	353.5	26.3	1136	8	AY279011	Zea mays	222	326	24.3	1311	8	AY323267	Zea mays
150	353.5	26.3	1152	8	AY279023	Zea mays	223	326	24.3	1549	8	AY323249	Zea mays

224	324	24.1	833	8	AY088274	AY088274 Arabidops	297	224.5	16.7	760	6	BD272991	BD272991 Materials
225	323	24.1	6090	1	U30252	U30252 Synchococc	298	224.5	16.7	760	6	AR216351	AR216351 Sequence
226	320.5	23.9	1320	8	AY323271	AY323271 Zea mays	299	224.5	16.7	760	6	AR432753	AR432753 Sequence
227	318.5	23.7	1309	8	AY323239	AY323239 Zea mays	300	224.5	16.7	760	6	BD005664	BD005664 Materials
228	318.5	23.7	1309	8	AY323256	AY323256 Zea mays	301	224.5	16.7	300800	1	SC0939112	AL939112 Streptomy
229	318.5	23.7	1309	8	AY323266	AY323266 Zea mays	302	224	16.7	534	6	AR236717	AR236717 Sequence
230	318	23.7	1537	8	AY323242	AY323242 Zea mays	303	220.5	16.4	110000	1	CP00000118	Continuation (19 o
231	318	23.7	1546	8	AY323244	AY323244 Zea mays	304	220.5	16.4	110000	1	CP00000119	Continuation (20 o
232	317	23.6	1306	8	AY323238	AY323238 Zea mays	305	219.5	16.3	133649	2	BX927362	BX927362 Danio rer
233	317	23.6	1306	8	AY323240	AY323240 Zea mays	306	219.5	16.3	261352	2	BX957311	BX957311 Danio rer
234	317	23.6	1306	8	AY323262	AY323262 Zea mays	307	218.5	16.3	101966	8	AE012563	AE012563 Arabidops
235	317	23.6	1306	8	AY323270	AY323270 Zea mays	308	218	16.2	299986	1	AE017240	AE017240 Mycobacte
236	317	23.6	1544	8	AY323246	AY323246 Zea mays	309	217.5	16.2	304282	1	AE016910	AE016910 Chromobac
237	311.5	23.2	486	8	AY651026	AY651026 Boehmeria	310	215.5	16.0	622	8	AB076979	AB076979 Avena sat
238	311.5	23.2	699	6	AX412281	AX412281 Sequence	311	215	16.0	110000	1	AP006618	Continuation (27 o
239	311.5	23.2	699	6	AX412282	AX412282 Sequence	312	215	16.0	300425	1	AP005044	AP005044 Streptomy
240	311.5	23.2	699	6	AX507044	AX507044 Sequence	313	214.5	16.0	292550	1	AP001513	AP001513 Bacillus
241	311.5	23.2	699	6	AX651360	AX651360 Sequence	314	207	15.4	528	6	AR236710	AR236710 Sequence
242	309	23.0	256879	3	AC116982	AC116982 Dictyoste	315	204.5	15.2	1231	8	AF168778	AF168778 Eucalyptu
243	307	22.9	930	8	AB000408	AB000408 Populus k	316	204.5	15.2	288437	1	AE017270	AE017270 Bacillus
244	307	22.9	1810	6	E09625	E09625 Streptomyce	317	204	15.2	110000	1	BX908798	Continuation (22 o
245	307	22.9	3267	1	STMACYA	D30759 Streptomyce	318	202.5	15.1	110000	1	AE000516	Continuation (3 of
246	307	22.9	50398	3	AC024771	AC024771 Caenorhab	319	202.5	15.1	341957	1	BX842572	BX842572 Mycobacte
247	307	22.9	206217	2	AC006754	AC006754 Caenorhab	320	202.5	15.1	343050	1	BX248334	BX248334 Mycobacte
248	305.5	22.7	965	8	ATHORF	L40031 Arabidops	321	202	15.0	399	6	BD224470	BD224470 Materials
249	304.5	22.7	112369	8	AC136449	AC136449 Medicago	322	202	15.0	399	6	AR216520	AR216520 Sequence
250	304.5	22.7	142064	2	AC148528	AC148528 Medicago	323	201.5	15.0	588	6	AR319743	AR319743 Sequence
251	303.5	22.6	14105	1	AE000743	AE000743 Aquifex a	324	201.5	15.0	3705	8	ATH242988	ATH242988 Arabidops
252	302.5	22.5	94091	8	ATE28A23	AE021961 Arabidops	325	200.5	14.9	632	6	AR227195	AR227195 Sequence
253	302.5	22.5	192861	8	ATCHRIV80	AL161584 Arabidops	326	196	14.6	83433	2	AP006501	Continuation (13 o
254	299.5	22.3	1010	8	AB035144	AB035144 Citrus na	327	190	14.1	300150	1	AP004594	AP004594 Oceanobac
255	298.5	22.2	1075	6	AR074146	AR074146 Sequence	328	185.5	13.8	13399	1	AE013088	AE013088 Theamoana
256	298.5	22.2	1075	6	BD224331	BD224331 Materials	329	185	13.8	50398	3	AC024771	AC024771 Caenorhab
257	298.5	22.2	1075	6	AR216381	AR216381 Sequence	330	185	13.8	110000	1	BX571966	Continuation (18 o
258	298.5	22.2	1075	6	AR432783	AR432783 Sequence	331	185	13.8	206217	2	AC006754	AC006754 Caenorhab
259	298.5	22.2	1075	6	BD005694	BD005694 Materials	332	184.5	13.7	265006	1	AE017259	AE017259 Wolbachia
260	298	22.2	3072	8	PT223620	AY232620 Populus t	333	183.5	13.7	287406	1	AE017280	AE017280 Bacillus
261	297.5	22.2	1308	8	AY579076	AY579076 Broussonet	334	183	13.6	594	6	BD224381	BD224381 Materials
262	294	21.9	1529	8	AY579076	AY579076 Broussonet	335	183	13.6	594	6	BD216431	BD216431 Sequence
263	291	21.7	1074	6	BD243145	BD243145 Sequence	336	183	13.6	594	6	AR432833	AR432833 Sequence
264	291	21.7	1074	6	BD243330	BD243330 Materials	337	181.5	13.5	505	6	AR236708	AR236708 Sequence
265	291	21.7	1074	6	AR216380	AR216380 Sequence	338	180.5	13.4	297850	1	AP006577	AP006577 Gloebact
266	291	21.7	1074	6	AR432782	AR432782 Sequence	339	180	13.4	607	6	BD074114	BD074114 Sequence
267	291	21.7	1074	6	BD005693	BD005693 Materials	340	180	13.4	607	6	BD224299	BD224299 Materials
268	290.5	21.6	2000	6	AX461218	AX461218 Sequence	341	180	13.4	607	6	BD273001	BD273001 Materials
269	290.5	21.6	89904	8	ATT25K17	AL049171 Arabidops	342	180	13.4	607	6	AR216349	AR216349 Sequence
270	290.5	21.6	196286	8	ATCHRIV64	AL161564 Arabidops	343	180	13.4	607	6	AR432751	AR432751 Sequence
271	287.5	21.4	1703	1	SYOPAPSA	M84476 Synchococc	344	180	13.4	607	6	BD005662	BD005662 Materials
272	286.5	21.3	109519	6	AX195929	AX195929 Sequence	345	179	13.3	29255	6	CQ363728	CQ363728 Sequence
273	285	21.2	2983	6	A98905	A98905 Sequence 2	346	179	13.3	110000	1	AE017283	Continuation (7 of
274	284	21.1	145828	8	AP005332	AP005332 Oryza sat	347	179	13.3	110000	1	AE017283	Continuation (8 of
275	284	21.1	154188	8	AP005633	AP005633 Oryza sat	348	178.5	13.3	142001	8	ATF21F14	ATF21F14 Sequence
276	280	20.8	3162	8	PCCOAMT	Z33878 P.crispum g	349	178	13.3	584	6	AX660579	AX660579 Arabidops
277	280	20.8	6662	8	PCCOAMTR	Z54483 P.crispum g	350	178	13.3	110000	1	AP006618	Continuation (50 o
278	279	20.8	651	6	AX196012	AX196012 Sequence	351	176.5	13.1	510	6	AR236698	AR236698 Sequence
279	277.5	20.7	3800	8	A98904	A98904 Sequence 1	352	176.5	13.1	600	6	AR236713	AR236713 Sequence
280	277.5	20.7	3800	8	PT223621	AY223621 Populus t	353	176.5	13.1	311000	1	CP0000112	CP0000112 Streptomy
281	276.5	20.6	343	6	AX400599	AX400599 Sequence	354	176	13.1	110000	1	CP00001109	Continuation (10 o
282	269	20.0	1944	1	AF145250	AF145250 Rhodother	355	176	13.1	110000	1	CP00001110	Continuation (11 o
283	266.5	19.8	8868	3	CEY32B12A	AL023834 Caenorhab	356	176	13.1	346357	1	BX842647	BX842647 Bdellovib
284	261.5	19.5	1673	8	AY6001140	AY6001140 Broussonet	357	175.5	13.1	320150	1	AP005033	AP005033 Streptomy
285	258	19.2	675	6	AR390021	AR390021 Sequence	358	174	13.0	296	6	BD224471	BD224471 Materials
286	244.5	18.2	110000	1	AP006841	Continuation (52 o	359	174	13.0	296	6	AR216521	AR216521 Sequence
287	244.5	18.2	347660	1	AP002994	AP002994 Mesorhizo	360	172.5	12.8	110000	1	AE017225	Continuation (42 o
288	235.5	17.5	30029	1	AE017178	AE017178 Porphyrom	361	172.5	12.8	110000	1	AE017334	Continuation (42 o
289	235.5	17.5	305961	1	AE016937	AE016937 Bacteroid	362	172.5	12.8	110000	1	AE017355	Continuation (43 o
290	232.5	17.3	323	8	AF534905	AF534905 Coffea ca	363	172.5	12.8	110000	1	CP00000142	Continuation (13 o
291	232	17.3	607	8	AY098515	AY098515 Ananas co	364	172.5	12.8	110000	1	CR543861	Continuation (13 o
292	229.5	17.1	536	8	AY161276	AY161276 Populus b	365	172.5	12.8	288814	1	AE017278	AE017278 Bacillus
293	229.5	17.1	234545	5	BX470214	BX470214 Zebrafish	366	172.5	12.8	290029	1	AE017038	AE017038 Bacillus
294	228	17.0	105863	8	AC004133	AC004133 Genomic s	367	172	12.8	10445	1	AE014716	AE014716 Bifidobac
295	224.5	16.7	760	6	AR074116	AR074116 Sequence	368	172	12.8	349980	6	AX492784	AX492784 Sequence
296	224.5	16.7	760	6	BD224301	BD224301 Materials	369	172	12.8	349980	6	AX553951	AX553951 Sequence

370	171.5	12.8	562	6	AR074144	Sequence	443	126	9.4	777	6	AX377804	Sequence
371	171.5	12.8	562	6	BD224329	Materials	444	125.5	9.3	705	6	CQ649678	Sequence
372	171.5	12.8	562	6	BD272987	Materials	445	125.5	9.3	20639	1	AE014228	Streptoco
373	171.5	12.8	562	6	AR216379	Sequence	446	125.5	9.3	349980	6	CQ655069	Sequence
374	171.5	12.8	562	6	AR432781	Sequence	447	125.5	9.3	349980	6	AX954529	Sequence
375	171.5	12.8	562	6	BD005692	Materials	448	124.5	9.3	708	6	AX607661	Sequence
376	171.5	12.8	301332	1	AE017012	Bacillus	C 449	124.5	9.3	6641	6	AX602145	Sequence
377	170	12.7	75216	6	AX704275	Sequence	C 450	124.5	9.3	167050	1	SAG766847	Streptoco
378	170	12.7	110000	1	AE000516	Continuation (14 o	C 451	124.5	9.3	292200	1	SC0939129	Streptomy
379	170	12.7	299450	1	BD248338	Myxobacte	452	124	9.2	1605	1	AF016233	Enterococ
380	170	12.7	349306	1	BX842575	Myxobacte	453	124	9.2	110000	1	AE017225	22
381	169	12.6	1389	6	AX414722	Sequence	454	124	9.2	110000	1	AE017334	22
382	169	12.6	240050	1	AL591979	Listeria	455	124	9.2	110000	1	AE017355	23
383	169	12.6	349980	6	AX641668	Sequence	456	124	9.2	293264	1	AE017031	Bacillus
384	169	12.6	349980	6	AX641669	Sequence	457	123	9.2	498	6	AR347999	Sequence
385	168.5	12.5	302325	1	AE017236	Myxobacte	C 458	123	9.2	3673	1	AF269748	Staphyloc
386	168	12.5	2233	6	AX416554	Sequence	C 459	123	9.2	3673	6	AR485702	Sequence
387	168	12.5	290507	1	AE017327	Listeria	C 460	123	9.2	3673	6	AX145066	Sequence
388	166.5	12.4	403	8	AY725190	Arachis h	C 461	122	9.2	300029	1	AE016748	Staphyloc
389	166.5	12.4	403	8	AY725191	Arachis h	462	122	9.1	201	11	BV202015	20798
390	166.5	12.4	403	8	AY725192	Arachis h	463	122	9.1	110000	1	CP000001	23
391	166.5	12.4	403	8	AY725193	Arachis h	464	121.5	9.0	711	6	AX568724	Sequence
392	166.5	12.4	403	8	AY725194	Arachis h	465	121.5	9.0	714	6	AR481634	Sequence
393	166	12.4	4560	1	LLVSPFEP	X99710 L.lactis OR	466	121.5	9.0	11309	6	CQ789017	Sequence
394	164.5	12.2	296750	1	AP003191	AP003191 Clostridi	467	121.5	9.0	11309	6	AR218876	Sequence
395	164	12.2	399	6	BD224469	Materials	468	121.5	9.0	11309	6	BD003788	Polynucle
396	164	12.2	399	6	AR216519	Sequence	469	121.5	9.0	11552	1	AE008462	Streptoco
397	164	12.2	333050	1	AL596168	Sequence	470	121.5	9.0	13378	1	AE007401	Streptoco
398	164	12.2	349980	6	AX413017	Sequence	471	121.5	9.0	111135	2	SPNEU1906	Streptoco
399	164	12.2	349980	6	AX417044	Sequence	472	121.5	9.0	349980	6	AX571762	Sequence
400	164	12.2	349980	6	AX417045	Sequence	473	121	9.0	518	6	CQ720861	Sequence
401	162.5	12.1	702	6	AR320113	Sequence	C 474	120	8.9	301550	1	AP003134	Staphyloc
402	162.5	12.1	12898	1	AE006403	Lactococc	C 475	120	8.9	303450	1	SC0939130	Streptomy
403	162	12.1	13325	1	AE005016	Halobacte	C 476	120	8.9	346300	1	AP003362	Staphyloc
404	161.5	12.0	348450	1	MLEPRTN4	AL583920 Mycobacte	C 477	119.5	8.9	298050	1	BX321861	Nitrosomo
405	159.5	11.9	299550	1	AP001511	AP001511 Bacillus	C 478	119	8.9	12014	1	AE010732	Methanusa
406	158	11.8	38675	1	MLU15180	U15180 Mycobacteri	C 479	118.5	8.8	1262	10	BC010402	Mus muscu
407	158	11.8	38675	6	AR345367	Sequence	480	118	8.8	507	6	AX207630	Sequence
408	158	11.7	110000	1	AE016822	Continuation (10 o	C 481	118	8.8	37768	3	U40414	Caenorhabdi
409	157	11.7	801	6	AR394036	Sequence	C 482	118	8.8	288404	1	AE017272	Bacillus
410	157	11.7	301278	1	AE015939	AE015939 Clostridi	C 483	116.5	8.7	10763	1	AE010544	Fusobacte
411	157	11.7	302132	1	AE016955	Enterococ	484	116	8.6	110000	1	BX571965	33
412	156	11.6	19024	6	BD193585	BD193585 Enterococ	485	115	8.6	639	6	BD163441	Novel pol
413	154	11.5	8367	1	AP0400582	AP400582 Acinetoba	486	115	8.6	639	6	AX121324	Sequence
414	154	11.5	110000	1	CR543861	Continuation (15 o	C 487	115	8.6	769	6	AX771879	Sequence
415	150.5	11.2	81866	6	NC64C2	Continuation (6 of	C 488	115	8.6	333150	1	AP005277	Sequence
416	149.5	11.1	508	6	AR236701	BX294009 Neurospor	C 489	115	8.6	349459	1	BX927151	Corynebac
417	149.5	11.1	110000	1	AE017333	Continuation (28 o	C 490	115	8.6	349980	6	AX127146	Sequence
418	149.5	11.1	110000	1	CP000002	Continuation (28 o	C 491	114.5	8.5	2868	1	AB049411	Acinetoba
419	147	10.9	1433	8	AF168779	AF168779 Eucalyptu	C 492	114.5	8.5	143109	8	OSJN00224	Oryza sat
420	147	10.9	199173	1	BSUB0014	Z99117 Bacillus su	C 493	114.5	8.5	300750	1	AP005217	Corynebac
421	146.5	10.9	110000	1	AE017180	Continuation (6 of	C 494	114	8.5	636	6	AX617408	Sequence
422	145	10.8	1504	8	AY267760	AY267760 Fusarium	495	114	8.5	1255	10	AF076156	Mus muscu
423	144	10.7	300050	1	AP004599	AP004599 Oceanobac	496	114	8.5	1605	8	PAN245505	Podospora
424	141	10.5	957	5	BX930132	BX930132 Gallus ga	C 497	114	8.5	110000	1	AE000516	19
425	139	10.3	51454	1	AE014157	AE014157 Streptoco	C 498	114	8.5	110000	1	BX571857	16
426	139	10.3	310950	1	AP005143	AP005143 Streptoco	C 499	114	8.5	291050	1	BX248340	Myxobacte
427	137	10.2	115339	8	AP003940	AP003940 Oryza sat	C 500	114	8.5	333750	1	AP004827	Staphyloc
428	137	10.2	174478	8	AP005467	AP005467 Oryza sat	C 501	114	8.5	347496	1	BX842577	Myxobacte
429	136	10.1	705	6	CQ649680	CQ649680 Sequence	C 502	113.5	8.5	5514	6	CQ587772	Sequence
430	136	10.1	10844	1	AE010060	AE010060 Streptoco	C 503	112	8.3	2086	6	AX394673	Sequence
431	136	10.1	11615	1	AE006576	AE006576 Streptoco	504	112	8.3	7912	10	RNCATOMET	Z12651 R.norvegicu
432	136	10.1	110000	1	CP000003	Continuation (11 o	C 505	112	8.3	110000	1	AE017856	17
433	136	10.1	110000	1	CP000003	Continuation (12 o	C 506	112	8.3	300052	1	BX571232	Myxobacte
434	134	10.0	324050	1	BX251410	BX251410 Tropherym	507	112	8.3	30015	1	AP005076	Vibrio pa
435	134	10.0	324227	1	AE016852	AE016852 Tropherym	C 508	112	8.3	300750	1	AP005217	Corynebac
436	131	9.8	304262	1	AE017005	AE017005 Bacillus	C 509	111.5	8.3	110000	1	AE017282	28
437	130.5	9.7	12012	1	AE014908	AE014908 Streptoco	510	111	8.3	495	6	AR485101	Sequence
438	130	9.7	10398	1	AE011847	AE011847 Xanthomon	511	111	8.3	495	6	AX144317	Sequence
439	128	9.5	2316	6	AX207632	AX207632 Sequence	C 512	111	8.3	13715	6	AR354077	Sequence
440	127.5	9.5	10069	1	AE007678	AE007678 Clostridi	C 513	111	8.3	13715	6	AR355633	Sequence
441	126.5	9.4	534	6	AX433853	AX433853 Sequence	C 514	111	8.3	38494	6	AR345349	Sequence
442	126	9.4	777	6	AX207628	AX207628 Sequence	C 515	111	8.3	38503	1	MSGB1912CS	L01536 M. leprae g



c 516	110.5	8.2	301443	1	AE017239	AE017239 Mycobacte	589	102	7.6	1405	5	BC082476	BC082476 Xenopus 1
517	110	8.2	236	6	BD224451	BD224451 Materials	c 590	102	7.6	1746	9	HSU14534	U14534 Human orpha
518	110	8.2	236	6	AR216501	AR216501 Sequence	c 591	102	7.6	1898	6	I46765	I46765 Sequence 1
519	110	8.2	236	6	AR432903	AR432903 Sequence	c 592	102	7.6	2084	11	BV177077	BV177077 sqnm92606
520	110	8.2	509	11	BX784390	BX784390 pinus pin	593	102	7.6	14138	1	AE004766	AE004766 Pseudomon
521	110	8.2	247910	1	AE017307	AE017307 Thermus t	c 594	102	7.6	14469	1	AE011498	AE011498 Leptospir
c 522	109.5	8.2	348411	1	AP003007	AP003007 Mesorhizo	c 595	102	7.6	21540	10	AC115937	AC115937 Mus muscu
c 523	109	8.1	11847	1	AE001918	AE001918 Deinococc	c 596	102	7.6	301250	1	AP005950	AP005950 Bradyrhiz
524	109	8.1	213732	1	AE001862	AE001862 Deinococc	c 597	102	7.6	303550	1	SC0939118	AL939118 Streptomy
525	108.5	8.1	1107	6	CQ812330	CQ812330 Sequence	598	102	7.6	305541	1	AE017290	AE017290 Leptospir
526	108.5	8.1	1107	9	HUMCOMTA	M65212 Homo sapien	599	102	7.6	348068	1	BX572604	BX572604 Rhodopseu
527	108.5	8.1	1213	9	BC011935	BC011935 Homo sapi	c 600	101.5	7.6	601	11	BV167609	BV167609 sqnm6022
528	108	8.0	320	4	AY340812	AY340812 Canis fam	c 601	101.5	7.6	2039	9	AK130031	AK130031 Homo sapi
c 529	108	8.0	10288	1	AE012905	AE012905 Chlorobiu	c 602	101.5	7.6	2084	11	BV177509	BV177509 sqnm95100
530	108	8.0	120528	9	AP000812	AP000812 Homo sapi	c 603	101.5	7.6	2084	11	BV179316	BV179316 sqnm10484
c 531	108	8.0	132544	1	AF521085	AF521085 Streptomy	604	101.5	7.6	5600	8	AY673000	AY673000 Triticum
c 532	108	8.0	155922	2	AP002513	AP002513 Homo sapi	605	101.5	7.6	6658	8	AY673001S2	AY673002 Triticum
533	107.5	8.0	1206	6	AX774876	AX774876 Sequence	606	101.5	7.6	153875	9	AC003682	AC003682 Homo sapi
534	107.5	8.0	1206	9	HUMCOMTC	M58525 Homo sapien	607	101.5	7.6	188324	2	BC530094	BC530094 Homo sapi
535	107.5	8.0	1291	6	CQ716680	CQ716680 Sequence	608	101.5	7.6	189326	9	AC018462	AC018462 Homo sapi
536	107.5	8.0	139628	2	AC150112	AC150112 Gallus ga	c 609	101	7.5	1543	8	AK120652	AK120652 Oriza sat
537	107.5	8.0	166863	2	AC150140	AC150140 Gallus ga	c 610	101	7.5	1820	9	BC035516	BC035516 Homo sapi
538	107.5	8.0	250950	1	AP005335	AP005335 Vibrio vu	c 611	101	7.5	129778	8	AC091123	AC091123 Oriza sat
c 539	107.5	8.0	302174	1	AE017241	AE017241 Mycobacte	c 612	101	7.5	154625	2	BC323047	BC323047 Danio rer
c 540	107.5	8.0	304490	1	AE016806	AE016806 Vibrio vu	c 613	101	7.5	163962	9	BS000233	BS000233 Pan trogl
c 541	107	7.9	10113	1	AE0110715	AE0110715 Methanosa	614	101	7.5	178158	8	AC084320	AC084320 Oriza sat
542	106.5	7.9	816	9	CR456997	CR456997 Homo sapi	c 615	101	7.5	348971	1	BX572594	BX572594 Rhodopseu
543	105.5	7.9	873	9	CR456422	CR456422 Homo sapi	616	100.5	7.5	1447	5	BC049292	BC049292 Xenopus 1
544	105.5	7.9	9463	1	SGRRTCLUS	X95596 S. griseus c	c 617	100.5	7.5	1688	6	AR035537	AR035537 Sequence
c 545	105.5	7.9	11464	1	AE005915	AE005915 Caulobact	c 618	100.5	7.5	1888	6	EL1457	EL1457 cDNA encodi
546	105.5	7.9	110000	1	AE017282_18	Continuation (19 o	c 619	100.5	7.5	1815	6	AR477499	AR477499 Sequence
c 547	105.5	7.9	110000	1	BX571966_09	Continuation (10 o	c 620	100.5	7.5	1934	9	BC007790	BC007790 Homo sapi
548	105.5	7.9	347625	1	BX248356	BX248356 Corynebac	c 621	100.5	7.5	1979	6	AR035536	AR035536 Sequence
c 549	105.5	7.9	347625	1	BX640416	BX640416 Bordetell	c 622	100.5	7.5	1979	6	EL1456	EL1456 cDNA encodi
550	105.5	7.9	349354	1	BX640416	BX640416 Bordetell	c 623	100.5	7.5	1987	6	AR448000	AR448000 Sequence
c 551	105	7.8	457	6	AX394671	AX394671 Sequence	c 624	100.5	7.5	2014	9	BC047750	BC047750 Homo sapi
c 552	105	7.8	110000	2	AP006502_14	Continuation (15 o	c 625	100.5	7.5	2070	9	BC074500	BC074500 Homo sapi
553	105	7.8	308050	1	SC0939124	AL939124 Streptomy	626	100.5	7.5	247151	2	AC126662	AC126662 Rattus no
554	104.5	7.8	1895	8	AK108846	AK108846 Oriza sat	627	100	7.4	2734	8	AK067366	AK067366 Oriza sat
c 555	104.5	7.8	180000	1	AF322012S1	AF322012 Bradyrhiz	c 633	100	7.4	6806	1	STMTN4556	M29297 S. fradiae c
556	104	7.7	299600	1	AP005941	AP005941 Bradyrhiz	c 634	100	7.4	10677	1	AE005967	AE005967 Caulobact
c 557	104.5	7.7	299600	1	AP005941	AP005941 Bradyrhiz	635	100	7.4	126845	8	AP005244	AP005244 Oriza sat
c 563	104	7.7	299850	1	AP005949	AP005949 Bradyrhiz	636	100	7.4	145311	1	AP003014	AP003014 Mesorhizo
564	103.5	7.7	1491	10	RATCATAA	M60753 R. norvegicu	c 637	100	7.4	164628	2	AC073646	AC073646 Homo sapi
565	103.5	7.7	1527	10	BC081850	BC081850 Rattus no	c 638	100	7.4	179937	2	AF546190	AF546190 Zea mays
566	103.5	7.7	1540	10	RATCATAB	M60754 R. norvegicu	639	100	7.4	230146	2	AC134057	AC134057 Rattus no
c 567	103.5	7.7	2138	1	STWSIGNA	L11648 Streptomyce	640	100	7.4	299991	1	AE016776	AE016776 Pseudomon
568	103.5	7.7	66669	1	AME16952	Y16952 Amycolatops	641	100	7.4	300450	1	AP005960	AP005960 Bradyrhiz
569	103.5	7.7	110000	2	LMFLCHR32_17	Continuation (18 o	642	99.5	7.4	3079	1	PDEMXXYZ	M92421 Paracoccus
c 570	103.5	7.7	233050	1	AL627271	AL627271 Salmonell	c 643	99.5	7.4	3949	5	AF327372	AF327372 Gallus ga
571	103.5	7.7	300247	1	AE016837	AE016837 Salmonell	c 644	99.5	7.4	9088	5	AF327372	AF327372 Gallus ga
c 572	103	7.7	3307	8	AK110307	AK110307 Oriza sat	645	99.5	7.4	295500	1	AP005954	AP005954 Bradyrhiz
c 573	103	7.7	10732	1	AE013407	AE013407 Methanosa	646	99.5	7.4	300350	1	AP006574	AP006574 Gloeobact
c 574	103	7.7	11877	1	AE011683	AE011683 Xanthomon	647	99.5	7.4	339681	1	AP003009	AP003009 Mesorhizo
c 575	103	7.7	44421	1	AY442931	AY442931 Agrobacte	c 648	99.5	7.4	348171	1	BX640412	BX640412 Bordetell
c 576	103	7.7	64492	1	AB086653	AB086653 Streptomy	c 649	99	7.4	2010	6	CQ785960	CQ785960 Sequence
c 577	103	7.7	109192	8	CNS08CCR	AL954153 Oriza sat	c 650	99	7.4	2030	6	HSU07132	U07132 Human stero
c 578	102.5	7.6	1525	8	AF066951	AF066951 Enteromor	c 651	99	7.4	2010	6	I36667	I36667 Sequence 1
c 579	102.5	7.6	2760	1	TAU62584	U62584 Thermus aqu	c 652	99	7.4	2030	6	I70211	I70211 Sequence 1
c 580	102.5	7.6	3003	6	CQ845922	CQ845922 Sequence	c 653	99	7.4	2505	6	AR023937	AR023937 Sequence 7
c 581	102.5	7.6	3003	9	AK131436	AK131436 Homo sapi	c 654	99	7.4	2505	6	I15438	I15438 Sequence 7
c 582	102.5	7.6	3978	6	CQ735548	CQ735548 Sequence	c 655	99	7.4	2685	6	AX924362	AX924362 Sequence
c 583	102.5	7.6	5502	9	HSMB08450	BX648302 Homo sapi	c 656	99	7.4	2685	6	AX924362	AX924362 Sequence
c 584	102.5	7.6	10245	1	AE004569	AE004569 Pseudomon	657	99	7.4	7528	6	CQ729217	CQ729217 Sequence
c 585	102.5	7.6	157424	8	AP003568	AP003568 Oriza sat	658	99	7.4	7536	9	AY451392	AY451392 Homo sapi
c 586	102.5	7.6	298550	1	AP005961	AP005961 Bradyrhiz	659	99	7.4	8461	6	CQ785963	CQ785963 Sequence
c 587	102.5	7.6	300129	1	AE017309	AE017309 Desulfovi	660	99	7.4	8461	6	CQ875346	CQ875346 Sequence
588	102.5	7.6	300531	1	AE016932	AE016932 Bacteroid	661	99	7.4	8472	9	BC063242	BC063242 Homo sapi

662	99	7.4	10029	1	AE010416	AE010416 Methanopy	c 735	97	7.2	310029	1	AE016868	AE016868 Pseudomon
663	99	7.4	10202	1	AE000483	AE000483 Pseudomon	736	97	7.2	348074	1	AE016868	AE016868 Pseudomon
664	99	7.4	10843	9	AY148100	AY148100 Homo sapi	737	97	7.2	349980	6	AE016868	AE016868 Pseudomon
665	99	7.4	110000	2	AP006484	AP006484 Cyanidios	738	96.5	7.2	1562	5	CR760877	CR760877 Xenopus t
666	99	7.4	138939	9	AC119675	AC119675 Homo sapi	739	96.5	7.2	11426	1	AE0044590	AE0044590 Pseudomon
667	99	7.4	163978	10	AC140411	AC140411 Mus muscu	740	96.5	7.2	22233	1	SPDBFB	X72850 Spingomona
668	99	7.4	193057	10	AL663067	AL663067 Mouse DNA	741	96.5	7.2	106707	2	AE019314	AE019314 Homo sapi
669	99	7.4	299450	1	AP005938	AP005938 Bradyrhiz	742	96.5	7.2	110000	2	AE016822_04	Continuation (5 of
670	99	7.4	300181	1	AE017318	AE017318 Desulfovi	743	96.5	7.2	128342	9	AL627313	Human DNA
671	99	7.4	346294	1	AP002299	AP002299 Mesorhizo	744	96.5	7.2	152462	10	AC131998	AC131998 Mus muscu
672	98.5	7.3	1217	9	BC000419	BC000419 Homo sapi	745	96.5	7.2	171525	2	AC145473	AC145473 Rattus no
673	98.5	7.3	1217	9	BC000419	BC000419 Homo sapi	746	96.5	7.2	182061	1	AC107869	AC107869 Mus muscu
674	98.5	7.3	1695	8	AC005867	AC005867 Homo sapi	747	96.5	7.2	195859	14	AF281817	AF281817 Tupaia he
675	98.5	7.3	2384	6	AX747042	AX747042 Sequence	748	96.5	7.2	219252	2	AC026760	AC026760 Mus muscu
676	98.5	7.3	2384	6	AX747042	AX747042 Sequence	749	96.5	7.2	242203	2	AC097860	AC097860 Rattus no
677	98.5	7.3	3147	6	BD132995	BD132995 Anti-bact	750	96.5	7.2	258888	2	AC109677	AC109677 Rattus no
678	98.5	7.3	3147	6	AR232445	AR232445 Sequence	751	96.5	7.2	272101	1	AE017302	AE017302 Thermus t
679	98.5	7.3	3147	6	AR256497	AR256497 Sequence	752	96.5	7.2	299750	1	AP005964	AP005964 Bradyrhiz
680	98.5	7.3	3147	6	AX189015	AX189015 Sequence	753	96	7.1	1657	9	AK098658	AK098658 Homo sapi
681	98.5	7.3	4355	1	EC0ARAJ	M64787 E.coli sbcc	754	96	7.1	2004	6	BD180143	BD180143 Highly th
682	98.5	7.3	5125	1	EC5BCC	X15981 E.coli sbcc	755	96	7.1	2588	1	CFICEXX	L11080 Cellulomona
683	98.5	7.3	8008	1	FAU93274	U93274 Pseudomonas	756	96	7.1	10066	14	BHV12US	Z23068 Bovine herp
684	98.5	7.3	11015	1	AE004736	AE004736 Pseudomon	757	96	7.1	15534	6	CQ776613	CQ776613 Sequence
685	98.5	7.3	16675	1	AE011814	AE011814 Xanthomon	758	96	7.1	15534	9	AB051895	AB051895 Homo sapi
686	98.5	7.3	77534	1	AF235504	AF235504 Streptomy	759	96	7.1	110000	2	AC151276_0	AC151276 Mus muscu
687	98.5	7.3	77536	6	BD235937	BD235937 Polyketid	760	96	7.1	110000	2	AP006497_2	Continuation (3 of
688	98.5	7.3	77536	6	AR271638	AR271638 Sequence	761	96	7.1	110000	8	AE016820_03	Continuation (4 of
689	98.5	7.3	77536	6	AR564393	AR564393 Sequence	762	96	7.1	160714	2	AC150149	AC150149 Gallus ga
690	98.5	7.3	110000	1	U00096_04	Continuation (5 of	763	96	7.1	202432	2	AC143119	AC143119 Macaca mu
691	98.5	7.3	110000	1	AP006618_23	Continuation (24 o	764	96	7.1	210472	9	AC035139	AC035139 Homo sapi
692	98.5	7.3	110000	8	AE016819_06	Continuation (7 of	765	96	7.1	233568	2	AC150275	AC150275 Mus muscu
693	98.5	7.3	128824	1	ECU73857_06	U73857 Escherichia	766	96	7.1	301191	1	AE017152	AE017152 Haemophil
694	98.5	7.3	168797	2	AC104882	AC104882 Mus muscu	767	96	7.1	308015	1	AE016783	AE016783 Pseudomon
695	98.5	7.3	202000	1	AP000038	AP000038 Aeropyrum	768	95.5	7.1	666	12	AY657499	AY657499 Synthetic
696	98.5	7.3	296300	1	AP005035	AP005035 Streptomy	769	95.5	7.1	2696	8	AK121206	AK121206 Oryza sat
697	98.5	7.3	302300	1	AP005034	AP005034 Streptomy	770	95.5	7.1	2926	1	AY667481	AY667481 Lysobacte
698	98.5	7.3	302550	1	AP006581	AP006581 Gloeobact	771	95.5	7.1	3173	6	E05949	E05949 DNA encodin
699	98	7.3	1782	6	BD158070	BD158070 Primer fo	772	95.5	7.1	110000	1	BX571965_24	Continuation (25 o
700	98	7.3	1782	6	AX879871	AX879871 Sequence	773	95.5	7.1	110000	1	CP000010_18	Continuation (19 o
701	98	7.3	1782	9	AK022862	AK022862 Homo sapi	774	95.5	7.1	110000	1	CP000011_12	Continuation (13 o
702	98	7.3	12772	1	AE004727	AE004727 Pseudomon	775	95.5	7.1	110000	8	AE016818_08	Continuation (9 of
703	98	7.3	76196	1	AY354515	AY354515 Streptomy	776	95.5	7.1	121960	2	AC151662	AC151662 basypus n
704	98	7.3	174363	9	AC135506	AC135506 Homo sapi	777	95.5	7.1	159119	1	AP006583	AP006583 Gloeobact
705	98	7.3	185146	2	AC104311	AC104311 Homo sapi	778	95.5	7.1	181731	2	CR792458	CR792458 Dario rer
706	98	7.3	215342	2	AC109322	AC109322 Homo sapi	779	95.5	7.1	192302	2	AC134315	AC134315 Lemur cat
707	98	7.3	279312	2	AC126572	AC126572 Rattus no	780	95.5	7.1	277000	1	SC0939109	SC0939109 Streptomy
708	98	7.3	310581	1	AE016863	AE016863 Pseudomon	781	95.5	7.1	298550	1	AP005029	AP005029 Streptomy
709	98	7.3	348971	1	BX572594	BX572594 Rhodosphe	782	95.5	7.1	299050	1	SC0939104	SC0939104 Streptomy
710	97.5	7.3	861	12	AY658649	AY658649 Synthetic	783	95.5	7.1	300350	1	AP006574	AP006574 Gloeobact
711	97.5	7.3	1632	6	AR301781	AR301781 Sequence	784	95.5	7.1	300861	1	AE016777	AE016777 Pseudomon
712	97.5	7.3	5525	8	AY672999	AY672999 Triticum	785	95.5	7.1	303550	1	SC0939131	SC0939131 Streptomy
713	97.5	7.3	10130	1	AE002085	AE002085 Deinococc	786	95.5	7.1	349672	1	BX640419	BX640419 Bordetell
714	97.5	7.3	20235	1	SERERYAB	M63677 S.erythraea	787	95.5	7.1	349726	1	BX640421	BX640421 Bordetell
715	97.5	7.3	20235	6	AR049368	AR049368 Sequence	788	95	7.1	1416	6	BD155975	BD155975 Primer fo
716	97.5	7.3	20235	6	AR095529	AR095529 Sequence	789	95	7.1	1416	6	AK076143	AK076143 Sequence
717	97.5	7.3	20444	1	SERERYABS	X62569 S.erythraea	790	95	7.1	1416	9	AK001168	AK001168 Homo sapi
718	97.5	7.3	24494	6	AR301774	AR301774 Sequence	791	95	7.1	2597	6	AX713562	AX713562 Sequence
719	97.5	7.3	42805	9	AC004221	AC004221 Homo sapi	792	95	7.1	2597	9	AK055133	AK055133 Homo sapi
720	97.5	7.3	189091	2	AC118207	AC118207 Mus muscu	793	95	7.1	3346	1	PS081032	PS081032 Pseudomonas
721	97.5	7.3	302650	1	AP005958	AP005958 Bradyrhiz	794	95	7.1	4941	6	CQ730770	CQ730770 Sequence
722	97.5	7.3	310550	1	SC0939113	SC0939113 Streptomy	795	95	7.1	4962	9	AB011162	AB011162 Homo sapi
723	97	7.2	1192	5	BX932533	BX932533 Gallus ga	796	95	7.1	4966	9	BC035577	BC035577 Homo sapi
724	97	7.2	2585	1	CFICEX	M15824 Cellulomona	797	95	7.1	4976	8	AK110228	AK110228 Oryza sat
725	97	7.2	12541	1	AE001956	AE001956 Deinococc	798	95	7.1	14568	1	AE000453	AE000453 Pseudomon
726	97	7.2	13026	1	AE002510	AE002510 Neisseria	799	95	7.1	110000	1	AP006840_28	Continuation (29 o
727	97	7.2	25184	1	AE008779	AE008779 Salmonell	800	95	7.1	110000	1	CP000011_11	Continuation (12 o
728	97	7.2	110000	1	AP006618_54	Continuation (55 o	801	95	7.1	110000	6	BD430793_02	Continuation (3 of
729	97	7.2	110000	1	CP000011_01	Continuation (2 of	802	95	7.1	147706	8	AC083945	AC083945 Oryza sat
730	97	7.2	241178	2	AC130508	AC130508 Rattus no	803	95	7.1	189458	10	AC134908	AC134908 Mus muscu
731	97	7.2	280558	1	AE017301	AE017301 thermus t	804	95	7.1	209384	2	AC151295	AC151295 Mus muscu
732	97	7.2	296282	2	AC111857	AC111857 Rattus no	805	95	7.1	213817	2	AC123649	AC123649 Mus muscu
733	97	7.2	299175	1	AP005023	AP005023 Streptomy	806	95	7.1	220577	2	AC068497	AC068497 Mus muscu
734	97	7.2	300704	1	AE017316	AE017316 Desulfovi	807	95	7.1	300029	8	AE017083	AE017083 Oryza sat

C 808	95	7.1	300181	1	AE017318	Deaulfovi	C 881	94	7.0	230993	2	AC150072	AC150072 Gallus ga
C 809	95	7.1	300425	1	AP005038	Streptomy	882	94	7.0	231350	2	AC150501	AC150501 Bos tauru
C 810	95	7.1	303400	1	AP006578	Gloeobact	883	94	7.0	231829	2	AC125936	AC125936 Rattus no
C 811	95	7.1	304681	2	AC016483	Mus muscu	884	94	7.0	233345	2	AC150066	AC150066 Gallus ga
C 812	95	7.1	307150	1	CNSPAX01		885	94	7.0	299850	1	AP005949	AP005949 Bradyrhiz
C 813	95	7.1	339650	1	SC0919108		C 886	94	7.0	300200	1	AP005962	AP005962 Bradyrhiz
C 814	95	7.1	349980	6	AX041106	Streptomy	C 887	94	7.0	300242	1	AE016790	AE016790 Pseudomon
C 815	94.5	7.0	534	6	CQ735395	Sequence	C 888	94	7.0	300450	1	AP005960	AP005960 Bradyrhiz
C 816	94.5	7.0	975	6	BD179645	Highly th	C 889	94	7.0	301332	1	AE017237	AE017237 Mycobacte
C 817	94.5	7.0	2184	3	DMHREC2C	X52591 Drosophila	C 890	94	7.0	302614	1	AE016778	AE016778 Pseudomon
C 818	94.5	7.0	2239	3	AF324956	AR166541	C 891	94	7.0	302950	1	SC0939130	SC0939130 Streptomy
C 819	94.5	7.0	2304	6	AR166541	Sequence 1	C 892	94	7.0	309050	1	AP003005	AP003005 Mesorhizo
C 820	94.5	7.0	2304	6	I49731	Sequence 1	C 893	94	7.0	332635	1	AL158031	AL158031 Homo sapi
C 821	94.5	7.0	2304	6	I74629	Drosophila	C 894	94	7.0	343504	2	AL158031	AL158031 Homo sapi
C 822	94.5	7.0	2311	6	DMXR2C	X53417 Drosophila	C 895	94	7.0	349552	1	AX569690	AX569690 Synchoco
C 823	94.5	7.0	2483	6	CQ580821	Sequence	C 896	94	7.0	349970	1	AX571659	AX571659 Wolinella
C 824	94.5	7.0	2506	3	AY069393	AY069393 Drosophila	C 897	93.5	7.0	801	5	AX933718	AX933718 Gallus ga
C 825	94.5	7.0	3412	9	HSM806839	AY672997 Triticum	C 898	93.5	7.0	1422	6	BD179676	BD179676 Highly th
C 826	94.5	7.0	4493	6	CQ580820	Sequence	C 899	93.5	7.0	1469	8	CRE577849	CRE577849 Chlamydom
C 827	94.5	7.0	5515	8	AY672997	Triticum	C 900	93.5	7.0	2299	8	AK111159	AK111159 Oryza sat
C 828	94.5	7.0	5516	8	AY672996	Triticum	C 901	93.5	7.0	5398	1	AB032524	AB032524 Streptomy
C 829	94.5	7.0	5570	8	AY672994	Triticum	C 902	93.5	7.0	10294	1	AE005909	AE005909 Caulobact
C 830	94.5	7.0	5582	8	AY672995	Triticum	C 903	93.5	7.0	10556	1	AE011660	AE011660 Xanthomon
C 831	94.5	7.0	14343	9	AY149894	AY149894 Homo sapi	C 904	93.5	7.0	11134	1	AE012473	AE012473 Xanthomon
C 832	94.5	7.0	14790	1	AE001885	AE001885 Deinococc	C 905	93.5	7.0	11819	1	AE011801	AE011801 Xanthomon
C 833	94.5	7.0	18737	6	CQ580721	Sequence	C 906	93.5	7.0	31800	2	AC015554	AC015554 Leishmani
C 834	94.5	7.0	18737	6	CQ580721	Sequence	C 907	93.5	7.0	41282	2	AC148873	AC148873 Chlamydom
C 835	94.5	7.0	45672	3	DMC22E5	AL031765 Drosophila	C 908	93.5	7.0	41987	1	AY498874	AY498874 Streptomy
C 836	94.5	7.0	46012	2	AL513225	AL513225 Drosophila	C 909	93.5	7.0	82232	1	AY458648	AY458648 Unculture
C 837	94.5	7.0	77556	2	AC017522	AC017522 Drosophila	C 910	93.5	7.0	110000	1	AP006618_05	AP006618_05 Continuation (6 of
C 838	94.5	7.0	110000	1	AE017180_16	Continuation (17 o	C 911	93.5	7.0	110000	1	AP006618_06	AP006618_06 Continuation (7 of
C 839	94.5	7.0	110000	1	AP006840_21	Continuation (22 o	C 912	93.5	7.0	110000	1	AP006618_12	AP006618_12 Continuation (13 o
C 840	94.5	7.0	110000	1	AX571965_14	Continuation (15 o	C 913	93.5	7.0	154746	14	HSV2HG52	HSV2HG52 Herpes simp
C 841	94.5	7.0	165725	2	AC024027	Homo sapi	C 914	93.5	7.0	165358	9	AL353782	AL353782 Human DNA
C 842	94.5	7.0	169618	3	AC105055	AC105055 Drosophila	C 915	93.5	7.0	166050	1	AL4646085	AL4646085 Ralstonia
C 843	94.5	7.0	177724	3	AC073765	AC073765 Mus muscu	C 916	93.5	7.0	230161	2	AC128213	AC128213 Rattus no
C 844	94.5	7.0	237619	2	AC073765	AC073765 Mus muscu	C 917	93.5	7.0	298900	1	AP005937	AP005937 Bradyrhiz
C 845	94.5	7.0	240264	2	AC107434	AC107434 Rattus no	C 918	93.5	7.0	299925	1	AP005039	AP005039 Streptomy
C 846	94.5	7.0	245134	2	AC126639	AC126639 Rattus no	C 919	93.5	7.0	302675	1	AP005024	AP005024 Streptomy
C 847	94.5	7.0	297800	1	AP006579	AP006579 Gloeobact	C 920	93.5	7.0	306550	1	AX248342	AX248342 Mycobacte
C 848	94.5	7.0	300100	1	SC0939123	SC0939123 Streptomy	C 921	93.5	7.0	308147	1	AE016915	AE016915 Mesorhizo
C 849	94.5	7.0	300143	1	AE017155	AE017155 Prochloro	C 922	93.5	7.0	329709	1	AP002997	AP002997 Chromobac
C 850	94.5	7.0	300933	3	AE003422	AE003422 Drosophila	C 923	93.5	7.0	346287	1	AX572595	AX572595 Rhodospseu
C 851	94	7.0	3058	8	AK110497	AK110497 Oryza sat	C 924	93.5	7.0	349260	1	AX572595	AX572595 Rhodospseu
C 852	94	7.0	3263	8	AK111218	AK111218 Oryza sat	C 925	93.5	7.0	349981	1	AX572602	AX572602 Rhodospseu
C 853	94	7.0	4382	14	MMSAAX	M96854 Moloney mur	C 926	93	6.9	331	11	AX546298	AX546298 Arabidops
C 854	94	7.0	7207	1	AF533147	AF533147 Bacillus	C 927	93	6.9	1410	6	E07846	E07846 DNA sequenc
C 855	94	7.0	9576	6	CQ859288	CQ859288 Sequence	C 928	93	6.9	1462	5	SSA416953	SSA416953 Salmo sal
C 856	94	7.0	9576	6	CQ873385	CQ873385 Sequence	C 929	93	6.9	1468	8	AK107128	AK107128 Oryza sat
C 857	94	7.0	13732	1	AE011982	AE011982 Xanthomon	C 930	93	6.9	1533	6	BD180585	BD180585 Highly th
C 858	94	7.0	15542	1	AE004504	AE004504 Pseudomon	C 931	93	6.9	1613	8	AK071802	AK071802 Oryza sat
C 859	94	7.0	17400	9	AF503925	AF503925 Homo sapi	C 932	93	6.9	1898	6	AX1676	AX1676 Sequence 1
C 860	94	7.0	58996	1	AB034704	AB034704 Rubriviva	C 933	93	6.9	1898	10	AF050165	AF050165 Mus muscu
C 861	94	7.0	82144	9	AC099660	AC099660 Homo sapi	C 934	93	6.9	1988	6	AX1678	AX1678 Sequence 3
C 862	94	7.0	86996	1	AC067718	AC067718 Rhodobacter	C 935	93	6.9	2183	8	AK119822	AK119822 Oryza sat
C 863	94	7.0	97995	9	AC067718	AC067718 Homo sapi	C 936	93	6.9	3051	6	CQ725223	CQ725223 Sequence
C 864	94	7.0	110000	1	AP006618_12	Continuation (13 o	C 937	93	6.9	3470	6	CQ849801	CQ849801 Sequence
C 865	94	7.0	110000	1	AP006840_25	Continuation (26 o	C 938	93	6.9	3470	9	AX126854	AX126854 Homo sapi
C 866	94	7.0	110000	1	AX571966_01	Continuation (2 of	C 939	93	6.9	5591	6	AX511491	AX511491 Sequence
C 867	94	7.0	110000	1	CR522870_10	Continuation (11 o	C 940	93	6.9	5595	9	AB020683	AB020683 Homo sapi
C 868	94	7.0	110000	2	CEY10558_2	Continuation (3 of	C 941	93	6.9	5828	14	MLMPROCG	MLMPROCG J02266 Moloney mur
C 869	94	7.0	123402	2	AC148071	AC148071 Dasypus n	C 942	93	6.9	5833	14	AF033813	AF033813 Moloney m
C 870	94	7.0	154605	2	AC046161	AC046161 Homo sapi	C 943	93	6.9	5833	14	REMSVX	REMSVX J01185 Genome Of m
C 871	94	7.0	156677	2	AC092550	AC092550 Homo sapi	C 944	93	6.9	7788	6	AX803724	AX803724 Sequence
C 872	94	7.0	166050	1	AL4646085	AL4646085 Ralstonia	C 945	93	6.9	8213	1	TSE007744	TSE007744 Thauera s
C 873	94	7.0	169247	9	AL669970	AL669970 Human DNA	C 946	93	6.9	10765	1	AE004555	AE004555 Pseudomon
C 874	94	7.0	180097	9	AC123978	AC123978 Papio anu	C 947	93	6.9	10829	1	AE004655	AE004655 Pseudomon
C 875	94	7.0	180159	8	AP003633	AP003633 Oryza sat	C 948	93	6.9	12891	1	AE004192	AE004192 Vibrio ch
C 876	94	7.0	186311	2	AC146295	AC146295 Mus muscu	C 949	93	6.9	13750	1	AY260903	AY260903 Rhodospir
C 877	94	7.0	193015	2	AC150074	AC150074 Gallus ga	C 950	93	6.9	37360	6	AX803722	AX803722 Sequence
C 878	94	7.0	199942	2	AC150038	AC150038 Gallus ga	C 951	93	6.9	62700	8	NC2E4	NC2E4 AL451022 Neurospor
C 879	94	7.0	220851	2	AC097956	AC097956 Rattus no	C 952	93	6.9	67523	1	SCU24241	SCU24241 Sorangium c
C 880	94	7.0	230278	14	MCU68299	U68299 Mouse cytom	C 953	93	6.9	110000	1	AE000516_04	AE000516_04 Continuation (5 of

C 954	93	6.9	110000	1	AE000516_05	Continuation (6 of	c1027	92.5	6.9	2517	6	AX317534	Sequence
C 955	93	6.9	110000	2	AP006495_1	Continuation (2 of	c1028	92.5	6.9	2520	6	AR410555	Sequence
C 956	93	6.9	110000	2	BP255276_07	Continuation (8 of	c1029	92.5	6.9	2520	6	AX317219	Sequence
C 957	93	6.9	110000	8	CR382130_23	Continuation (24 of	c1030	92.5	6.9	2520	6	AX317502	Sequence
C 958	93	6.9	139999	8	AC018727	AC018727 Oryza sat	c1031	92.5	6.9	2520	6	AX317538	Sequence
C 959	93	6.9	148179	9	AP001631	AP001631 Homo sapi	c1032	92.5	6.9	2520	6	AX317540	Sequence
C 960	93	6.9	184026	1	AP006619	AP006619 Nocardia	c1033	92.5	6.9	2520	6	AX317570	Sequence
C 961	93	6.9	188585	10	AC114404	AC114404 Mus muscu	c1034	92.5	6.9	2520	6	AX317574	Sequence
C 962	93	6.9	189050	1	AL646077	AL646077 Ralstonia	c1035	92.5	6.9	2520	6	AX317580	Sequence
C 963	93	6.9	206389	2	AC110327	AC110327 Rattus no	c1036	92.5	6.9	2526	6	AX317580	Sequence
C 964	93	6.9	213050	1	AL646067	AL646067 Ralstonia	c1037	92.5	6.9	2526	6	AR410413	Sequence
C 965	93	6.9	222932	2	AC145345	AC145345 Mus muscu	c1038	92.5	6.9	2526	6	AR410418	Sequence
C 966	93	6.9	255838	2	AC109061	AC109061 Rattus no	c1039	92.5	6.9	2526	6	AR410473	Sequence
C 967	93	6.9	29850	1	SC093912_7	AL939127 Streptomy	c1040	92.5	6.9	2526	6	AR410475	Sequence
C 968	93	6.9	298750	1	AP005375	AP005375 Thermosyn	c1041	92.5	6.9	2526	6	AR410508	Sequence
C 969	93	6.9	300029	8	AE017122	AE017122 Oryza sat	c1042	92.5	6.9	2526	6	AR410509	Sequence
C 970	93	6.9	302835	1	AE012555	AE012555 Xylella f	c1043	92.5	6.9	2526	6	AR410510	Sequence
C 971	93	6.9	318136	1	BX572101	BX572101 Prochloro	c1044	92.5	6.9	2526	6	AR410540	Sequence
C 972	93	6.9	340000	9	AP001748	AP001748 Homo sapi	c1045	92.5	6.9	2526	6	AR562302	Sequence
C 973	93	6.9	342416	1	EX842573	EX842573 Mycobacte	c1046	92.5	6.9	2526	6	AR562307	Sequence
C 974	93	6.9	349142	1	EX572559	EX572559 Rhodopseu	c1047	92.5	6.9	2526	6	AR562362	Sequence
C 975	92.5	6.9	2178	8	NCMOM72	XS3735 N. crassa M	c1048	92.5	6.9	2526	6	AR562397	Sequence
C 976	92.5	6.9	2433	6	AX317584	AX317584 Sequence	c1049	92.5	6.9	2526	6	AR562398	Sequence
C 977	92.5	6.9	2445	6	AX317568	AX317568 Sequence	c1050	92.5	6.9	2526	6	AR562399	Sequence
C 978	92.5	6.9	2445	6	AX317572	AX317572 Sequence	c1051	92.5	6.9	2526	6	AR562429	Sequence
C 979	92.5	6.9	2445	6	AX317576	AX317576 Sequence	c1052	92.5	6.9	2526	6	AR567947	Sequence
C 980	92.5	6.9	2445	6	AX317578	AX317578 Sequence	c1053	92.5	6.9	2526	6	AR567951	Sequence
C 981	92.5	6.9	2493	6	AX317586	AX317586 Sequence	c1054	92.5	6.9	2526	6	AR567953	Sequence
C 982	92.5	6.9	2499	6	AX317582	AX317582 Sequence	c1055	92.5	6.9	2526	6	AR567955	Sequence
C 983	92.5	6.9	2508	6	AX317398	AX317398 Sequence	c1056	92.5	6.9	2526	6	AX317100	Sequence
C 984	92.5	6.9	2508	6	AX317402	AX317402 Sequence	c1057	92.5	6.9	2526	6	AX317101	Sequence
C 985	92.5	6.9	2508	6	AX317404	AX317404 Sequence	c1058	92.5	6.9	2526	6	AX317114	Sequence
C 986	92.5	6.9	2508	6	AX317406	AX317406 Sequence	c1059	92.5	6.9	2526	6	AX317115	Sequence
C 987	92.5	6.9	2508	6	AX317408	AX317408 Sequence	c1060	92.5	6.9	2526	6	AX317116	Sequence
C 988	92.5	6.9	2508	6	AX317412	AX317412 Sequence	c1061	92.5	6.9	2526	6	AX317129	Sequence
C 989	92.5	6.9	2508	6	AX317414	AX317414 Sequence	c1062	92.5	6.9	2526	6	AX317264	Sequence
C 990	92.5	6.9	2508	6	AX317416	AX317416 Sequence	c1063	92.5	6.9	2526	6	AX317270	Sequence
C 991	92.5	6.9	2508	6	AX317420	AX317420 Sequence	c1064	92.5	6.9	2526	6	AX317346	Sequence
C 992	92.5	6.9	2508	6	AX317423	AX317423 Sequence	c1065	92.5	6.9	2526	6	AX317370	Sequence
C 993	92.5	6.9	2508	6	AX317428	AX317428 Sequence	c1066	92.5	6.9	2526	6	AX317372	Sequence
C 994	92.5	6.9	2508	6	AX317436	AX317436 Sequence	c1067	92.5	6.9	2526	6	AX317376	Sequence
C 995	92.5	6.9	2511	6	AR309013	AR309013 Sequence	c1068	92.5	6.9	2526	6	AX317380	Sequence
C 996	92.5	6.9	2511	6	AR317144	AR317144 Sequence	c1069	92.5	6.9	2526	6	AX317384	Sequence
C 997	92.5	6.9	2511	6	AR410409	AR410409 Sequence	c1070	92.5	6.9	2526	6	AX317388	Sequence
C 998	92.5	6.9	2511	6	AR474890	AR474890 Sequence	c1071	92.5	6.9	2526	6	AX317392	Sequence
C 999	92.5	6.9	2511	6	AR562298	AR562298 Sequence	c1072	92.5	6.9	2526	6	AX317396	Sequence
C1000	92.5	6.9	2511	6	AR567945	AR567945 Sequence	c1073	92.5	6.9	2526	6	AX317449	Sequence
C1001	92.5	6.9	2511	6	AX317259	AX317259 Sequence	c1074	92.5	6.9	2526	6	AX317452	Sequence
C1002	92.5	6.9	2511	6	AX555663	AX555663 Sequence	c1075	92.5	6.9	2526	6	AX317456	Sequence
C1003	92.5	6.9	2511	6	AX698681	AX698681 Sequence	c1076	92.5	6.9	2526	6	AX317468	Sequence
C1004	92.5	6.9	2511	6	BD095937	BD095937 PBN-1 end	c1077	92.5	6.9	2526	6	AX317494	Sequence
C1005	92.5	6.9	2514	6	AR410541	AR410541 Sequence	c1078	92.5	6.9	2526	6	AX317555	Sequence
C1006	92.5	6.9	2514	6	AR562430	AR562430 Sequence	c1079	92.5	6.9	2526	6	AX698683	Sequence
C1007	92.5	6.9	2514	6	AX317130	AX317130 Sequence	c1080	92.5	6.9	2526	6	AX698688	Sequence
C1008	92.5	6.9	2514	6	AX317451	AX317451 Sequence	c1081	92.5	6.9	2526	6	AX698691	Sequence
C1009	92.5	6.9	2514	6	AX317472	AX317472 Sequence	c1082	92.5	6.9	2526	6	AX698694	Sequence
C1010	92.5	6.9	2514	6	AX317496	AX317496 Sequence	c1083	92.5	6.9	2532	6	AX317460	Sequence
C1011	92.5	6.9	2517	6	AR410420	AR410420 Sequence	c1084	92.5	6.9	2532	6	AX317464	Sequence
C1012	92.5	6.9	2517	6	AR410524	AR410524 Sequence	c1085	92.5	6.9	2619	6	AX317560	Sequence
C1013	92.5	6.9	2517	6	AR562309	AR562309 Sequence	c1086	92.5	6.9	2643	6	AX317556	Sequence
C1014	92.5	6.9	2517	6	AR562413	AR562413 Sequence	c1087	92.5	6.9	3135	6	AX317578	Sequence
C1015	92.5	6.9	2517	6	AX317066	AX317066 Sequence	c1088	92.5	6.9	4373	10	AX131166	AK131166 Mus muscu
C1016	92.5	6.9	2517	6	AX317125	AX317125 Sequence	c1089	92.5	6.9	5956	9	AB058752	AB058752 Homo sapi
C1017	92.5	6.9	2517	6	AX317481	AX317481 Sequence	c1090	92.5	6.9	6245	1	AF202779	AF202779 Rhodobact
C1018	92.5	6.9	2517	6	AX317492	AX317492 Sequence	c1091	92.5	6.9	7282	1	AF548455	AF548455 Delftia a
C1019	92.5	6.9	2517	6	AX317498	AX317498 Sequence	c1092	92.5	6.9	11159	1	AE012066	AE012066 Xanthomon
C1020	92.5	6.9	2517	6	AX317506	AX317506 Sequence	c1093	92.5	6.9	11267	1	AE004919	AE004919 Pseudomon
C1021	92.5	6.9	2517	6	AX317510	AX317510 Sequence	c1094	92.5	6.9	11791	1	AE004763	AE004763 Pseudomon
C1022	92.5	6.9	2517	6	AX317514	AX317514 Sequence	c1095	92.5	6.9	14253	1	AE015066	AE015066 Shigella
C1023	92.5	6.9	2517	6	AX317518	AX317518 Sequence	c1096	92.5	6.9	36078	2	AC151616	AC151616 Emiliania
C1024	92.5	6.9	2517	6	AX317522	AX317522 Sequence	c1097	92.5	6.9	39263	1	AY281354	AY281354 Unculture
C1025	92.5	6.9	2517	6	AX317526	AX317526 Sequence	c1098	92.5	6.9	54184	9	AL713889	AL713889 Human DNA
C1026	92.5	6.9	2517	6	AX317530	AX317530 Sequence	c1099	92.5	6.9	110000	1	AE016822_12	Continuation (13 o

1100	92.5	6.9	110000	1	BX571965_35	Continuation (36 o	cl173	91.5	6.8	2505	6	AR562433	Sequence
1101	92.5	6.9	110000	1	BX571966_26	Continuation (27 o	cl174	91.5	6.8	2505	6	AX317152	Sequence
1102	92.5	6.9	110000	1	BX571966_29	Continuation (30 o	cl175	91.5	6.8	2505	6	BD059535	FEN-1 end
1103	92.5	6.9	110000	1	CP000010_25	Continuation (26 o	cl176	91.5	6.8	2511	6	AR309012	Sequence
1104	92.5	6.9	150372	2	AC150103	Gallus ga	cl177	91.5	6.8	2511	6	AR317143	Sequence
1105	92.5	6.9	189505	9	AC092138	Homo sapi	cl178	91.5	6.8	2511	6	AR410362	Sequence
1106	92.5	6.9	197615	5	BX470161	Zebrafish	cl179	91.5	6.8	2511	6	AR562251	Sequence
1107	92.5	6.9	203050	1	AL646071	Rattus no	cl180	91.5	6.8	2511	6	AR567943	Sequence
1108	92.5	6.9	241270	2	AC120095	Rattus no	cl181	91.5	6.8	2511	6	AX317241	Sequence
1109	92.5	6.9	250891	2	AC118119	Rattus no	cl182	91.5	6.8	2511	6	AX698678	Sequence
1110	92.5	6.9	262530	2	AC111916	Rattus no	cl183	91.5	6.8	2511	6	BD095936	FEN-1 end
1111	92.5	6.9	265693	2	AC122319	Mus muscu	cl184	91.5	6.8	2640	6	I40148	Sequence 30
1112	92.5	6.9	292309	1	AE016979	Shigella	1185	91.5	6.8	2653	6	BD155996	Primer fo
1113	92.5	6.9	299450	1	AP006580	Gloeobact	1186	91.5	6.8	2653	6	AX544044	Sequence
1114	92.5	6.9	299525	1	AP005045	Streptomy	1187	91.5	6.8	2653	6	AX876185	Sequence
1115	92.5	6.9	301700	1	AP005948	Bradyrhiz	1188	91.5	6.8	2653	9	AK001186	Homo sapi
1116	92.5	6.9	301708	1	AE016792	Pseudomon	1189	91.5	6.8	2943	6	AR405900	Sequence
1117	92.5	6.9	304500	1	AP005953	Bradyrhiz	cl190	91.5	6.8	3221	1	TTHPOLA	Thermus the
1118	92.5	6.9	305584	1	AP005953	Chromobac	cl191	91.5	6.8	3221	6	E09501	DNA encodin
1119	92.5	6.9	338579	1	AP003004	Mesorhizo	1192	91.5	6.8	3488	8	AK101762	Oryza sat
1120	92.5	6.9	349061	1	NMA222491	Neisseria	cl193	91.5	6.8	5022	1	AF112365	Streptomy
1121	92	6.9	1035	6	AX079056	Sequence	cl194	91.5	6.8	5260	12	AB025788	Expressio
1122	92	6.9	1987	1	PASSSDAPF	X78478 Pseudomon	1195	91.5	6.8	7324	1	AF090329	Pseudomon
1123	92	6.9	2396	6	CQ581775	Sequence	1196	91.5	6.8	9972	1	AE003913	Xylella f
1124	92	6.9	2590	6	CQ599964	Sequence	cl197	91.5	6.8	10029	1	AE012481	Xanthomon
1125	92	6.9	2682	9	BC023554	Homo sapi	1198	91.5	6.8	10029	1	AE012523	Xanthomon
1126	92	6.9	2720	9	BC017210	Homo sapi	cl199	91.5	6.8	10087	1	AE004058	Xylella f
1127	92	6.9	2820	9	BC023551	Homo sapi	1200	91.5	6.8	10189	1	AE004715	Pseudomon
1128	92	6.9	2894	6	CQ599979	Sequence	cl201	91.5	6.8	10426	1	AE004699	Pseudomon
1129	92	6.9	2955	8	AK100088	Oryza sat	1202	91.5	6.8	11160	1	AE009150	Agrobacte
1130	92	6.9	4256	3	AY122255	Drosophill	1203	91.5	6.8	11252	1	AE005760	Caulobact
1131	92	6.9	5008	6	CQ849971	Sequence	1204	91.5	6.8	11258	1	AE011803	Xanthomon
1132	92	6.9	5008	9	AK127044	Homo sapi	1205	91.5	6.8	11665	1	AE008115	Agrobacte
1133	92	6.9	5286	1	SCACTT6	X63449 S.coelicolo	cl206	91.5	6.8	11786	1	AE004927	Pseudomon
1134	92	6.9	10369	1	AE005059	Halobacte	cl207	91.5	6.8	12675	1	AE011822	Xanthomon
1135	92	6.9	13197	1	AE004503	Pseudomon	1208	91.5	6.8	20021	1	AE004730	Pseudomon
1136	92	6.9	14423	1	AE004532	Pseudomon	1209	91.5	6.8	35335	3	AC016161	Leishmani
1137	92	6.9	15280	9	AB107036	Homo sapi	cl210	91.5	6.8	61450	8	AP006556	Oryza sat
1138	92	6.9	24123	1	AF086815	Acidovor	cl211	91.5	6.8	76196	1	AY354515	Streptomy
1139	92	6.9	74542	1	BX571965_40	Continuation (41 o	cl212	91.5	6.8	101385	5	CNS09898	Tetradon
1140	92	6.9	102042	2	AC150097	Gallus ga	1213	91.5	6.8	110000	1	BX571965_11	Continuation (12 o
1141	92	6.9	106332	14	AY150217	Ambystoma	1214	91.5	6.8	110000	1	CP000010_06	Continuation (7 of
1142	92	6.9	110000	1	AE016822_15	Continuation (16 o	1215	91.5	6.8	110000	1	CP000010_07	Continuation (8 of
1143	92	6.9	110000	1	AE017282_24	Continuation (25 o	cl216	91.5	6.8	140933	8	AP005063	Oryza sat
1144	92	6.9	110000	1	AP006840_30	Continuation (31 o	1217	91.5	6.8	141166	10	AC122423	Mus muscu
1145	92	6.9	110000	1	AY316747_2	Continuation (3 of	1218	91.5	6.8	154019	9	AC151486	Pan trogl
1146	92	6.9	110000	1	CP000010_30	Continuation (31 o	1219	91.5	6.8	156840	2	AC146810	Zea mays
1147	92	6.9	110000	2	LMFLCHR12_00	Continuation (2 of	cl220	91.5	6.8	158749	8	AY360394	Oryza sat
1148	92	6.9	110000	2	LMFLCHR12_01	Continuation (17 o	1221	91.5	6.8	160541	8	AP004458	Oryza sat
1149	92	6.9	110000	2	LMFLCHR32_16	Continuation (17 o	cl222	91.5	6.8	160681	2	AC118586	Pan trogl
1150	92	6.9	166421	8	AP003106	Oryza sat	cl223	91.5	6.8	163194	3	LMFP214	Leishmani
1151	92	6.9	24273	2	AC106167	Rattus no	1224	91.5	6.8	164901	8	AY360393	Oryza sat
1152	92	6.9	245482	2	AC098630	Rattus no	cl225	91.5	6.8	174714	9	AC025280	Homo sapi
1153	92	6.9	252109	2	AC150037	Gallus ga	cl226	91.5	6.8	180623	9	AC092341	Homo sapi
1154	92	6.9	254439	2	AC150047	Gallus ga	1227	91.5	6.8	181161	2	AC092347	Homo sapi
1155	92	6.9	269985	2	AC127669	Rattus no	cl228	91.5	6.8	196204	9	AC073957	Homo sapi
1156	92	6.9	298300	1	AP005025	Streptomy	1229	91.5	6.8	226460	2	AC114157	Rattus no
1157	92	6.9	299350	1	SME591786	Sinorhizo	1230	91.5	6.8	247592	9	U52111	Homo sapien
1158	92	6.9	300029	1	AE016787	Pseudomon	1231	91.5	6.8	263875	2	AC094237	Rattus no
1159	92	6.9	300950	1	AP005940	Bradyrhiz	cl232	91.5	6.8	270418	1	AE017303	Thermus t
1160	91.5	6.8	1274	5	CR761306	Xenopus t	cl233	91.5	6.8	299925	1	AP005043	Streptomy
1161	91.5	6.8	1707	3	AF012276	Toxoplasma	1234	91.5	6.8	300425	1	AP005044	Streptomy
1162	91.5	6.8	1787	9	HSPG5UT	Z14129 H.sapiens p	cl235	91.5	6.8	300817	1	AE016756	Escherich
1163	91.5	6.8	2004	9	AY619993	Homo sapi	1236	91.5	6.8	313800	1	SC0939114	Streptomy
1164	91.5	6.8	2004	9	AY619994	Homo sapi	1237	91.5	6.8	314100	1	SC0939106	Streptomy
1165	91.5	6.8	2499	6	AR410430	Sequence	1238	91.5	6.8	325483	1	AP005050	Streptomy
1166	91.5	6.8	2499	6	AR562319	Sequence	cl239	91.5	6.8	333500	1	AP003590	Nostoc sp
1167	91.5	6.8	2499	6	AX317076	Sequence	1240	91.5	6.8	906	6	AR386351	Sequence
1168	91.5	6.8	2505	6	AR023938	Sequence	cl241	91	6.8	1092	12	AY659078	Synthetic
1169	91.5	6.8	2505	6	I15439	Sequence 9	1242	91	6.8	1125	12	AY659325	Synthetic
1170	91.5	6.8	2505	6	AR309011	Sequence	1243	91	6.8	1500	6	BD180484	Highly th
1171	91.5	6.8	2505	6	AR317142	Sequence	cl244	91	6.8	1509	6	AX751797	Sequence
1172	91.5	6.8	2505	6	AR410544	Sequence	1245	91	6.8	1906	6	E01303	cdna encodi

1246	91	6.8	2016	4	BOVMIS	M13151 Bovine Muel	cl1319	90.5	6.7	3034	10	AK122327	Mus muscu
1247	91	6.8	2085	6	AX078521	AX078521 Sequence	cl1320	90.5	6.7	3065	6	AR262597	Sequence
1248	91	6.8	2299	6	AX664177	AX664177 Sequence	cl1321	90.5	6.7	3077	9	BC006278	Homo sapi
1249	91	6.8	2749	6	CQ767748	CQ767748 Sequence	cl1322	90.5	6.7	3306	10	AB017609	Mus muscu
1250	91	6.8	2749	6	AR5252737	AR5252737 Sequence	cl1323	90.5	6.7	3337	6	E30802	Novel prote
1251	91	6.8	2749	6	AR528644	AR528644 Sequence	cl1324	90.5	6.7	3660	10	AB017608	Mus muscu
1252	91	6.8	2749	6	AX403629	AX403629 Sequence	cl1325	90.5	6.7	3674	6	E30801	Novel prote
1253	91	6.8	2749	6	AX454474	AX454474 Sequence	cl1326	90.5	6.7	3680	10	BC017126	Mus muscu
1254	91	6.8	2749	6	AX464252	AX464252 Sequence	cl1327	90.5	6.7	4449	10	CGU29946	Cricetulus
1255	91	6.8	2749	6	AX490952	AX490952 Sequence	cl1328	90.5	6.7	5054	1	AF042276	Pseudomon
1256	91	6.8	2749	9	AY358364	AY358364 Homo sapi	cl1329	90.5	6.7	5054	6	AX105316	Sequence
1257	91	6.8	2873	1	SHU41627	SHU41627 Streptomyce	cl1330	90.5	6.7	8775	3	AY061650	AY061650 Toxoplas
1258	91	6.8	3456	1	RSF543650	RSF543650 Rhodobact	cl1331	90.5	6.7	10029	1	AE012488	Xanthomon
1259	91	6.8	6175	1	AF064527	AF064527 Rhodocier	cl1332	90.5	6.7	10312	1	AE009781	Pyrobacul
1260	91	6.8	7312	9	HUMCACNL1G	L29536 Homo sapien	cl1333	90.5	6.7	10419	1	AE001865	Deinococc
1261	91	6.8	7417	9	HUMCACNL1E	L29534 Homo sapien	cl1334	90.5	6.7	10506	1	AE004806	Pseudomon
1262	91	6.8	7499	9	HUMCACN	L29529 Homo sapien	cl1335	90.5	6.7	10761	1	AE014547	Brucella
1263	91	6.8	8940	9	HUMLVDCCB	L04569 Homo sapien	cl1336	90.5	6.7	10963	1	AE011744	Xanthomon
1264	91	6.8	10057	1	AE004871	AE004871 Pseudomon	cl1337	90.5	6.7	11243	1	AE012067	Xanthomon
1265	91	6.8	10061	1	AE004314	AE004314 Vibrio ch	cl1338	90.5	6.7	12423	1	AE005155	Halobacte
1266	91	6.8	10429	1	AE004875	AE004875 Pseudomon	cl1339	90.5	6.7	12985	1	AE009710	Brucella
1267	91	6.8	10518	1	AE012117	AE012117 Xanthomon	cl1340	90.5	6.7	13341	1	AE003964	Xylella f
1268	91	6.8	10895	1	AE004521	AE004521 Pseudomon	cl1341	90.5	6.7	14618	10	AF260753	Cricetulu
1269	91	6.8	10950	1	AE012119	AE012119 Xanthomon	cl1342	90.5	6.7	43514	9	AC005545	Continuation (31 o
1270	91	6.8	10978	1	AE004940	AE004940 Pseudomon	cl1343	90.5	6.7	110000	1	BX571965_30	Continuation (14 o
1271	91	6.8	11031	1	AE004648	AE004648 Pseudomon	cl1344	90.5	6.7	110000	1	CP000010_04	Continuation (5 of
1272	91	6.8	12201	1	AE012255	AE012255 Xanthomon	cl1345	90.5	6.7	110000	2	LMFLCHR33_08	Continuation (9 of
1273	91	6.8	13138	1	AE012166	AE012166 Xanthomon	cl1346	90.5	6.7	127952	8	OSJN000063	AL060706 Oryza sat
1274	91	6.8	15446	1	AE000710	AE000710 Aquifex a	cl1347	90.5	6.7	135638	1	AF484556	Streptomy
1275	91	6.8	110000	1	AE000516_31	Continuation (32 o	cl1348	90.5	6.7	156002	8	OSJN000050	AL060626 Oryza sat
1276	91	6.8	110000	1	AE000516_32	Continuation (33 o	cl1349	90.5	6.7	158170	9	AC016757	Homo sapi
1277	91	6.8	110000	1	AE016822_00	AE016822 Leifsonia	cl1350	90.5	6.7	184631	2	AC141913	Rattus no
1278	91	6.8	110000	1	AE017282_13	Continuation (14 o	cl1351	90.5	6.7	191762	10	AC107770	Mus muscu
1279	91	6.8	110000	1	BX571965_30	Continuation (31 o	cl1352	90.5	6.7	204050	1	AL646073	Ralsconia
1280	91	6.8	110000	1	CP000010_04	Continuation (5 of	cl1353	90.5	6.7	210010	2	AL646135	Pan trogl
1281	91	6.8	110000	2	AP006494_7	Continuation (8 of	cl1354	90.5	6.7	210614	1	AB088224	Streptomy
1282	91	6.8	110000	2	AP006501_07	Continuation (8 of	cl1355	90.5	6.7	220622	2	AC118570	Lemur cat
1283	91	6.8	110000	2	LMFLCHR33_08	Continuation (9 of	cl1356	90.5	6.7	229800	1	AP005028	Streptomy
1284	91	6.8	138203	1	AY310323	AY310323 Streptomy	cl1357	90.5	6.7	299800	1	AP005028	Streptomy
1285	91	6.8	152881	10	AC124353	AC124353 Mus muscu	cl1358	90.5	6.7	308050	1	SC0939124	Streptomy
1286	91	6.8	168916	10	AC1124373	AC1124373 Mus muscu	cl1359	90.5	6.7	340000	1	AP005274	Coryneb
1287	91	6.8	174139	2	AC116700	AC116700 Mus muscu	cl1360	90.5	6.7	346274	1	BX640443	Bordetell
1288	91	6.8	178376	2	AC125512	AC125512 Papio anu	cl1361	90.5	6.7	346301	1	BX640443	Bordetell
1289	91	6.8	193798	2	AC145535	AC145535 Lemur cat	cl1362	90.5	6.7	348014	1	BX640430	Bordetell
1290	91	6.8	196216	9	AC099343	AC099343 Homo sapi	cl1363	90.5	6.7	348071	1	BX927148	Coryneb
1291	91	6.8	202555	9	AC034139	AC034139 Homo sapi	cl1364	90.5	6.7	34876	1	BX842581	Mycobacte
1292	91	6.8	255809	2	AC108312	AC108312 Rattus no	cl1365	90.5	6.7	349876	1	BX640442	Bordetell
1293	91	6.8	272101	1	AE017302	AE017302 Therius t	cl1366	90.5	6.7	349980	6	AX120085	Sequence
1294	91	6.8	299425	1	AP005037	AP005037 Streptomy	cl1367	90.5	6.7	934	1	AY186970	Geothermo
1295	91	6.8	299425	1	AP005049	AP005049 Streptomy	cl1368	90.5	6.7	1069	6	AR452916	Sequence
1296	91	6.8	299886	1	AE017240	AE017240 Mycobacte	cl1369	90.5	6.7	1069	8	BT009567	Triticum
1297	91	6.8	300550	1	AP005030	AP005030 Streptomy	cl1370	90.5	6.7	1176	1	AB014153	Micromono
1298	91	6.8	300900	1	AP005939	AP005939 Bradyrhiz	cl1371	90.5	6.7	1194	1	AB014944	Rhodobact
1299	91	6.8	301482	1	AE016916	AE016916 Chromobac	cl1372	90.5	6.7	2016	6	AX653225	Sequence
1300	91	6.8	301995	1	AE016779	AE016779 Pseudomon	cl1373	90.5	6.7	2427	8	AF110494	Neurospor
1301	91	6.8	303226	1	AE016774	AE016774 Pseudomon	cl1374	90.5	6.7	2451	8	AY604047	Oryza sat
1302	91	6.8	307050	1	BX294140	BX294140 Pirellula	cl1375	90.5	6.7	2826	8	AX100795	Oryza sat
1303	91	6.8	329000	3	TB6CHRIA3	TB6CHRIA3	cl1376	90.5	6.7	3115	1	AF225972	Ralsconia
1304	91	6.8	346362	1	BB640439	BB640439 Bordetell	cl1377	90.5	6.7	3867	10	BC055076	BC055076 Mus muscu
1305	91	6.8	346510	1	AP003011	AP003011 Mesorhizo	cl1378	90.5	6.7	6676	1	AF031590	Streptomy
1306	91	6.8	347894	1	BX640431	BX640431 Bordetell	cl1379	90.5	6.7	8651	1	AY124589	Agromyces
1307	91	6.8	348411	1	AP003007	AP003007 Mesorhizo	cl1380	90.5	6.7	9427	1	AE011711	Xanthomon
1308	91	6.8	348442	1	BX640446	BX640446 Bordetell	cl1381	90.5	6.7	9589	1	SC0001205	Streptomy
1309	91	6.8	348676	1	BX842581	BX842581 Mycobacte	cl1382	90.5	6.7	10592	1	AE005729	Caulobact
1310	90.5	6.7	906	6	BD179555	BD179555 Highly th	cl1383	90.5	6.7	10901	1	AE012469	Xanthomon
1311	90.5	6.7	909	1	AB085185	AB085185 Thermus t	cl1384	90.5	6.7	11828	1	AE013561	Methanosa
1312	90.5	6.7	1568	8	AC104988	AC104988 Oryza sat	cl1385	90.5	6.7	11828	1	AF187159	Streptomy
1313	90.5	6.7	1755	6	BD180277	BD180277 Highly th	cl1386	90.5	6.7	12198	1	AE004632	Pseudomon
1314	90.5	6.7	1319	5	CR761885	CR761885 Xenopus t	cl1387	90.5	6.7	12249	1	AE004670	Pseudomon
1315	90.5	6.7	2377	1	AB108682	AB108682 Streptomy	cl1388	90.5	6.7	12372	1	AE004670	Pseudomon
1316	90.5	6.7	2526	6	AR410471	AR410471 Sequence	cl1389	90.5	6.7	15816	1	AB091692	Sphingomo
1317	90.5	6.7	2526	6	AR562360	AR562360 Sequence	cl1390	90.5	6.7	21931	1	AY149472	Acinetoba
1318	90.5	6.7	2526	6	AX317099	AX317099 Sequence	cl1391	90.5	6.7	49999	6	AX015917	Sequence



1392	90	6.7	79370	1	UNK4311260	1465	89.5	6.7	2877	4	SSPHGPX	X76008 S.scrofa ph
1393	90	6.7	79506	9	AL137247 Human DNA	1466	89.5	6.7	4740	1	SPU60417	U60417 Streptomyce
1394	90	6.7	87668	1	AY365053 Wauteria	1467	89.5	6.7	4762	10	BC053083	BC053083 Mus muscu
1395	90	6.7	95437	3	AC139742 Leishmani	1468	89.5	6.7	5540	1	RCNIFA	M86823 Rhodobacter
1396	90	6.7	110000	1	AE016822 17	1469	89.5	6.7	5823	9	HSN806092	BX537963 Homo sapi
1397	90	6.7	110000	1	AE017180_34	1470	89.5	6.7	6462	6	AX153794	AX153794 Sequence
1398	90	6.7	110000	1	BX571966_10	1471	89.5	6.7	10029	1	AE005827	AE005827 Caulobact
1399	90	6.7	110000	1	BX571966_11	1472	89.5	6.7	10176	1	AE014563	AE014563 Brucella
1400	90	6.7	110000	1	CP000010_22	1473	89.5	6.7	10667	1	AE002529	AE002529 Neisseria
1401	90	6.7	110000	8	CR382132_37	1474	89.5	6.7	10816	1	AE009191	AE009191 Agrobacte
1402	90	6.7	110000	8	CR382135_03	1475	89.5	6.7	10861	1	AE008157	AE008157 Agrobacte
1403	90	6.7	126928	2	AC096673	1476	89.5	6.7	11162	1	AE011767	AE011767 Xanthomon
1404	90	6.7	127403	2	AC098842	1477	89.5	6.7	11601	8	AF335504	AF335504 Oryza sat
1405	90	6.7	134431	14	AY386265 Bovine pa	1478	89.5	6.7	12010	1	AE005218	AE005218 Escherich
1406	90	6.7	138929	8	AP000616 Oryza sat	1479	89.5	6.7	13393	1	AE011910	AE011910 Xanthomon
1407	90	6.7	139226	8	OSJN00274	1480	89.5	6.7	15470	1	AE004513	AE004513 Pseudomon
1408	90	6.7	143113	8	AP000559 Oryza sat	1481	89.5	6.7	19771	1	PPEA3NIF	X99694 Plasmid pEA
1409	90	6.7	146366	2	AC091846	1482	89.5	6.7	34071	6	AX153790	AX153790 Sequence
1410	90	6.7	149270	9	AC091912 Homo sapi	1483	89.5	6.7	39214	9	BX664700	BX664700 Human DNA
1411	90	6.7	153351	9	AC092675	1484	89.5	6.7	42559	9	AC005258	AC005258 Homo sapi
1412	90	6.7	155525	2	AP007206 Oryza sat	1485	89.5	6.7	42717	6	AX153789	AX153789 Sequence
1413	90	6.7	156677	9	AC021087 Homo sapi	1486	89.5	6.7	62709	2	AC117730	AC117730 Mus muscu
1414	90	6.7	161844	2	AC147451 Ocolemur	1487	89.5	6.7	67480	7	AY129334	AY129334 Mycobacte
1415	90	6.7	163039	8	OSJN00156	1488	89.5	6.7	71120	2	AP005417	AP005417 Oryza sat
1416	90	6.7	164104	2	AC021571	1489	89.5	6.7	84371	2	AP001963	AP001963 Homo sapi
1417	90	6.7	169950	2	AC084049 Homo sapi	1490	89.5	6.7	110000	1	AE016822	Continuation (6 of
1418	90	6.7	171280	2	AC024186 Homo sapi	1491	89.5	6.7	110000	1	AP006618	Continuation (52 o
1419	90	6.7	171384	2	AC136212 Gallus ga	1492	89.5	6.7	110000	1	AP006840	Continuation (32 o
1420	90	6.7	174839	9	AL157395 Human DNA	1493	89.5	6.7	110000	1	CP000010	Continuation (19 o
1421	90	6.7	175231	10	AC034108 Mus muscu	1494	89.5	6.7	110000	2	AC098940	Continuation (2 of
1422	90	6.7	178000	1	SC0590463	1495	89.5	6.7	110000	2	AP006496	Continuation (13 o
1423	90	6.7	181105	2	AP002394	1496	89.5	6.7	110000	2	LMFLCHR34	Continuation (23 o
1424	90	6.7	183349	2	AC027501	1497	89.5	6.7	116621	2	AC150102	AC150102 Gallus ga
1425	90	6.7	191996	9	AC092275	1498	89.5	6.7	123323	9	AP001816	AP001816 Homo sapi
1426	90	6.7	192366	10	AC068906	1499	89.5	6.7	123620	8	AC103891	AC103891 Oryza sat
1427	90	6.7	195791	2	AC018997 Homo sapi	1500	89.5	6.7	123620	8	AC103891	Oryza sat
1428	90	6.7	197635	2	AC019079 Homo sapi							
1429	90	6.7	197701	9	AC091941 Homo sapi							
1430	90	6.7	201050	1	AL646064 Ralstonia							
1431	90	6.7	208524	1	AE016925 Chromobac							
1432	90	6.7	210301	9	AF307337 Homo sapi							
1433	90	6.7	225646	10	AC024915 Mus muscu							
1434	90	6.7	227773	10	AC034109 Mus muscu							
1435	90	6.7	230918	2	AC114190 Rattus no							
1436	90	6.7	242808	10	AC024069 Mus muscu							
1437	90	6.7	247910	1	AE017307 Thermus t							
1438	90	6.7	260860	2	AC125982 Rattus no							
1439	90	6.7	273785	1	SMES91793							
1440	90	6.7	298550	1	AP005047 Streptomy							
1441	90	6.7	300349	1	AE017319 Desulfovi							
1442	90	6.7	303550	1	SC0939118							
1443	90	6.7	308147	1	AE016915 Chromobac							
1444	90	6.7	333800	1	SMES91792							
1445	90	6.7	347365	1	BX569691 Synchoco							
1446	90	6.7	347800	1	AP000060 Aropyrum							
1447	90	6.7	348247	1	BX842579 Mycobacte							
1448	90	6.7	348706	1	BX640445 Bordetell							
1449	90	6.7	348764	1	BX569689 Synchoco							
1450	90	6.7	348866	1	BX640426 Bordetell							
1451	89.5	6.7	660	6	CQ744105 Sequence							
1452	89.5	6.7	962	6	AR198362 Sequence							
1453	89.5	6.7	1052	6	A37840 Sequence 10							
1454	89.5	6.7	1052	6	AR069878 Sequence							
1455	89.5	6.7	1052	6	AR099274 Sequence							
1456	89.5	6.7	1052	6	AR124159 Sequence							
1457	89.5	6.7	1052	6	CQ761077 Sequence							
1458	89.5	6.7	1052	6	AR442766 Sequence							
1459	89.5	6.7	1079	8	AF315118 Populus e							
1460	89.5	6.7	1456	10	BC024087 Mus muscu							
1461	89.5	6.7	1533	8	AK100881 Oryza sat							
1462	89.5	6.7	1535	8	AK061493 Oryza sat							
1463	89.5	6.7	1656	8	AK061220 Oryza sat							
1464	89.5	6.7	2781	5	AY374500 Tetraodon							

## ALIGNMENTS

RESULT 1	LOCUS	SEQUENCE	789 bp	DNA	linear	PAT 03-FEB-2004
CQ721501	CQ721501	Sequence 7435 from Patent WO02068579.				
DEFINITION	CQ721501	Sequence 7435 from Patent WO02068579.				
ACCESSION	CQ721501	Sequence 7435 from Patent WO02068579.				
VERSION	CQ721501.1	GI:42282358				
KEYWORDS	CQ721501.1	GI:42282358				
SOURCE	CQ721501	Homo sapiens (human)				
ORGANISM	CQ721501	Homo sapiens				
REFERENCE	CQ721501	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	CQ721501	Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.				
TITLE	CQ721501	Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof				
JOURNAL	CQ721501	Patent: WO 02068579-A 7435 06-SEP-2002;				
FEATURES	CQ721501	PE Corporation (NY) (US)				
source	CQ721501	Location/Qualifiers				
ORIGIN	CQ721501	1. .789				
Alignment Scores:	CQ721501	/organism="Homo sapiens"				
Pred. No.:	CQ721501	/mol_type="unassigned DNA"				
Score:	CQ721501	/db_xref="taxon:9606"				
Percent Similarity:	CQ721501	5.28e-95				
Best Local Similarity:	CQ721501	1343.00				
Query Match:	CQ721501	100.00%				
DB:	CQ721501	Mismatches: 0				
	CQ721501	Indels: 0				
	CQ721501	Gaps: 6				

US-10-017-407A-306 (1-262) x CQ721501 (1-789)

```
Qy 1 MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla 20
Db 1 ATGACCCAGCGGTGCCCCGGCTCTCGTCCCGCCGCGCTGGCCCTGGGCTCAGCGCA 60
Qy 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgArgCysProTrpArgGly 40
Db 61 CTGGCGCGCCCTTGCCACTGGCCCTCTTCTGGGAGGCGGTGCCCCCATGGCGAGGC 120
Qy 41 ArgArgGluGlnCysLeuLeuProGluAAspSerArgLeuTrpGlnTrpLeuLeuSer 60
Db 121 CGCGGAGAGCAGTGCCTTCCCGCCAGCAGCAGCGCTGTGGCAGTATCTTCTGAGC 180
Qy 61 ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuThrLeuGluGlnPro 80
Db 181 CGCTCCATGCGGAGCAGCCCGCGCTGCGAAGCCTGAGGCTGGAGGAGCGCG 240
Qy 81 GlnGlyAspSerMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeu 100
Db 241 CAGGGGGATTCTATGATGACCTGCGAGCAGGCGCCAGCTCTTGCGCAACCTGGCGGCTC 300
Qy 101 IleGlnAlaLysLysAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAla 120
Db 301 ATCCAGGCCAAGAAGCGCTGACCTGGGCACTTCCGCGCTACTCCGCCCTGGCCCTG 360
Qy 121 AlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnPro 140
Db 361 GCCTTGGCGCTGCCCGGACCGGGCGGTGGTGGCTGGAGGTGGACCGCGAGCCCGC 420
Qy 141 GlnProLysGlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArgIleArg 240
Db 661 CAACCTCCGAAAGGGAGCGTGGCGCGGAGTGTGTGCGAAACCTAAACGAAACGATCCG 720
Qy 241 ArgAspValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPhe 260
Db 721 CGGAGCTCAGGGTCTACATCAGCCCTCTGCCCCCTGGGCGATGGACTCACCTTGGCCTTC 780
Qy 261 LysIle 262
Db 781 AGATC 786
```

## RESULT 2

```
AX338456
LOCUS
DEFINITION
ACCESSION
VERSION
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
```

AX338456  
Sequence 3 from Patent WO0183719.  
AX338456  
AX338456.1 GI:18128895  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
Meyers, R.A. and Williamson, M.  
25692, a novel human o-methyltransferase family member and uses  
thereof

JOURNAL Patent: WO 0183719-A 3 08-NOV-2001;  
Millennium Pharmaceuticals, Inc. (US)FEATURES  
source

1..789  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Alignment Scores:  
Pred. No.: 5.28e-95 Length: 789  
Score: 1343.00 Matches: 262  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-017-407A-306 (1-262) x AX338456 (1-789)

```
Qy 1 MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla 20
Db 1 ATGACCCAGCGGTGCCCCGGCTCTCGTGGCGCGCGCTGGCCCTGGGCTCAGCGCA 60
Qy 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgArgCysProTrpArgGly 40
Db 61 CTGGCGCGCCCTTGCCACTGGCCCTCTTCTGGGAGGCGGTGCCCCCATGGCGAGGC 120
Qy 41 ArgArgGluGlnCysLeuLeuProGluAAspSerArgLeuTrpGlnTrpLeuLeuSer 60
Db 121 CGCGGAGAGCAGTGCCTTCCCGCCAGCAGCAGCGCTGTGGCAGTATCTTCTGAGC 180
Qy 61 ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuThrLeuGluGlnPro 80
Db 181 CGCTCCATGCGGAGCAGCCCGCGCTGCGAAGCCTGAGGCTGGAGGAGCGCG 240
Qy 81 GlnGlyAspSerMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeu 100
Db 241 CAGGGGGATTCTATGATGACCTGCGAGCAGGCGCCAGCTCTTGCGCAACCTGGCGGCTC 300
Qy 101 IleGlnAlaLysLysAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAla 120
Db 301 ATCCAGGCCAAGAAGCGCTGACCTGGGCACTTCCGCGCTACTCCGCCCTGGCCCTG 360
Qy 121 AlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnPro 140
Db 361 GCCTTGGCGCTGCCCGGACCGGGCGGTGGTGGCTGGAGGTGGACCGCGAGCCCGC 420
Qy 141 GlnProLysGlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArgIleArg 160
Db 421 GAGCTGGGACGCGCCCTGTGGAGGAGCGCGGAGCGGAGCAGATCGACCTCCGCGCTG 480
Qy 161 LysProAlaLeuGluThrLeuAspGluLeuAlaAlaGluAlaGlyGluAlaGlyThrPheAsp 180
Db 481 AAGCCCGCTTCGAGACCCCTGGACAGCTGCTGGCGGCGGAGCGGAGCCCGACCTTCGAC 540
Qy 181 ValAlaValValAspAlaAspLysGluAsnCysSerAlaTyrTyrGluArgCysLeuGln 200
Db 541 GTGGCGGTGGTGGATGCGGACAGGAGAACTGCTCCGCCCTACTACGAGCGCTGCCCTG 600
Qy 201 LeuLeuArgProGlyIleLeuAlaValLeuAlaValLeuArgValLeuTrpArgGlyLysValLeu 220
Db 601 CTGCTGCGACCGGAGGATCTCTCGCGTCTCAGAGTCTTGTGGCGCGGAGGAGGTGCTG 660
Qy 221 GlnProLysGlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArgIleArg 240
Db 661 CAACCTCCGAAAGGGAGCGTGGCGCGGAGTGTGTGCGAAACCTAAACGAAACGATCCG 720
Qy 241 ArgAspValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPhe 260
Db 721 CGGAGCTCAGGGTCTACATCAGCCCTCTGCCCCCTGGGCGATGGACTCACCTTGGCCTTC 780
Qy 261 LysIle 262
Db 781 AGATC 786
```



Db	781	AGATC 786				
RESULT 3						
LOCUS	BC023663					
DEFINITION	Homo sapiens catechol-O-methyltransferase domain containing 1, mRNA (CDNA clone MGC:29637 IMAGE:4897624), complete cds.					
ACCESSION	BC023663					
VERSION	BC023663.2	GI:40226187				
KEYWORDS	MGC.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	1 (bases 1 to 913)					
AUTHORS	Strausberg, R.D., Collins, F.S., Wagner, L.H., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Shenmen, C.M., Schuler, G.D., Altshuler, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schetz, T.E., Brownstein, M.J., Usslin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalusz, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.					
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences					
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	99 (26)	16899-16903 (2002)			
PUBMED	12477932					
REFERENCE	2 (bases 1 to 913)					
AUTHORS	Strausberg, R.					
TITLE	Direct Submission					
JOURNAL	Submitted (05-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA					
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>					
COMMENT	On Dec 19, 2003 this sequence version replaced gi:23959051.					
	Contact: MGC help desk					
	Email: <a href="mailto:cgabbs-remail.nih.gov">cgabbs-remail.nih.gov</a>					
	Tissue Procurement: ATCC					
	cDNA Library Preparation: Rubin Laboratory					
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)					
	DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;					
	Web site: <a href="http://www.nisc.nih.gov/">http://www.nisc.nih.gov/</a>					
	Contact: <a href="mailto:nisc.mgc@nih.gov">nisc.mgc@nih.gov</a>					
	Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakeley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Mastello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.					
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a>						
Series: IRAL Plate: 39 Row: j Column: 6						
This clone was selected for full length sequencing because it passed the following selection criteria: GenomScan gene prediction, Similarity but not identity to protein.						
FEATURES	Location/Qualifiers					
source	1..913					

/organism="Homo sapiens"		
/mol_type="mRNA"		
/db_xref="taxon:9606"		
/clone="MGC:29637 IMAGE:4897624"		
/tissue_type="Brain, neuroblastoma"		
/clone_lib="NIH_MGC_19"		
/lab_host="DH10B-R"		
/note="Vector: pOT7"		
1..913		
/gene="COMTD1"		
/note="synonym: FLJ23841"		
/db_xref="LocusID:118881"		
6..794		
/gene="COMTD1"		
/codon_start=1		
/product="catechol-O-methyltransferase domain containing 1"		
/protein_id="AAH23663.1"		
/db_xref="GI:40226188"		
/db_xref="LocusID:118881"		
/translation="MTQPVRLSPALALGSAAALGAFATGFLGRRCPPMWRREGRCLLPEDSLRMQYLLSRMREHPALRSRLTLLEQPGDSMTCEQALANLARILRKPALDILGTFYGSALALALPADGRVVTCEVDAOPPELGRPLRQAAEAHKIDLRKPALETIDLLAAGACTFDVAVDGVKENCISAYYERCIQLLRPGGILAVLRVLWRGKVIQPPKGDVAACVRNLRIRDRVYIISLLPLGDLTLIAFKI"		
Alignment Scores:		
Pred. No.: 6	21e-95	Length: 913
Score: 1343.00	Matches: 262	
Percent Similarity: 100.00%	Conservative: 0	
Best Local Similarity: 100.00%	Mismatches: 0	
Query Match: 100.00%	Indels: 0	
DB: 9	Gaps: 0	
US-10-017-407A-306 (1-262) x BC023663 (1-913)		
QY 1	MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAa	20
DB 6	ATGACCCAGCGGTGCCCGGCTCTCGTGC CGCGCGCTGGCCCTCGAGCGCA	65
QY 21	LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgArgCysProProTrpArgGly	40
DB 66	CTGGCGCGCGCTTCGCCACTGGCCTCTTCTCTGGGAGCGCGTGCCTCCATGGCAGGC	125
QY 41	ArgArgGluGlnCysLeuLeuProGluAspSerArgLeuTrpGlnTyrLeuLeuSer	60
DB 126	CGCGAGAGCAGTGCCTGCTTCTCCCGGAGACAGCGCTGTGGCAGTATCTTCGAGC	185
QY 61	ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuLeuThrLeuGluGlnPro	80
DB 186	CGCTCCATCGGGAGACCCCGCGCTCGGAAGCCTGAGGCTGTGACCTCGAGCAGCGC	245
QY 81	GlnGlyAspSerMetMetThrCysGluGlnAlaGlnLeuLeuAlaLeuAlaArgLeu	100
DB 246	CAGGGGGATTCTATGATGACCTGCGAGCAGCGCCAGCTCTTGGCCAACTGGCGCGCTC	305
QY 101	IleGlnAlaIleValysAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeu	120
DB 306	ATCCAGGCCAGAGAGCGGCTGGACCTGGGCACCTTTCACGGGGTACTCCGGCCCTGGCCCTG	365
QY 121	AlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnProPro	140
DB 366	GCCCTGGCGCTGCCCGGAGCGCGCGTGTGACCTGCGAGGTGGAGCGCGAGCCCCCG	425
QY 141	GluLeuGlyArgProLeuTrpArgGlnAlaGlnAlaGluHisIleAspLeuArgLeu	160
DB 426	GAGCTGGGACGGCCCTGTGGAGCAGCGCGAGCGGAGCACAAGATCGACCTCCGCTG	485
QY 161	LysProAlaLeuGluThrLeuAspGluLeuAlaGlyGluAlaGlyThrPheAsp	180
DB 486	AAGCCCGCTTGGAGACCTTGGAGAGCTGTGGCGAGCTGTGTGGCGGCGCGGCGGCGACCTTCGAC	545

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:29637 IMAGE:4897624"
/tissue_type="Brain, neuroblastoma"
/clone_lib="NIH_MGC_19"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
1..913
/gene="COMTD1"
/note="synonym: FLJ23841"
/db_xref="LocustID:118881"
6..794
/gene="COMTD1"
/codon_start=1
/product="catechol-O-methyltransferase domain containing
1"
/protein_id="AAH23663.1"
/db_xref="GI:40226188"
/translation="MTQPVRLSPVPAALGSAALGAATGATGLGRRCPWRGRREQ
CLLPEDSRMQYLLSRSMREHPLRSRLRLTLEQPGQSMMTCEQAQLANLARIQ
AKKALDLGTCTGYSALALALALPADGRVVTCEVDQPPELGRPLRQAEAKHKIDRL
KPALTDLDELLAAGAGTFDVAVDADKENCASAYVERCLQLLRPGGILAVLVRGK
VLQPPKGDVAECVRLNERIRDRVYIISLLPLGDLTLAFKI"

```

## ORIGIN

```

Alignment Scores:
Pred. No.:      6 21e-95      Length:      913
Score:          1343.00      Matches:     262
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:               9          Gaps:      0

US-10-017-407A-306 (1-262) x BC023663 (1-913)

QY      1 MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla 20
Db      6 ATGACCCAGCCGGTGCCTCCGTCGCCGCGCGCTGCGCTGAGCGGCTCAGCGCA 65

QY     21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgArgCysProProTrpArgGly 40
Db     66 CTGGGCGCGCCCTTCGCCACTGCGCTCTTCTCTGGGAGCGGCTGCCCGCGAGGC 125

QY     41 ArgArgGluGlnCysLeuLeuProProGluAspSerArgLeuTrpGlnTrpLeuLeuSer 60
Db    126 CGCGGAGAGACAGTGCCTGCTTCCCCCGAGGACAGCCGCTGTCGAGCATCTTCTGAGC 185

QY     61 ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuLeuThrLeuGluGlnPro 80
Db    186 CGCTCCATCGGGGAGGACCCCGGCGCTGCGAGCGCTGAGGCTGCTGAGGAGCGCG 245

QY     81 GlnGlyAspSerMetMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeu 100
Db    246 CAGGGGGATTCCTATGATGACCTCGCAGCAGGCGCCAGCTCTTGGCCCAACCTGGCGGCTC 305

QY    101 IleGlnAlaLysIleAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeu 120
Db    306 ATCCAGGCCCAAGAGCGCTGAGACCTTGGGCACCTTCCGGGCTACTCCGGCTTGGCCCTG 365

QY    121 AlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnProPro 140
Db    366 GCCTTGGCGCTGCCCGCGGACCGGCGCGTGTGACCTGCGAGGTGCGAGCGCGCGCCCG 425

QY    141 GluLeuGlyArgProLeuTrpArgGlnAlaGluAlaGluHisLysIleAspLeuArgLeu 160
Db    426 GAGCTGGGACGGCCCTGTGGAGGCGAGCGCGAGGCGAGCACAAAGATCGACCTCCGGCTG 485

QY    161 LysProAlaLeuGluThrLeuAspGluLeuLeuAlaAlaGlyGluAlaGlyThrPheAsp 180
Db    486 AAGCCCGCTTGGAGACCTTGGAGCGCTGTCGCGGCGGCGGAGCGGCGGCGGCGGCGGCG 545

```

```
QY 181 ValAlaValAlaAspAlaAspLysGluAsnCysSerAlaTyrTyrGluArgCysLeuGln 200
Db 546 GTGGCGTGGTGGATCGGACAGGAGAACTGCTCGCCCTACTACAGCGCTGCGTGCAG 605
QY 201 LeuLeuArgProGlyGlyLeuAlaValLeuArgValLeuTrpArgGlyLysValLeu 220
Db 606 CTGCTGCGACCGGAGGCATCTCGCGCTCTCAGAGTCCTGCGCGCGGGAAGGTGCTG 665
QY 221 GlnProProLysGlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArgLys 240
Db 666 CAACTCCGAAAGGGACGTGGCGCGAGTGTGTGCGAAACCTAAACGAACGATCCGG 725
QY 241 ArgAspValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPhe 260
Db 726 CGGAGCTCAGGGTCTACATCAGCTCTTGGCCCTGGGGGATGGACTCACCTTGGCCTTC 785
QY 261 LysIle 262
Db 786 AAGATC 791

RESULT 4
BD222712
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Lal,P., Tang,X.T., Gorgone,G.A., Corley,N.C., Guegler,K.J.,
Baughn,M.R., Akerblom,I.B., Young,J.A., Yue,H., Patterson,C.,
Reddy,R., Hillman,J.L. and Bandman,O.
Human signal peptide-containing protein
Patent: JP 2002519030-A 58 02-JUL-2002;
INCYTE PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002519030-A/58
PD 02-JUN-2002
PF 25-JUN-1999 JP 2000557363
PR 26-JUN-1998 US 60/090762,31-JUL-1998 US 60/094983 PR
01-OCT-1998 US 60/102686 11-DEC-1998 US 60/112129 PI PREETI
LAL,Y TOM TANG,GINA A GORGONE,NEIL C CORLEY,KARL J PI GUEGLER,
PI MARIAH R BAUGHN,INGRID E AKERBLOW,JANICE AU YOUNG,HENRY YUE,
PI CHANDRA PATTERSON,ROOPA REDDY,JENNIFER L HILLMAN,OLGA BANDMAN
PC C12N15/09,A61K38/00,A61K39/395,A61K45/00,A61P9/00,A61P15/00,
PC A61P25/00,
PC A61P29/00,A61P35/00,A61P43/00,C07K14/47,C07K16/18,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,C12P21/02,C12Q1/68,G01N33/68//C12P21/08, PC
C12N15/00,
PC A61K37/02,C12N5/00
CC Incyte Clone No: 2816821
FH Key Location/Qualifiers
FT source 1..985
FT Location/Qualifiers
1..985
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

FEATURES
source
Location/Qualifiers
1..985
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 6,76e-95 Length: 985
Score: 1343.00 Matches: 262
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
```

```
US-10-017-407A-306 (1-262) x BD222712 (1-985)
QY 1 MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla 20
Db 84 ATGACCCAGCCCGTGGCCCGGCTCTCCGTGCCCCGCGCTGGCCCTTGGGCTCAGCGCGCA 143
QY 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgArgCysProProTrpArgGly 40
Db 144 CTGGGCGCGCCTTCGCCACTGCGCTCTTCTTGGGGAGGCGGTGCCCCCATGGCGAGGC 203
QY 41 ArgArgGluGlnCysLeuLeuProProGluAspSerArgLeuTrpGlnTyrIleLeuSer 60
Db 204 CGCGGAGAGCAGTGCCTGCTTCCCCCGAGGACAGCCGCTGTGGCAGTATCTTCTGAGC 263
QY 61 ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuThrLeuGluGlnPro 80
Db 264 CGCTCATCGGGAGACCCCGCGCTGCGAAGCCGTGAGGCTGTGACCTGGAGCAGCCG 323
QY 81 GlnGlyAspSerMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeu 100
Db 324 CAGGGGGATTCTATGATGACCTGCGAGCAGGCCAGCTCTTGCCCAACCTGGCGGGCTC 383
QY 101 IleGlnAlaLysLysAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeu 120
Db 384 ATCCAGGGCCAGAGAGCGCTGGACCTGGGCACCTTTCACGGGCTACTCCGCCCTGGCCCTG 443
QY 121 AlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnProPro 140
Db 444 GCCCTGGCGCTCCCGCGGACGCGGCGGTGGTGTGACTGCGAGGTGACGCGCAGCCCGC 503
QY 141 GluLeuGlyArgProLeuTrpArgGlnAlaGluAlaGluHisLysIleAspLeuArgLeu 160
Db 504 GAGCTGGGACGGCCCTGTGGAGGCGAGCCGAGGCGGAGCACAAGATCGACCTCGGGCTG 563
QY 161 LysProAlaLeuGluThrLeuAspGluLeuLeuAlaAlaGlyGluAlaGlyThrPheAsp 180
Db 564 AAGCCCGCTTGGAGACCTTGGACGAGCTGTGGCGGCGGCGGAGCCGCGACCTTCGAC 623
QY 181 ValAlaValAlaAspAlaAspLysGluAsnCysSerAlaTyrTyrGluArgCysLeuGln 200
Db 624 GTGGCGTGGTGGATGCGGACAAGGAGAACTCTCTCGCCCTACTACGAGCGCTGCTTGGCAG 683
QY 201 LeuLeuArgProGlyGlyIleLeuAlaValLeuArgValLeuTrpArgGlyLysValLeu 220
Db 684 CTGCTGCGACCCGAGGAGCATCTCGCGCTCTCAGAGTCTTGGCGCGGGAAGGTGCTG 743
QY 221 GlnProProLysGlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArgLys 240
Db 744 CAACTCCGAAAGGGAGCGTGGCGCGGAGTGTGTGCGAAACCTAAACGAACGATCCCG 803
QY 241 ArgAspValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPhe 260
Db 804 CGGAGCTCAGGGTCTACATCAGCTCTTGGCCCTGGGGGATGGACTCACCTTGGCCTTC 863
QY 261 LysIle 262
Db 864 AAGATC 869

RESULT 5
AX201342
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

AX201342
Sequence 21 from Patent WO0153486.
AX201342
AX201342.1 GI:15391164
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Ashkenazi,A.J., Goddard,A., Godowski,P.J., Gurney,A.L.,
Hillan,K.J., Marsters,S.A., Pan,J., Pitti,R.M., Roy,M.A., Smith,V.,
Stone,D.M., Watanabe,C.K. and Wood,W.I.
```

TITLE Compositions and methods for the treatment of tumour  
JOURNAL Patent: WO 0153486-A 21 26-JUL-2001;  
Genentech, Inc. (US)  
FEATURES Location/Qualifiers  
source 1..989  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Alignment Scores:  
Pred. No.: 6,79e-95 Length: 989  
Score: 1343.00 Matches: 262  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
US-10-017-407A-306 (1-262) x AX201342 (1-989)  
QY 1 MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla 20  
DB 84 ATGACCCAGCGGTGCGCGCTCTCGTCCCGCGCGCTGGCCCTGGGCTCAGCGCA 143  
QY 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgArgCysProProTyrArgGly 40  
DB 144 CTGGGCGCGCTTCGCCACTGGCCCTCTTCCTGGGAGCGGCTGCCCTCCATGCGAGGC 203  
QY 41 ArgArgGluGlnCysLeuLeuProGluAspSerArgLeuTyrGlnTyrLeuLeuSer 60  
DB 204 CGCGGAGAGCAGTCTGCTTCCCGCGAGGACAGCGCTGGCAGTATCTTCTGAGC 263  
QY 61 ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuLeuThrLeuGlnPro 80  
DB 264 CGCTCCATGCGGAGCACCAGCGCGCTGCGAAGCTGAGGCTGCTGACCTGGAGCAGCG 323  
QY 81 GlnGlyAspSerMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeu 100  
DB 324 CAGGGGGATTCTATGATGACCTCGGAGCGCGCTGCGGAGCGGCTGCGGAGCGGCTC 383  
QY 101 IleGlnAlaLysLeuAlaPheAlaThrGlyLeuPheLeuGlyArgArgCysLeuGln 120  
DB 384 ATCCAGGCCAAGAGCGCTGGACCTGGGACACCTTCACGGGCTACTCCGGCCCTGGGCTG 443  
QY 121 AlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnProPro 140  
DB 444 GCCTCGGAGCGGCGCTGCGGAGCGGCTGCGGAGCGGCTGCGGAGCGGCTGCGGAGCG 503  
QY 141 GluLeuGlyArgProLeuTyrArgGlnAlaGluAlaGluHisLysIleAspLeuArgLeu 160  
DB 504 GAGCTGGGACGGCCCTGTGGAGCGAGCGCGGAGCGGAGCACAAGATCGACCTCGGCTG 563  
QY 161 LysProAlaLeuGluThrLeuAspGluLeuLeuAlaAlaGlyGluAlaGlyThrPheAsp 180  
DB 564 AAGCCCGCTTGGAGACCTTGGACAGAGCTGCTGGCGGCGGCGGAGCGGCGGCTGCGAC 623  
QY 181 ValAlaValAlaAspAlaAspLysGluAsnCysSerAlaTyrTyrGluArgCysLeuGln 200  
DB 624 GTGGCGTGTGGATCGGACAGGAGAACTGCTCCGCCCTACTACGAGCGCTCGCTGCAG 683  
QY 201 LeuLeuArgProGlyGlyIleLeuAlaValLeuArgValLeuTyrArgGlyLysValLeu 220  
DB 684 CTGCTCGGACCGGAGGCACTCTCGCGCTCTCAGAGTCTGCTGGCGCGGAGGCTGCTG 743  
QY 221 GlnProProLysGlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArgIleArg 240  
DB 744 CAACCTCCCAAGAGGAGCGTGGCGGCGGAGTGTGTGCGAAACATAACCAACGATCCGG 803  
QY 241 ArgAspValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPhe 260  
DB 804 CGGAGCTCAGGGTCTACATGACCTCTCTGCGCCCTGGCGGATGGATCTACCTTGGCCTTC 863  
QY 261 LysIle 262

|||||  
864 AGATC 869  
RESULT 6  
AX697237  
LOCUS AX697237  
DEFINITION Sequence 305 from Patent WO0078961.  
ACCESSION AX697237  
VERSION AX697237.1 GI:29498404  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS  
1 Ferrara, N., Stewart, T. A., Williams, P. M., Baker, K. P., Desnoyers, L.,  
Eaton, D. L., Gao, W. Q., Pan, J., Botstein, D., Fong, S., Goddard, A.,  
Godowski, P. J., Gurney, A. L., Smith, V., Tumas, D., Wood, W. I.,  
Grimaldi, C. J., Hillan, K. J., Paoni, N. F., Roy, M. A., and Watanabe, C. K.  
Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 0078961-A 305 28-DEC-2000;  
Genentech Inc. (US)  
FEATURES Location/Qualifiers  
source 1..989  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Alignment Scores:  
Pred. No.: 6,79e-95 Length: 989  
Score: 1343.00 Matches: 262  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
US-10-017-407A-306 (1-262) x AX697237 (1-989)  
QY 1 MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla 20  
DB 84 ATGACCCAGCGGTGCGCGCTCTCGTCCCGCGCGCTGGCCCTGGGCTCAGCGCA 143  
QY 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgArgCysProProTyrArgGly 40  
DB 144 CTGGGCGCGCTTCGCCACTGGCCCTCTTCCTGGGAGCGGCTGCCCTCCATGCGAGGC 203  
QY 41 ArgArgGluGlnCysLeuLeuProGluAspSerArgLeuTyrGlnTyrLeuLeuSer 60  
DB 204 CGCGGAGAGCAGTCTGCTTCCCGCGAGGACAGCGCTGGCAGTATCTTCTGAGC 263  
QY 61 ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuLeuThrLeuGlnPro 80  
DB 264 CGCTCCATGCGGAGCACCAGCGCGCTGCGAAGCTGAGGCTGCTGACCTGGAGCAGCG 323  
QY 81 GlnGlyAspSerMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeu 100  
DB 324 CAGGGGGATTCTATGATGACCTCGGAGCGCGCTGCGGAGCGGCTGCGGAGCGGCTC 383  
QY 101 IleGlnAlaLysLeuAlaPheAlaThrGlyLeuPheLeuGlyArgArgCysLeuGln 120  
DB 384 ATCCAGGCCAAGAGCGCTGGACCTGGGACACCTTCACGGGCTACTCCGGCCCTGGGCTG 443  
QY 121 AlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnProPro 140  
DB 444 GCCTCGGAGCGGCGCTGCGGAGCGGCTGCGGAGCGGCTGCGGAGCGGCTGCGGAGCG 503  
QY 141 GluLeuGlyArgProLeuTyrArgGlnAlaGluAlaGluHisLysIleAspLeuArgLeu 160  
DB 504 GAGCTGGGACGGCCCTGTGGAGCGAGCGCGGAGCGGAGCACAAGATCGACCTCGGCTG 563  
QY 161 LysProAlaLeuGluThrLeuAspGluLeuLeuAlaAlaGlyGluAlaGlyThrPheAsp 180  
DB 564 AAGCCCGCTTGGAGACCTTGGACAGAGCTGCTGGCGGCGGCGGAGCGGCGGCTGCGAC 623  
QY 181 ValAlaValAlaAspAlaAspLysGluAsnCysSerAlaTyrTyrGluArgCysLeuGln 200  
DB 624 GTGGCGTGTGGATCGGACAGGAGAACTGCTCCGCCCTACTACGAGCGCTCGCTGCAG 683  
QY 201 LeuLeuArgProGlyGlyIleLeuAlaValLeuArgValLeuTyrArgGlyLysValLeu 220  
DB 684 CTGCTCGGACCGGAGGCACTCTCGCGCTCTCAGAGTCTGCTGGCGCGGAGGCTGCTG 743  
QY 221 GlnProProLysGlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArgIleArg 240  
DB 744 CAACCTCCCAAGAGGAGCGTGGCGGCGGAGTGTGTGCGAAACATAACCAACGATCCGG 803  
QY 241 ArgAspValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPhe 260  
DB 804 CGGAGCTCAGGGTCTACATGACCTCTCTGCGCCCTGGCGGATGGATCTACCTTGGCCTTC 863  
QY 261 LysIle 262



DEFINITION Sequence 1 from Patent WO0183719.  
 ACCESSION AX338454  
 VERSION AX338454.1 GI:18128893  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1  
 AUTHORS Meyers, R.A. and Williamson, M.  
 TITLE 25692, a novel human o-methyltransferase family member and uses thereof  
 JOURNAL Patent: WO 0183719-A 1 08-NOV-2001;  
 FEATURES Millennium Pharmaceuticals, Inc. (US)  
 source Location/Qualifiers  
 1. 1037  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:9606"  
 113. 901  
 /note="unnamed protein product"  
 /codon\_start=1  
 /protein\_id="CAD20539.1"  
 /db\_xref="GI:18128894"  
 /translation="MTQPVRLSVPAALALGSALCAAFATGLFLGRCPWRGRREQ  
 CLPPEDSLMQVLLSRMREHPALRSLLTLEQPGDSMMTCQAOQLLANLIQL  
 AKKALDLGFTGYTSALALAPADGRVTVCEVDAQPELGRPLMRQAEKHIDILRL  
 KPALETLDLAAAGAGTVDVADKENCASAYRERCLQLLRPGGILAVLRVLRGK  
 VLQPPKGDVAACEVRNLNERIRDRVRYISLLPLGDLTLAFKI"  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 7,16e-95 Length: 1037  
 Score: 1343.00 Matches: 262  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0  
 US-10-017-407A-306 (1-262) x AX338454 (1-1037)  
 QY 1 MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla 20  
 DB 113 ATGACCCAGCGGTGCGCCGCTCTCCGTGCGCGCGCGCTGGCCCTGAGCGCA 172  
 QY 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgCysProTtpArgGly 40  
 DB 173 CTGGGCGCGCCTTCGCCACTGCGCTCTCTCTGGGAGGCGGTGCCCCCATGGCGAGGC 232  
 QY 41 ArgArgGluGlnCysLeuLeuProProGluAspSerArgLeuTrpGlnTyrLeuLeuSer 60  
 DB 233 CGGCGAGAGCAGTGCCTGCTTCCCCCGGAGGACAGCGCGCTGGCGAGTATCTTCGAGC 292  
 QY 61 ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuLeuThrLeuGluGlnPro 80  
 DB 293 CGCTCATCGGAGACCGCGCGCTGCGAAGCTGAGGCTGCTGACCTGGAGCAGCGC 352  
 QY 81 GlnGlyAspSerMetMetThrCysGluGlnAlaGlnLeuAlaAlaLeuAlaArgLeu 100  
 DB 353 CAGGGGGATTCATGATGACCTCGAGCAGGCGCCAGCTCTTGCCCAACCTGGCGCGGCTC 412  
 QY 101 IleGlnAlaLysLysAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeu 120  
 DB 413 ATCCAGGCCAAGAAGCGCTGGACCTGGGCACCTTCACGGCTACTCCGCCCTGGCCCTG 472  
 QY 121 AlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnProPro 140  
 DB 473 GCGCTGGCGCTGCGCGGAGCGCGGTGTGTACCTGCGAGGTGACGCGCAGCGCCCGC 532  
 QY 141 GluLeuGlyArgProLeuTrpArgGlnAlaGluAlaGluHisLysIleAspLeuArgLeu 160  
 DB 533 GAGCTGGGAGCGGCCCTGTGTGGAGGCGGCGGAGCGGAGCACAAGATGACCTCCGGCTG 592

QY 161 LysProAlaLeuGluThrLeuAspGluLeuLeuAlaAlaGlyGluAlaGlyThrPheAsp 180  
 DB 593 AAGCCCGCCTTGGAGACCCCTGGACGAGCTGCTGCGCGCGGAGCGCGACCTTCGAC 652  
 QY 181 ValAlaValValAspAlaAspLysGluAsnCysSerAlaTyrTyrGluArgCysLeuGln 200  
 DB 653 GTGGCCGTGTGTGATCGGACAGGAGAACTGCTCCGCCCTACTACGAGCGCTCCCTCGAG 712  
 QY 201 LeuLeuArgProGlyGlyIleLeuAlaValLeuArgValLeuTrpArgGlyLysValLeu 220  
 DB 713 CTGCTCGGACCGGAGGATCCTCGCGCTCCTCAGAGTCTCTGTGCGCGGAGAGGTGCTG 772  
 QY 221 GlnProLysGlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArgIleArg 240  
 DB 773 CAACTCCGAAAGGAGCGTGGCGCGCGAGTGTGTGCGAAACCTAAACGAAACGATCCGG 832  
 QY 241 ArgAspValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPhe 260  
 DB 833 CGGAGCTCAGGGTCTACATCAGCTCTGCCCCCTGGCGATGAGTACCTTGGCCTTC 892  
 QY 261 LysIle 262  
 DB 893 AGATC 898  
 RESULT 9  
 BC047774  
 LOCUS  
 DEFINITION Homo sapiens catechol-O-methyltransferase domain containing 1, mRNA  
 (CDNA clone MGC:54273 IMAGE:5761696), complete cds.  
 ACCESSION BC047774  
 VERSION BC047774.1 GI:28839536  
 KEYWORDS MGC.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1041)  
 AUTHORS Strausberg, R.D., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaby, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalusz, D.E., Schnerk, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
 TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 PUBMED 12477932  
 REFERENCE 2 (bases 1 to 1041)  
 AUTHORS Strausberg, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (03-MAR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 1A03, Bethesda, MD 20892-2590, USA  
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 COMMENT Contact: MGC help desk  
 Email: [cgabs@mail.nih.gov](mailto:cgabs@mail.nih.gov)  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)  
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 94305  
 Web site: <http://www-shgc.stanford.edu>  
 Contact: (Dickson, Mark) [med@paxil.stanford.edu](mailto:med@paxil.stanford.edu)  
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/HLN at: <http://image.llnl.gov>  
 Series: IRAC Plate: 98 Row: 9 Column: 5  
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21389376.

## FEATURES

source

1. .1041  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="MGC:54273 IMAGE:5761696"  
 /tissue type="Lung, Spleen, fetal, pooled"  
 /clone\_lib="NIH MGC\_122"  
 /lab\_host="DH10E"  
 /note="Vector: pCMV-SPORT6"

gene

1. .1041  
 /gene="COMTD1"  
 /note="synonym: FLJ23841"  
 /db\_xref="LocusID:118881"

CDS

85..873  
 /gene="COMTD1"  
 /codon\_start=1  
 /product="catechol-O-methyltransferase domain containing 1"

/protein\_id="AAH47774.1"  
 /db\_xref="GI:28839537"  
 /db\_xref="LocusID:118881"

/translation="MTQPVRLSVPAALGSAALGAAPATGLFGRCPWRGRREQ  
 CLLPEDSLWYLLSRWRPALRSLRLLEQPGDSMTTQQAQLANLARLIQ  
 AKALDLFTGVSALALAPADGRVVTCEVDAQPELGRPLWRQAEAKHIDLRL  
 KPALETDLAAGAGTDFVAVDADKENCASAYVERCLQLLRPGGILLAVLRWRGK  
 VLQPPKGDVAECVRNLNERIRDRVYISLLPLDGLTLAFKI"

## ORIGIN

## Alignment Scores:

Pred. No.: 7,19e-95 Length: 1041  
 Score: 1343.00 Matches: 262  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-10-017-407A-306 (1-262) x BC047774 (1-1041)

QY 1 MetThrGlnProValProArgLeuSerValProAlaLeuAlaLeuGlySerAlaAla 20  
 DB 85 ATGACCCAGCGCGTCCCGCGCTCTCCGTGCCGCGCGCTGGCCCTGGGCTCAGCCGCA 144  
 QY 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgArgCysProTrpArgGly 40  
 DB 145 CTGGGCGCGCGCTCTCCGCTCTCTCTCTGGGAGGCGGTGCGCCCTCCATGGCGAGCG 204  
 QY 41 ArgArgGluGlnCysLeuLeuProGluAAspSerArgLeuTrpGlnTyrLeuLeuSer 60  
 DB 205 CGGCGAGAGCAGTGCCTGCTTCCCGCCGAGGACAGCGCGCTGTGGCAGTATCTTCGAGC 264  
 QY 61 ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuLeuThrLeuGlnPro 80  
 DB 265 CGCTCCATCGGAGACCGCGCGCTGCCAAGCCTGAGGCTGTGACCTGGAGCAGCGC 324  
 QY 81 GlnGlyAspSerMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeu 100  
 DB 325 CAGGGGGATTCATGATGACCTCGAGAGCGCCAGCTCTTGGCCAACTGGCGCGGCTC 384  
 QY 101 IleGlnAlaLysLysAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeu 120  
 DB 385 ATCCAGGCCAAGAAGCGCTGGACCTGGGCACCTTCACGGGCTACTCCGCGCTGGCCCTG 444

QY 121 AlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAlaAspAlaGlnProPro 140  
 DB 445 GGCCTGGCGCTGCCCGCGAGCGGGCGCTGGTGGACCTGGAGGTGGAGCGGAGCCCCCG 504  
 QY 141 GluLeuGlyArgProLeuTrpArgGlnAlaGluAlaGluHisLysLysLeuAspLeuArgLeu 160  
 DB 505 GAGCTGGGACGCGCCCTGTGGAGGAGGCGGAGCGGAGGAGCACAAGATCGACCTCCGGCTG 564  
 QY 161 LysProAlaLeuGluThrLeuAspGluLeuLeuAlaGlyGluAlaGlyThrPheAsp 180  
 DB 565 AAGCCCGCTTCGAGACCTCGACGAGCTGTGGCGGCGGAGCGGAGCGGACCTTCGAC 624  
 QY 181 ValAlaValValAspAlaAspLysGluAsnCysSerAlaTyrTyrGluArgCysLeuGln 200  
 DB 625 GTGGCGGTGGTGGATGGGAGCAAGAGAACTGCTCGCCCTACTACGAGCGCTGCTGCGAG 684  
 QY 201 LeuLeuArgProGlyGlyLeuLeuAlaValLeuArgValLeuTrpArgGlyLysValLeu 220  
 DB 685 CTGCTGGGACCGGAGGACCTCTCGCGCTCCTCAGAGTCTGTGGCGCGGAGGTTGCTG 744  
 QY 221 GlnProProLysGlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArgIleArg 240  
 DB 745 CAACCTCCGAAAGGGGACGTGGCGCGCGAGTGTGCGAAACCTAAACGACGATCCCG 804  
 QY 241 ArgAspValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPhe 260  
 DB 805 CGGAGCTCAGGCTTACATCAGCTCTCTGCGCCCTGGGCGAGTGGACTACCTTGGCTTC 864  
 QY 261 LysIle 262  
 DB 865 AAGATC 870

RESULT 10  
 AK074421  
 LOCUS Homo sapiens cDNA FLJ23841 fis, clone KAT04516.  
 DEFINITION AK074421  
 ACCESSION AK074421  
 VERSION AK074421.1 GI:18677019  
 KEYWORDS oligo capping; fis (full insert sequence).  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 Watanabe, K., Kumagai, A., Itakura, S., Yamazaki, M., Tashiro, H.,  
 Ota, T., Suzuki, Y., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T.,  
 Nakamura, Y., Isogai, T. and Sugano, S.  
 NEDO human cDNA sequencing project  
 1 Unpublished  
 2 (bases 1 to 988)  
 Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T.,  
 Shibahara, T., Tanaka, T. and Nakamura, Y.  
 Direct Submission  
 Submitted (14-FEB-2002) Sumio Sugano, Institute of Medical Science,  
 University of Tokyo, Laboratory of Genome Structure, Human Genome  
 Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan  
 (E-mail: [flcdna@ims.u-tokyo.ac.jp](mailto:flcdna@ims.u-tokyo.ac.jp), Tel: 81-3-5449-5286,  
 Fax: 81-3-5449-5416)  
 NEDO human cDNA sequencing project supported by Ministry of  
 Economy, Trade and Industry of Japan; cDNA full insert sequencing;  
 Research Association for Biotechnology; cDNA library construction,  
 5'- & 3'-end one pass sequencing; Department of Virology and Human  
 Genome Center, Institute of Medical Science, University of Tokyo  
 (partly supported by Science and Technology Agency).  
 Location/Qualifiers  
 1. .988  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="KAT04516"  
 /cell\_line="KATO III"  
 /cell\_type="signet-ring cell carcinoma"

FEATURES  
 source  
 1. .988  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="KAT04516"  
 /cell\_line="KATO III"  
 /cell\_type="signet-ring cell carcinoma"







```
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="MGC:58496 IMAGE:6535487"
/tissue_type="Brain, mouse"
/clone_lib="NIH MGC 144"
/lab_host="DH10B"
/notes="Vector: pDNR-LIB"
1. 946
/genes="Comtd1"
/db_xref="LocusID:69156"
/db_xref="MGI:1916406"
34_822
/genes="Comtd1"
/codon_start=1
/product="catechol-O-methyltransferase domain containing
1"
/protein_id="AAH49670.1"
/db_xref="GI:29612505"
/db_xref="LocusID:69156"
/db_xref="MGI:1916406"
/translation="MAQPVRLSIPAAALGSAALGAATFATGLLLGKRWPPNGSRROE
RLPPEDNPLWYLLSRMSRHPALRSLLTLEOQGDMMTCEQAQLANLARLIK
AKKALDLGFTGVSALALALPEAGRVVTCVDAPPKLGRPMKQAEVQKIDLR
OPALOTLDELLAAGEAGTFDIAVVDADKENTAYRERCLQLLRPGGVLAFLVLRGE
VLQPPRNKTEVCVRNLNERILRDARVYISLLPLDGLSLAFKI"
ORIGIN
Alignment Scores:
Pred. No.: 1.87e-80 Length: 946
Score: 1156.00 Matches: 224
Percent Similarity: 92.37% Conservative: 18
Best Local Similarity: 85.50% Mismatches: 20
Query Match: 86.08% Indels: 0
DB: 10 Gaps: 0
US-10-017-407a-306 (1-262) x BC049670 (1-946)
QY 1 MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla 20
Db 34 ATGGCTCAGCGCGCTCGCTGCTATCTATCCAGCGCGCATGCGCCCTGGCGCTCGCGCGCG 93
QY 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGlyArgGlyCysProProTrpArgGly 40
Db 94 CTGGCGCGCGCTCTGCTACTGCTCTCTGCTGGGGAACGGTGGCTCTCATGGGGGTCC 153
QY 41 ArgArgGluGlnCysLeuLeuProProGluAspSerArgLeuTrpGlnTrpLeuLeuSer 60
Db 154 AGCGGCAAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 213
QY 61 ArgSerMetArgGluHisProAlaLeuArgSerLeuArgLeuLeuThrLeuGluGlnPro 80
Db 214 CGCTCCATGAGAGAGACCGCGCGCTGCGAGCTCGACCTGCTGACCTGGAGCAGCGCG 273
QY 81 GlnGlyAspSerMetThrCysGluGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeu 100
Db 274 CAGGGGATTCATGATGACCTGTGAACAGGCCACGCTTCTGCGCCAACTGGCGCGGCTC 333
QY 101 IleGlnAlaLysLysAlaLeuAspLeuGlyThrPheThrGlyTyrSerAlaLeuAlaLeu 120
Db 334 ATTAAGGCCCAAGAAAGCTCTGGATCTGGGTACTTTTTCACGGGCTACTCGGCCCTTGGCCCTA 393
QY 121 AlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnProPro 140
Db 394 GCCTTGGCGCTTCCGAGGCTGGCGCGCTGGTGTGACCTGCGAGGTTCACGAGAGCCCCCG 453
QY 141 GluLeuGlyArgProLeuTrpArgGlnAlaGluAlaGluHisLysIleAspLeuArgLeu 160
Db 454 AGCTGGGACGGCCCACTGGGAAGCAGCGCAGAGTCTGAGCAGAGATCGACCTTCGGCTG 513
QY 161 LysProAlaLeuGluThrLeuAspGluLeuLeuAlaAlaGlyGluAlaGlyThrPheAsp 180
Db 514 CAGCGCGCGCTGCGAGACATTTGATGAGTCTCTAGCGCGCGCGGAGCGCGGACCTTCGAC 573
```

181 ValAlaValAlaAspAlaAspLysGluAsnCysSerAlaTyrTyrGluArgCysLeuGln 200  
574 ATAGCGCTGGTGGAGCGGACCAAGAGAACTGTACCGCTACTACGAGGCGGTCTGTGCAG 633  
201 LeuLeuArgProGlyGlyIleLeuAlaValLeuArgValLeuTrpArgGlyLysValLeu 220  
634 CTCCTAGTCTCCGAGGCGTCTGCTGCTACTCAGAGTCTGTGGCGCGGAGAGTGTCTG 693  
221 GlnProProLysGlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArgIleArg 240  
694 CAGCCTCAGCCCGGAGGAAAGAGACTGTGTAATGTGTGGGAACTGTGAACGACGATCTCTG 753  
241 ArgAspValArgValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPhe 260  
754 AGGAGCGCAGGCTTACATCAGCTCTGCGCCCTGGATGATGATGATGATGATGATGATGAT 813  
261 LysIle 262  
814 AGATC 819

RESULT 12  
AL390034/c  
LOCUS  
DEFINITION Human DNA sequence from clone Rp11-375G3 on chromosome 10, complete sequence.  
ACCESSION AL390034 GI:18041549  
VERSION AL390034.23  
KEYWORDS HTG.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 38679)  
Wray, P.  
Direct Submission  
Submitted (01-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humrey@sanger.ac.uk  
On Jan 2, 2002 this sequence version replaced gi:18032099.  
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.  
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TrEMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at  
http://www.sanger.ac.uk/Projects/C\_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at  
http://www.sanger.ac.uk/HGP/Chr10  
Rp11-375G3 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see  
http://www.chori.org/bacpac/home.htm  
VECTOR: pBAC3.6  
IMPORTANT: This sequence is not the entire insert of clone Rp11-375G3. It may be shorter because we sequence overlapping sections only once, except for a short overlap.  
The true left end of clone Rp11-39K21 is at 36680 in this sequence. The true right end of clone Rp11-48715 is at 2000 in this sequence.

Location/Qualifiers

```
source      1. .38679
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            /chromosome="10"
            /clone="RP11-375G3"
            /clone_lib="RPCI-11.2"
            /notes="Sequence from uni-directional dgrp big dye
            terminator reads only."
misc_feature 29061..29121
ORIGIN
Alignment Scores:
Pred. No.:      9,46e-69      Length:      38679
Score:          1028.00      Matches:      261
Percent Similarity: 42.10%      Conservative: 0
Best Local Similarity: 42.10%      Mismatches: 1
Query Match:      76.55%      Indels:      359
DB:              9          Gaps:        6

US-10-017-407A-306 (1-262) x AL390034 (1-38679)
QY      1 MetThrGlnProValProArgLeuSerValProAlaAlaLeuGlySerAlaAla 20
DB      9448 ATGACCCAGCGGTGCCCCGGCTCTCGTGCCCGCGCGCTGGCCCTGAGCGCA 9389
QY      21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeu----- 31
DB      9388 CTGGGCGCGCCTTCGCCACTGGCCTCTTCTGGGTGAGCAGGACCTGGTCCC GGCGGGC 9329
QY      31 ----- 31
DB      9328 GGGTGGCGGGCGCAGAGTAGGGCGGGCGTGGCTCAGGTTAATCCAACACCTCTCCCC 9269
QY      32 ---- GlyArgArgCysProProTrpArgGlyArgGluGlnCysLeuLeuProProG 50
DB      9268 GTCAGGGAGCGGTGCCCCCATGCGAGCGCGGAGCAGTGGCTGCTTCCCCCGGA 9209
QY      50 uAspSerArgLeuTrpGlnTyrLeuLeuSerArgSerMetArgGluHisProAlaLeuAr 70
DB      9208 GGACAGCGCGCTGTGGCAGTATCTTCTGAGCGCTCCATCGGGAGCAGCCCGCGGTGCG 9149
QY      70 gSerLeuArgLeu----- 74
DB      9148 AAGCCTGAGGCTGGTCAGCAGGCGCGGAGCGGAAACGGGCGTCCCTCTCGACCCCTGCG 9089
QY      74 ----- 74
DB      9088 GGTCCACAGTGGCTGTGACCTTGGGTGGGCGCTGGGCCCTCCCTGGGGCTTCCGGCTTC 9029
QY      74 ----- 74
DB      9028 CTTGGGCGGGTGGGTGGGCGTTCGAGAGGGCCAGTCCCCCAGGCCACGCCAGAACCG 8969
QY      74 ----- 74
DB      8968 CGCCCTGGGGCTTGGGACCCCCAGGGCGAAGGTGGGTGACCTGTCATGGCTGGTGCCACC 8909
QY      75 ----- LeuThrLeuGluGlnProGlnGlyAspSerMetMetThrCysG 89
DB      8908 CTCCTCCTTCACGACGCTGACCTCGAGCGCGCAGCGGAGTTCATGATGACCTGGCGA 8849
QY      89 uGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeuLleGlnAlaLysLeAlaLeuAspLe 109
DB      8848 GCAGGCCCCAGCTCTTGCCCAACCTGGGCGGCTCATCCAGGCCAAGAGGGCGTGGACCT 8789
QY      109 u----- 109
DB      8788 GGGTAGGGGACGCGCGCGGGATCCCGAGGGCGGAGGTTTCCGGGCGGACCCCACTCT 8729
QY      110 ----- GlyThrPheThrGlyTyrSerAlaLeuAla 120
DB      8728 GGGCTGAGCCCGTCTGTGTCTGGTCCCGAGGCACTTTCACGGGCTACTCGGGCTTCCGGCC 8669
```

```
QY      120 euAlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnProp 140
DB      8668 TGGCCCTGGCGCTGCCCGCGAGCGGGCGCTGGTGACTCTGCGAGGTGGAGCGCGAGCCCC 8609
QY      140 roGluLeuGlyArgProLeuTrpArg----- 148
DB      8608 CGGAGCTGGGACGGCCCCCTGTGGAGGCAGGTGAGCGCCCGCGCTAGCTCTGCGAGCCCCA 8549
QY      149 ----- GlnAlaGluAlaGluHisLysIleAsp 157
DB      8548 GGGGGGGGCGCAAGCGGTGACCCGCTCCCTCCGAGGCCCGAGCGGGAGCAACAGATCGAC 8489
QY      158 LeuArgLeuLysProAlaLeuGluThrLeu----- 167
DB      8488 CTCGGCTGAAGCCCGCTTGGAGACCT- GGTGTAGCACCGAAGCGGAAGGCTTTGA 8430
QY      167 ----- 167
DB      8429 AGCCATTTCATTCAAAACGAGGCTGCTGTGTGGCGAGCTGTGACTGGGCCCTGCGCGGCGAG 8370
QY      167 ----- 167
DB      8369 GTTAAGGGCAGGGCGGTTGTACAGAGCCCGGGCGGCTGGGAGGGGCTCAGGGGCGG 8310
QY      168 ----- AspGluLeuLeuAla 172
DB      8309 CCGGGCGCGGAGCTCAGCGCACCTGCCCTCCCTCCCGCGCAAGACGAGCTGCTGGCG 8250
QY      173 AlaGlyGluAlaGlyThrPheAspValAlaValValAspAlaAspLysGluAsnCysSer 192
DB      8249 GCGGGCGAGCGCGGACCTTCGACGTGGCGTGGTGGATCGGACAAAGAGAACTGCTCC 8190
QY      193 AlaTyrTyrGluArgCysLeuGlnLeuLeuArgProGlyGlyIleLeuAlaValLeuArg 212
DB      8189 GCCTACTACGAGCGCTGCTGCGAGCTGCTGCGAGCCCGAGGAGCATCTCGCGCTCTCAGA 8130
QY      212 ----- 212
DB      8129 GTAAGGGATCCACTGCGGGGAGGAGAAAGACCCCTGTGCGGCGGGTCCCATCTTTTC 8070
QY      212 ----- 212
DB      8069 CTTGACTCTCTTATATACCCAAAGCCCAACCCAGTCCAGTCCAGTACAGTACACCCCT 8010
QY      212 ----- 212
DB      8009 CCGGGGCTCGGGCCCGGTACCCAGGCTTTCCTCCGCTTTGGTTCTCTCCAGCTCTGG 7950
QY      212 ----- 212
DB      7949 TCACCTCCTCGCGGGACCTCCCTCGAGGCCCGGCTCCCGCCAGACACCTCCCTCC 7890
QY      212 ----- 212
DB      7889 GAGACCCCGCTTTCCTGCTGGGACCTCCCTCCAGAGCCCGGCTCCCGCGGGCACCT 7830
QY      212 ----- 212
DB      7829 CCCTCCAGTCCCGGCTTCGCGCCGAGACCTCCCTCCGAAAGCCCGCTCCAGGCG 7770
QY      213 ----- ValLeuTrpArgGlyLysValLeuGlnProProLys 224
DB      7769 CCGTTGGCCCGGCTCCCGGAGTCTCTGTGGCGGGAGGCTGTCGCACTCCGAAA 7710
QY      225 GlyAspValAlaAlaGluCysValArgAsnLeuAsnGluArgIleArgArgAspValArg 244
DB      7709 GGGGACGTGGCGCGCGAGTGTGCGAAACCTAAACGAAACGATCCGGGCGGAGCTCAGG 7650
QY      245 ValTyrIleSerLeuLeuProLeuGlyAspGlyLeuThrLeuAlaPheLysIle 262
DB      7649 GTCTACATCAGGCTCTGCGGCTGGGCGATGGACTCACCTTGGCTTCAAGATC 7596
```

## RESULT 13

## AC027393/c

## LOCUS

## DEFINITION

## SEQUENCE, 28 unordered pieces.

## ACCESSION

## AC027393

## VERSION

## HTG; HTGS\_PHASE1; HTGS\_DRAFT.

## KEYWORDS

## SOURCE

## ORGANISM

## Homo sapiens

## Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

## 1 (bases 1 to 169612)

## Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Baetien,V., Beda,F., Boguslavsky,L., Bouckgater,B., Brown,A., Burkett,G., Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mienga,V., Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N., Pisanic,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.

## Direct Submission

## Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

## 3 (bases 1 to 169612)

## Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Baetien,V., Beda,F., Boguslavsky,L., Bouckgater,B., Brown,A., Burkett,G., Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mienga,V., Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N., Pisanic,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.

## TITLE

## JOURNAL

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## On May 25, 2000 this sequence version replaced gi:7652066.

## All repeats were identified using RepeatMasker:

## Smit, A.F.A. &amp; Green, P. (1996-1997)

## http://ftp.genome.washington.edu/RM/RepeatMasker.html

## ----- Genome Center

## Center: Whitehead Institute/ MIT Center for Genome Research

## Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>  
 Contact: [sequence\\_submission@genome.wi.mit.edu](mailto:sequence_submission@genome.wi.mit.edu)

----- Project Information

Center project name: L6572

Center clone name: 770\_D\_23

----- Summary Statistics

Sequencing vector: M13; M7815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 155213 bases at least Q40

Consensus quality: 162022 bases at least Q30

Consensus quality: 164973 bases at least Q20

Insert size: 179000; agarose-fp

Insert size: 166912; sum-of-contigs

Quality coverage: 4.1 in Q20 bases; agarose-fp

Quality coverage: 4.4 in Q20 bases; sum-of-contigs

-----

\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 28 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

\* 1 1191: contig of 1191 bp in length  
 \* 1192 1291: gap of 100 bp  
 \* 1292 2404: contig of 1113 bp in length  
 \* 2405 2504: gap of 100 bp  
 \* 2505 3705: contig of 1201 bp in length  
 \* 3706 3805: gap of 100 bp  
 \* 3806 4734: contig of 929 bp in length  
 \* 4735 4834: gap of 100 bp  
 \* 4835 6570: contig of 1736 bp in length  
 \* 6571 8583: contig of 1913 bp in length  
 \* 8584 8683: gap of 100 bp  
 \* 8684 10290: contig of 1607 bp in length  
 \* 10291 10390: gap of 100 bp  
 \* 10391 11338: contig of 1548 bp in length  
 \* 11339 12038: gap of 100 bp  
 \* 12039 15839: contig of 3801 bp in length  
 \* 15840 15939: gap of 100 bp  
 \* 15940 19203: contig of 3264 bp in length  
 \* 19204 19303: gap of 100 bp  
 \* 19304 22581: contig of 3278 bp in length  
 \* 22582 22681: gap of 100 bp  
 \* 22682 24947: contig of 2266 bp in length  
 \* 24948 25047: gap of 100 bp  
 \* 25048 28167: contig of 3120 bp in length  
 \* 28168 28267: gap of 100 bp  
 \* 28268 32083: contig of 3816 bp in length  
 \* 32084 32183: gap of 100 bp  
 \* 32184 35533: contig of 3350 bp in length  
 \* 35534 35633: gap of 100 bp  
 \* 35634 41517: contig of 5884 bp in length  
 \* 41518 41617: gap of 100 bp  
 \* 41618 47143: contig of 5526 bp in length  
 \* 47144 47243: gap of 100 bp  
 \* 47244 51694: contig of 4451 bp in length  
 \* 51695 51795: contig of 5776 bp in length  
 \* 51796 57570: gap of 100 bp  
 \* 57571 63190: contig of 5520 bp in length  
 \* 63191 63290: gap of 100 bp  
 \* 63291 70708: contig of 7418 bp in length  
 \* 70709 70808: gap of 100 bp  
 \* 70809 78988: contig of 8180 bp in length  
 \* 78989 79088: gap of 100 bp  
 \* 79089 86527: contig of 7439 bp in length  
 \* 86528 99114: contig of 100 bp  
 \* 99115 99214: gap of 100 bp

\* 99215 110221: contig of 11007 bp in length  
 \* 110222 110321: gap of 100 bp  
 \* 110322 123287: contig of 12966 bp in length  
 \* 123288 123387: gap of 100 bp  
 \* 123388 147877: contig of 24490 bp in length  
 \* 147878 147977: gap of 100 bp  
 \* 147978 169612: contig of 21635 bp in length.

## FEATURES

## source

Location/Qualifiers

1. 169612

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

/chromosome="10"

/map="10"

/clone="RP11-770D23"

/clone\_lib="RPC1-11 Human Male BAC"

1. 1191

/note="assembly\_fragment"

1292..2404

/note="assembly\_fragment"

2505..3705

/note="assembly\_fragment"

3806..4734

/note="assembly\_fragment"

clone\_end:17

/vector\_side:right

4835..6570

/note="assembly\_fragment"

6671..8583

/note="assembly\_fragment"

8684..10290

/note="assembly\_fragment"

clone\_end:SP6

/vector\_side:left

10391..11938

/note="assembly\_fragment"

12039..15839

/note="assembly\_fragment"

15940..19203

/note="assembly\_fragment"

19304..22581

/note="assembly\_fragment"

22682..24947

/note="assembly\_fragment"

25048..28167

/note="assembly\_fragment"

28268..32083

/note="assembly\_fragment"

32184..35533

/note="assembly\_fragment"

35634..41517

/note="assembly\_fragment"

41618..47143

/note="assembly\_fragment"

47244..51694

/note="assembly\_fragment"

## Alignment Scores:

Pred. No.: 4,95e-68 Length: 169612  
 Score: 1028.00 Matches: 261  
 Percent Similarity: 42.10% Conservative: 0  
 Best Local Similarity: 42.10% Mismatches: 1  
 Query Match: 76.55% Indels: 359  
 DB: 2 Gaps: 6

US-10-017-407A-306 (1-262) x AC027393 (1-169612)

QY 1 MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla 20  
 |||||  
 Db 142098 ATGACCCACCGGTGCCCCGGCTCTCCGTGCCCGCCCGCTGGCCCTGGGCTCAGCCGCA 142039  
 |||||  
 QY 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeu----- 31  
 |||||

Db 142038 CTGGGGCGCGCCTTCCGCCACTGGCCCTTCTCCTGGGTGAGCAGACCTGGTCCCGCGCGGC 141979  
 QY 31 ----- 31  
 Db 141978 GGGTGGCGGGCGCAGAGTAGGCGCGCGTGGCTCAGGTTAATCAACACCTCTCTCC 141919  
 QY 32 ---- GlyArgArgCysProProTrrArgGlyArgArgGluGlnCysLeuLeuProProG 50  
 |||||  
 Db 141918 GTCAGGGAGCGGTGCCCCCATGGCGAGCGCGGAGAGCAGTGGCTGTCTCCCGCGCA 141859  
 QY 50 uAapSerArgLeuTrrGlnTyrLeuLeuSerArgSerMetArgGluHisProAlaLeuAr 70  
 |||||  
 Db 141858 GGACACCGCCCTGTGGCAGTAATCTTCTGAGCCCTCCATGCGGGAGACCCCGCGCTGCG 141799  
 QY 70 gSerLeuArgLeu----- 74  
 |||||  
 Db 141798 AAGCCTGAGGCTGGTCAGCAGGCGCGGAGCGGAACGGCGGTCCCTCTCGACCCCTGCG 141739  
 QY 74 ----- 74  
 Db 141738 GGTCCACACGTGGCTGTGTGACCTTGGGCTGGGCGCTTGGCCCTCTCGGCTTC 141679  
 QY 74 ----- 74  
 Db 141678 CTTGGGCGGGGTGCGGTGGGCGTTCCGAAGGGCCAGTCCCCCAGGCCACGCCCAACCG 141619  
 QY 74 ----- 74  
 Db 141618 CGCCCTGGGGCTTGGGACCCCGGCGAGAGGTGGGTGACCTGTCATGGCTGGTGCACC 141559  
 QY 75 ----- LeuThrLeuGluGlnProGlnGlyAapSerMetMetThrCysG 89  
 |||||  
 Db 141558 CTCTCTTTTACGCGAGCTGACCTGGAGCAGCGCAGGGGGATTCTATGATGACCTGCGA 141499  
 QY 89 uGlnAlaGlnLeuLeuAlaAsnLeuAlaArgLeuLleGlnAlaLysLeuAlaLeuHeple 109  
 |||||  
 Db 141498 GCAGGCCAGCTCTTGGCCAACTGGCGCGGTCTATCCAGGCCAAGAGCGCTGGACCT 141439  
 QY 109 u----- 109  
 Db 141438 GGGTAGGGCAGCGCGCGGGATCCCGGAGGGCGGAGTTTCCGGCGCCGACCCCTCT 141379  
 QY 110 ----- GlyThrPheThrGlyTyrSerAlaLeuAlaL 120  
 |||||  
 Db 141378 GGGCTGAGCCCTCTGTGTCCTGCTCCAGGACCTTCACTGGGCTACTCCGCTGCGCC 141319  
 QY 120 euAlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGlnProp 140  
 |||||  
 Db 141318 TGGCCCTGGCGTGGCCCGGACGGGCGGTGGTGTGACCTGCGAGGTGGACGCGCAGCCCC 141259  
 QY 140 roGluLeuGlyArgProLeuTrrArg----- 148  
 |||||  
 Db 141258 CGGAGCTGGGACGGCCCTTGTGGAGGCGAGTGGAGCGCCCGCGCTAGCTCTGCAGCCCCA 141199  
 QY 149 ----- GlnAlaGluAlaGluHisLysLleAap 157  
 |||||  
 Db 141198 GCGCGGGCGCAACGGCTGACCGCTCCCTCCGCGAGCGCGGAGCACAAGATCGAC 141139  
 QY 158 LeuArgLeuLysProAlaLeuGluThrLeu----- 167  
 |||||  
 Db 141138 CTCCGCTGAAGCCCGCTTGGAGACCTT- GGGTGAACACCGAAGCGGAGGGGCTTTGA 141080  
 QY 167 ----- 167  
 Db 141079 AGCCATTATTGCAAAACGAGGCTGTGTGTGSCCGAGTGTGACTGGGCTTCCCGGGCAG 141020  
 QY 167 ----- 167  
 Db 141019 GTTAAGGCGAGGCGCGTGTGTACAGAGCCCGGCGGCTTGGAGGGGCTTCAGGGCGC 140960  
 QY 168 ----- AspGluLeuLeuAla 172  
 |||||  
 Db 140959 CCGGGCGCGGACTACGCGCACCTGCTCCCTCCCTCCCGCCGACAGACGCTGCTGGCG 140900



QY 192 SerAlaTyTrGluArgCysLeuGlnLeuLeuArgProGlyGlyLeuAlaValLeu 211  
 Db 77136 ACCGCCTACTACGAGCGCTGTCTGCAGCTCTACGTCCCGAGCGTGTCTCGTACTC 77077  
 QY 212 Atg----- 212  
 Db 77076 AGAGTAAGACTAGCTAAGCAAACTGCTGTTTGTGTGGTGAGTACCCTTTCTC 77017  
 QY 212 ----- 212  
 Db 77016 AGCTCTTCCACCCACCCCGCCGCCCCAAAGCCACCAGATATCATAGTCTCC 76957  
 QY 212 ----- 212  
 Db 76956 CGCCCTCTGCTAAAGCTCTGGTCTGCTACCCCTCCAGCGGCCGCCCTC 76897  
 QY 213 -----ValLeuTrpArgGlyLysValLeuGlnProProlGlyAspValAlaA1a 229  
 Db 76896 CATCTGTAGTCTGTGGCGGAGAGTGTCTGACGCTCAGCCCGAGCAAGACTGTT 76837  
 QY 230 GluCysValArgAsnLeuAsnGluArgIleArgAspValArgValTrpIleSerLeu 249  
 Db 76836 GAATGTGTGGGAACCTGAACGACCATCTGAGGAGCCGAGGCTTACATCAGCCTC 76777  
 QY 250 LeuProLeuGlyAspGlyLeuThrLeuAlaPheLysIle 262  
 Db 76776 CTGCCCTTGATGATGCTCTCTCTTGGGCTTTAAGATC 76738  
 RESULT 15  
 AC132590  
 LOCUS Mus musculus BAC clone RP24-273G1 from chromosome 14, complete  
 DEFINITION sequence.  
 ACCESSION AC132590  
 VERSION AC132590.3 GI:38564396  
 KEYWORDS HTG.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 161371)  
 Swearingen-Shahid,S., Shahid,S., Meyer,R. and Haglund,K.  
 The sequence of Mus musculus BAC clone RP24-273G1  
 Unpublished (2001)  
 REFERENCE 2 (bases 1 to 161371)  
 AUTHORS Wilson.R.  
 TITLE Sequencing of Mus musculus  
 JOURNAL Unpublished (2001)  
 REFERENCE 3 (bases 1 to 161371)  
 AUTHORS McPherson,J.D. and Waterston,R.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-SEP-2002) Genome Sequencing Center, 4444 Forest Park  
 Parkway, St. Louis, MO 63108, USA  
 REFERENCE 4 (bases 1 to 161371)  
 AUTHORS McPherson,J.D. and Waterston,R.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (10-OCT-2002) Genome Sequencing Center, 4444 Forest Park  
 Parkway, St. Louis, MO 63108, USA  
 REFERENCE 5 (bases 1 to 161371)  
 AUTHORS Wilson.R.K.  
 TITLE Direct Submission  
 JOURNAL Submitted (27-NOV-2003) Genome Sequencing Center, 4444 Forest Park  
 Parkway, St. Louis, MO 63108, USA  
 REFERENCE 6 (bases 1 to 161371)  
 AUTHORS Wilson.R.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-JAN-2004) Department of Genetics, Washington  
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
 On Nov 27, 2003 this sequence version replaced gi:23683300.  
 ----- Genome Center  
 Center: Washington University Genome Sequencing Center  
 Center code: WUGSC  
 Web site: http://genome.wustl.edu

Contact: submissions@watson.wustl.edu  
 ----- Summary Statistics  
 Center project name: M\_BB0273G01  
 -----

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:  
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

#### MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu

#### SOURCE INFORMATION:

The RPCI-24 BAC library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org

#### NEIGHBORING SEQUENCE INFORMATION:

This sequence is the entire insert of the clone. This clone is overlapped by AC129590.

FEATURES	source
repeat_region	1..161371 /organism="Mus musculus" /mol_type="genomic DNA" /db_xref="taxon:10090" /chromosome="14" /map="14" /clone_lib="RPCI-24" /rpt_family="ERV1"
repeat_region	1..348 /rpt_family="B2"
repeat_region	545..734 /rpt_family="Alu"
repeat_region	1040..1179 /rpt_family="MaLR"
repeat_region	2711..3080 /rpt_family="ERVK"
repeat_region	2868..3129 /rpt_family="MIR"
repeat_region	3139..3301 /rpt_family="ACHobo"
repeat_region	3382..3467 /rpt_family="L2"
repeat_region	3750..3815 /rpt_family="B4"
repeat_region	4246..4403 /rpt_family="B4"
repeat_region	4411..4650 /rpt_family="B2"
repeat_region	4592..4700 /rpt_family="MaLR"
repeat_region	4863..5081 /rpt_family="L1"
repeat_region	5928..6041 /rpt_family="BCL_MM"
repeat_region	6055..6138 /rpt_family="L1"
repeat_region	6149..6318 /rpt_family="L1"
repeat_region	6420..6753

```

repeat_region /rpt_family="L1"
6816_..7201
repeat_region /rpt_family="MaLR"
7250_..7399
repeat_region /rpt_family="Alu"
7596_..7996
repeat_region /rpt_family="L1"
8057_..8187
repeat_region /rpt_family="B2"
8191_..8692
repeat_region /rpt_family="L1"
8693_..8879
repeat_region /rpt_family="B2"
8880_..9031
repeat_region /rpt_family="L1"
15222_..15472
repeat_region /rpt_family="L1"
15491_..15703
repeat_region /rpt_family="B2"
15739_..15887
repeat_region /rpt_family="MaLR"
15888_..16190
repeat_region /rpt_family="MaLR"
16161_..16277
repeat_region /rpt_family="MaLR"
16247_..16353
repeat_region /rpt_family="MaLR"
16347_..16564
repeat_region /rpt_family="MaLR"
16571_..18968
repeat_region /rpt_family="L1"
18971_..19521
repeat_region /rpt_family="MaLR"
19522_..19658
repeat_region /rpt_family="L1"
19721_..20605
repeat_region /rpt_family="L1"
20607_..20663
repeat_region /rpt_family="ERV1"
20768_..20896
repeat_region /rpt_family="Alu"
21122_..21261
repeat_region /rpt_family="L1"
21264_..21420
repeat_region /rpt_family="B4"
21551_..21620
repeat_region /rpt_family="L1"
21649_..21775
repeat_region /rpt_family="Alu"
21900_..21974
repeat_region /rpt_family="ID"
22014_..22073
repeat_region /rpt_family="ID"
22267_..22310
repeat_region /rpt_family="L1"
22417_..22678
repeat_region /rpt_family="B4"
22729_..22864
repeat_region /rpt_family="Alu"
22867_..22980
repeat_region /rpt_family="L1"
23172_..23351
repeat_region /rpt_family="L1"
23419_..23574
repeat_region /rpt_family="B2"
23776_..24006
repeat_region /rpt_family="B4"
24929_..25063
repeat_region /rpt_family="Alu"
25146_..25492
repeat_region /rpt_family="MaLR"
25532_..25626
repeat_region /rpt_family="MIR"

```

```

repeat_region 25639_..25873
/rpt_family="L2"
repeat_region 25937_..26018
/rpt_family="Alu"
repeat_region 26021_..26107
/rpt_family="MIR"
repeat_region 26205_..26315
/rpt_family="MIR"
repeat_region 27582_..27640
/rpt_family="MIR"
repeat_region 28143_..28277

Alignment Scores:
Pred. No.: 7,09e-56 Length: 161371
Score: 870.50 Matches: 223
Percent Similarity: 44.84% Conservatives: 16
Best Local Similarity: 41.84% Mismatches: 23
Query Match: 64.82% Indels: 275
DB: 10 Gaps: 7

US-10-017-407A-306 (1-262) x AC132590 (1-161371)
QY 1 MetThrGlnProValProArgLeuSerValProAlaAlaLeuAlaLeuGlySerAlaAla 20
Db 44910 ATGGCTCAGCCCGTCCCTCGGCTATCTATCCAGCGCAGCTGGCCCTGGGCTCGGCCGG 44969
QY 21 LeuGlyAlaAlaPheAlaThrGlyLeuPheLeuGly----- 32
Db 44970 CTGGCGCGCGCTTCGTACTGGTCTCTTGTCTGGGTAGCTGGGCTGGGCTGCTGCAGTC 45029
QY 33 -----ArgArgCys----- 35
Db 45030 CGGGGAATGGGAGGAGGGCGGAGAGCCGAGACCCCGTCAGAA--TGCAGGCC 45088
QY 36 -----ProProTrpArgGlyArgGlu 43
Db 45089 TGACTCGGCACCTCTCCCGCAGCGAAGACCGTGGGCTCCATGGGGTCCAGCGGCAA 45148
QY 44 GlnCysLeuLeuProGluAspSerArgLeuTrpGlnTrpLeuLeuSerArgSerMet 63
Db 45149 GAGCGCTGCTGCCACCTGAGGACAAATCCCTGTGGCAGTATCTGCTAGCGCTCATG 45208
QY 64 ArgGluHisProAlaLeuArgSerLeuArgLeu----- 74
Db 45209 AGAGAGCACC CGCGCTGCGGAGCCTGCGACTGGTCTGAGTGGGACCGAAGACCG 45268
QY 74 ----- 74
Db 45269 CTCCCCACTTCCAGCGTGGTGGACCTCAGTGGCTGTGTGACCTTTGAGCTAGGCAGAAAC 45328
QY 74 ----- 74
Db 45329 CCTCTCTGGGCTTCGGGTTCCCTGAGACCTGTCCTCTAGGCCACACCCGCCACCGAG 45388
QY 74 ----- 74
Db 45389 CCCCTGAATGATTCAAACCTCAGGGGGAGGTGGGGGGGTGACTGGTATGATGGCAC 45448
QY 75 -----LeuThrLeuGluGlnProGlnGlyAspSerMetMetThrCys 88
Db 45449 CTCCTCTCTCCACACAGCTGACCTGGAGCAGCGCAGGGGGATTTCATGATGACCTGT 45508
QY 89 GluGlnAlaGlnLeuAlaAsnLeuAlaArgLeuLleGlnAlaLysLysAlaLeuAsp 108
Db 45509 GAACAGGGCCAGCTTCTGGCCAACTGGCGCGGCTCATTAAGGCCAAGAAAGCTCTGGAT 45568
QY 109 Leu----- 109
Db 45569 CT-GGGTAGGRACAGCAGCCATGGTCTCTGGAACACAGGGTTCACAGGSCAGCCCTGCAC 45627
QY 110 -----GlyThrPheThrGlyTrpSerAlaLeu 118
Db 45628 CCTGAACAGCTTGACAGTGTGTCCCTTTCCACAGGTACTTTTCACGGGCTACTCGGCCCTG 45687

```



```
QY 119 AlaLeuAlaLeuAlaLeuProAlaAspGlyArgValValThrCysGluValAspAlaGln 138
Db 45688 GCCTAGCCTTGGCGCTTCGGAGGCTGGCGGCTGGTGCACCTGCGAGGTTGACGCAGAG 45747
QY 139 ProGluLeuGlyArgProLeuTyrArg-
Db 45748 CCCCCAAGCTGGGACGGCCCAATGTGGAA-GCAGGTGAGAGCCCCACACCTGGCGCGGTT 45806
QY 149 -----GlnAlaGluAlaGlu 153
Db 45807 CGGGCTCCGGCTCGGGGGCGTGGCGGCTGACCGGCTCCTTCGCGAGGCGAGAAGTGGAG 45866
QY 154 HisLysIleAspLeuArgLeuLysProAlaLeuGluThrLeu----- 167
Db 45867 CAGAAGATCGACCTTCGGCTGCAGCCGCGCTTCGAGACATT-GGGTGAGCACCAGTGGCG 45925
QY 167 ----- 167
Db 45926 GAGGGACCCAGACAGCACTGTCCAACCCCGGGGAAACAAACTGGCGACCTGTAGCAGCCC 45985
QY 168 -----AspGluLeuLeu 171
Db 45986 GCTGAGACCCCTAGCTCAGCCAGCGGCACATGCCCTCTGTCCCTGTTAAGATGAGCTCCTA 46045
QY 172 AlaAlaGlyGluAlaGlyThrPheAspValAlaValValAspAlaAspLysGluAsnCys 191
Db 46046 GCGCGGGCGAGGCGCGAACCCTTCGACATAGCGGTGGTGACGCGGACAAAGAGAACTGT 46105
QY 192 SerAlaTyrTyrGluArgCysLeuGlnLeuLeuArgProGlyGlyIleLeuAlaValLeu 211
Db 46106 ACCGCTACTACAGCGCTGTCTGCAGCTCCTACGTCCCGGAGCGGTGCTCGCTGTACTC 46165
QY 212 Arg----- 212
Db 46166 AGAGTAAGGACTAGCTAAGGCANAACTGTGTCTTGTGGTGGGTACCACCTCTTCTC 46225
QY 212 ----- 212
Db 46226 AGCTCTTCCACCCACCCAGCCCGGCGCCCAAGCCCAAGCCAGAGTATCATAGGTCC 46285
QY 212 ----- 212
Db 46286 CGCCCCCTCTGGCTAAAGCTCTGGGTGGCTACCCCCCACTTCCGACGGCCCCCGCCCTC 46345
QY 213 -----ValLeuTyrArgGlyLysValLeuGlnProProLysGlyAspValAlaAla 229
Db 46346 CATCTGTAGTCTCTGTGGCGGAGAGTGTCTGACGCTCAGCCCGAGGAACAAGACTGTT 46405
QY 230 GluCysValArgAsnLeuAsnGluArgIleArgArgAspValArgValTyrIleSerLeu 249
Db 46406 GAATGTGTGGGAACCTGAACGAACGCATCTCTGAGGGAGCCAGGGTCTACATCAGCCTC 46465
QY 250 LeuProLeuGlyAspGlyLeuThrLeuAlaPheLysIle 262
Db 46466 CTGCCCCCTGGATGATGGCTCTCTCTTGGCCTTTAAGATC 46504
```

Search completed: April 20, 2005, 02:24:17  
Job time : 4825 secs

**THIS PAGE BLANK (0870)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 19, 2005, 15:50:43 ; Search time 697 Seconds  
(without alignments)  
8608.289 Million cell updates/sec

Perfect score: 989  
Sequence: 1 gcggccgcgagtcgagga.....caaaaaaaaaaaaaaaaaa 989

Scoring table: IDENTITY\_NUC

Gapop 10.0 ; Gapext 1.0

Searched: 5622541 seqs, 303335566 residues

Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Published Applications NA.\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq.\*
- 17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq.\*
- 18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*
- 19: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 20: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 21: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 22: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
34	989	100.0	989	16	US-10-210-951-21
35	989	100.0	989	16	US-10-211-884-21
36	989	100.0	989	16	US-10-211-884-21
37	989	100.0	989	16	US-10-013-909A-305
38	989	100.0	989	17	US-10-211-858-21
39	989	100.0	989	17	US-10-211-858-21
40	989	100.0	989	17	US-10-307-817-121
41	989	100.0	989	17	US-10-307-817-125
42	989	100.0	989	17	US-10-307-817-125
43	989	100.0	989	17	US-10-307-817-125
44	989	100.0	989	17	US-10-307-817-125
45	989	100.0	989	17	US-10-307-817-125
46	989	100.0	989	17	US-10-307-817-125
47	989	100.0	989	17	US-10-307-817-125
48	989	100.0	989	17	US-10-307-817-125
49	989	100.0	989	17	US-10-307-817-125
50	989	100.0	989	17	US-10-307-817-125
51	989	100.0	989	17	US-10-307-817-125
52	989	100.0	989	17	US-10-307-817-125
53	989	100.0	989	17	US-10-307-817-125
54	989	100.0	989	17	US-10-307-817-125
55	989	100.0	989	17	US-10-307-817-125
56	989	100.0	989	17	US-10-307-817-125
57	989	100.0	989	17	US-10-307-817-125
58	989	100.0	989	17	US-10-307-817-125
59	989	100.0	989	17	US-10-307-817-125
60	989	100.0	989	17	US-10-307-817-125
61	989	100.0	989	17	US-10-307-817-125
62	989	100.0	989	17	US-10-307-817-125
63	989	100.0	989	17	US-10-307-817-125
64	989	100.0	989	17	US-10-307-817-125
65	989	100.0	989	17	US-10-307-817-125
66	989	100.0	989	17	US-10-307-817-125
67	989	100.0	989	17	US-10-307-817-125
68	989	100.0	989	17	US-10-307-817-125
69	989	100.0	989	17	US-10-307-817-125
70	989	100.0	989	17	US-10-307-817-125
71	989	100.0	989	17	US-10-307-817-125
72	989	100.0	989	17	US-10-307-817-125
73	989	100.0	989	17	US-10-307-817-125
74	989	100.0	989	17	US-10-307-817-125
75	989	100.0	989	17	US-10-307-817-125
76	989	100.0	989	17	US-10-307-817-125
77	989	100.0	989	17	US-10-307-817-125

Sequence 23102, A  
Sequence 632, App  
Sequence 1360, Ap  
Sequence 1452, Ap  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 2, Appli  
Sequence 49671, A  
Sequence 45, Appl  
Sequence 43, Appl  
Sequence 23149, A  
Sequence 13, Appl  
Sequence 108865,  
Sequence 41, Appl  
Sequence 35, Appl  
Sequence 1, Appli  
Sequence 53820, A  
Sequence 1, Appli  
Sequence 27082, A  
Sequence 53827, A  
Sequence 7777, Ap  
Sequence 77, Appl  
Sequence 138013,  
Sequence 25410, A  
Sequence 61896, A  
Sequence 28379, A  
Sequence 12827, A  
Sequence 138007,  
Sequence 33, Appl  
Sequence 12284, A  
Sequence 3691, Ap  
Sequence 16291, A  
Sequence 37, Appl  
Sequence 31, Appl  
Sequence 138010,  
Sequence 2642, Ap  
Sequence 138002,  
Sequence 3140, Ap  
Sequence 113175,  
Sequence 41715, A  
Sequence 5, Appli  
Sequence 26100, A  
Sequence 53821, A  
Sequence 14336, A  
Sequence 2377, Ap  
Sequence 2526, Ap  
Sequence 62449, A  
Sequence 11, Appl  
Sequence 113176,  
Sequence 140246,  
Sequence 138015,  
Sequence 24738, A  
Sequence 138003,  
Sequence 53825, A  
Sequence 23965, A  
Sequence 84, Appl  
Sequence 1, Appli  
Sequence 7, Appli  
Sequence 32, Appl  
Sequence 179664,  
Sequence 27818, A  
Sequence 146, App  
Sequence 36, Appl  
Sequence 37, Appl  
Sequence 113171,  
Sequence 53814, A  
Sequence 53809, A  
Sequence 275, App  
Sequence 298, App  
Sequence 5814, Ap  
Sequence 1, Appli  
Sequence 108605,  
Sequence 21, Appl  
Sequence 305, App  
Sequence 21, Appl  
Sequence 121, App  
Sequence 125, App  
Sequence 1, Appli  
Sequence 521, App  
Sequence 3, Appli  
Sequence 123, App  
Sequence 182, App  
Sequence 22407, A

151	96.8	9.8	1012	15	US-10-174-693-94	Sequence 94, Appl	224	59.6	6.0	399	15	US-10-174-693-194	Sequence 194, Appl
152	96.8	9.8	1026	15	US-10-174-693-6	Sequence 6, Appli	225	59.6	6.0	7185	16	US-10-329-079-48	Sequence 48, Appl
153	93	9.4	1257	18	US-10-425-115-66941	Sequence 66941, A	226	59.6	6.0	61944	16	US-10-329-079-34	Sequence 34, Appl
154	88	8.9	931	9	US-09-452-239-17	Sequence 17, Appl	227	59.2	6.0	4667	18	US-10-723-860-5759	Sequence 5759, Ap
155	88	8.9	1423	17	US-09-452-239-47	Sequence 47, Appl	228	59	6.0	3501	18	US-10-437-963-22161	Sequence 22161, A
156	87.8	8.9	534	9	US-09-452-239-47	Sequence 47, Appl	229	59	6.0	4667	18	US-10-723-860-5759	Sequence 5759, Ap
157	86.8	8.8	641	18	US-10-437-963-77651	Sequence 77651, A	230	59	6.0	10800	17	US-10-037-417-5	Sequence 5, Appli
158	86.8	8.8	995	18	US-10-767-795-3303	Sequence 3303, Ap	231	59	6.0	10809	17	US-10-037-417-1	Sequence 1, Appli
159	86.6	8.8	567	18	US-10-767-701-12825	Sequence 12825, A	232	58.8	5.9	688	17	US-10-425-114-4767	Sequence 4767, Ap
160	85.6	8.7	617	18	US-10-021-323-15391	Sequence 15391, A	233	58.8	5.9	743	17	US-10-425-114-18343	Sequence 18343, A
161	85.6	8.7	962	9	US-09-452-239-23	Sequence 23, Appl	234	58.8	5.9	1056	15	US-10-156-761-4663	Sequence 4663, Ap
162	85.6	8.7	1023	9	US-09-452-239-25	Sequence 25, Appl	235	58.8	5.9	1384	17	US-10-156-761-4663	Sequence 31776, A
163	85.6	8.7	1044	17	US-10-424-599-95805	Sequence 95805, A	236	58.8	5.9	1384	18	US-10-425-114-31776	Sequence 32933, A
164	85.6	8.7	1512	18	US-10-739-930-3516	Sequence 3516, Ap	237	58.8	5.9	2487	18	US-10-437-963-10147	Sequence 10147, A
165	84	8.5	1072	9	US-09-770-443-132	Sequence 132, App	238	58.8	5.9	5858	19	US-10-488-056-14	Sequence 14, Appl
166	79.6	8.0	1333	18	US-10-767-795-6335	Sequence 6335, Ap	239	58.6	5.9	1257	15	US-10-156-761-5999	Sequence 5999, Ap
167	79.2	8.0	980	9	US-09-452-239-21	Sequence 21, Appl	240	58.4	5.9	646	18	US-10-425-115-43431	Sequence 43431, A
168	79.2	8.0	1508	17	US-10-424-599-18320	Sequence 18320, A	241	58.4	5.9	1053	18	US-10-437-963-43823	Sequence 43823, A
169	78.8	8.0	658	17	US-10-425-114-23426	Sequence 23426, A	242	58.2	5.9	828	15	US-10-156-761-4574	Sequence 4574, Ap
170	78.8	8.0	889	17	US-10-425-114-1908	Sequence 1908, Ap	243	58	5.9	89421	9	US-09-976-059-1	Sequence 1, Appli
171	77	7.8	1058	17	US-10-424-599-100655	Sequence 100655, A	244	57.8	5.8	3606	15	US-10-156-761-2645	Sequence 2645, Ap
172	76.2	7.7	760	15	US-10-174-693-25	Sequence 25, Appl	245	57.6	5.8	897	18	US-10-767-701-14332	Sequence 14332, A
173	76	7.7	1159	18	US-10-425-115-53828	Sequence 53828, A	246	57.6	5.8	1323	15	US-10-156-761-4750	Sequence 4750, Ap
174	74.4	7.5	929	9	US-09-452-239-19	Sequence 19, Appl	247	57.6	5.8	1721	18	US-10-437-963-44166	Sequence 44166, A
175	73.8	7.5	1725	18	US-10-437-963-64453	Sequence 64453, A	248	57.4	5.8	1029	10	US-09-938-901-5	Sequence 5, Appli
176	72.8	7.4	546	18	US-10-021-323-10069	Sequence 10069, A	249	57.4	5.8	1875	15	US-10-156-761-3143	Sequence 3143, Ap
177	72.6	7.3	876	18	US-10-437-963-41905	Sequence 41905, A	250	57.4	5.8	2241	15	US-10-156-761-3171	Sequence 3171, Ap
178	70.6	7.1	1350	9	US-09-925-301-266	Sequence 266, App	251	57.2	5.8	554	17	US-10-425-114-17961	Sequence 17961, A
179	70.2	7.1	345	18	US-10-425-115-53808	Sequence 53808, A	252	57.2	5.8	755	18	US-10-767-701-609	Sequence 609, App
180	69.4	7.0	1206	17	US-10-240-425-1322	Sequence 1322, A	253	57	5.8	972	18	US-10-425-115-17653	Sequence 17653, A
181	69.4	7.0	1206	18	US-10-283-975A-192	Sequence 192, App	254	57	5.8	1113	19	US-10-762-107-25	Sequence 25, Appl
182	69.4	7.0	1311	13	US-10-087-192-1325	Sequence 1325, Ap	255	57	5.8	1671	15	US-10-156-761-2058	Sequence 2058, Ap
183	69.4	7.0	1327	13	US-10-044-090-642	Sequence 642, App	256	57	5.8	3774	15	US-10-156-761-2845	Sequence 2845, Ap
184	68.4	6.9	3072	18	US-10-437-963-79828	Sequence 79828, A	257	57	5.8	36602	19	US-10-762-107-1	Sequence 1, Appli
185	68	6.9	749	18	US-10-767-795-6336	Sequence 6336, Ap	258	56.8	5.7	879	17	US-10-425-114-30199	Sequence 30199, A
186	67.2	6.8	969	18	US-10-437-963-21877	Sequence 21877, A	259	56.8	5.7	907	17	US-10-425-114-30210	Sequence 30210, A
187	67	6.8	1149	17	US-10-258-951-13	Sequence 13, Appl	260	56.8	5.7	1182	17	US-10-458-201-19	Sequence 19, Appl
188	66.8	6.8	1074	15	US-10-174-693-54	Sequence 54, Appl	261	56.8	5.7	1471	18	US-10-437-963-67675	Sequence 67675, A
189	66.8	6.8	1075	15	US-10-174-693-55	Sequence 55, Appl	262	56.8	5.7	1486	17	US-10-425-114-3685	Sequence 3685, Ap
190	66.6	6.7	529	18	US-10-425-115-121105	Sequence 121105, A	263	56.8	5.7	1582	18	US-10-425-115-138009	Sequence 138009, A
191	66.4	6.7	744	17	US-10-239-463-1	Sequence 1, Appli	264	56.8	5.7	3306	15	US-10-156-761-6845	Sequence 6845, Ap
192	66.2	6.7	912	9	US-09-452-239-27	Sequence 27, Appl	265	56.8	5.7	11604	17	US-10-458-201-13	Sequence 13, Appl
193	66	6.7	997	17	US-10-424-599-71962	Sequence 71962, A	266	56.8	5.7	15120	17	US-10-458-201-1	Sequence 1, Appli
194	66	6.7	1389	15	US-10-156-761-5082	Sequence 5082, Ap	267	56.8	5.7	22976	17	US-10-650-507-19	Sequence 19, Appl
195	65.8	6.7	575	18	US-10-425-115-140243	Sequence 140243, A	268	56.8	5.7	36401	19	US-10-925-357-1	Sequence 116, App
196	65	6.6	578	18	US-10-767-701-26345	Sequence 26345, A	269	56.8	5.7	41936	19	US-09-967-768A-116	Sequence 6261, Ap
197	64.6	6.5	553	17	US-10-264-049-1169	Sequence 1169, Ap	270	56.8	5.7	1190	18	US-10-437-963-36882	Sequence 36882, A
198	64.2	6.5	584	18	US-10-425-115-53810	Sequence 53810, A	271	56.8	5.7	1377	18	US-10-411-910A-228	Sequence 228, App
199	64.2	6.5	600	9	US-09-452-239-39	Sequence 39, Appl	272	56.6	5.7	1014	18	US-10-437-963-58666	Sequence 58666, A
200	64	6.5	1065	18	US-10-437-963-18368	Sequence 18368, A	273	56.6	5.7	3014	15	US-10-259-165-329	Sequence 329, App
201	63.6	6.4	510	9	US-09-452-239-9	Sequence 9, Appli	274	56.6	5.7	3414	15	US-10-132-134-35	Sequence 35, Appl
202	63.4	6.4	897	15	US-10-156-761-3542	Sequence 3542, Ap	275	56.6	5.7	25085	16	US-10-132-134-35	Sequence 25, Appl
203	63.2	6.4	966	15	US-10-156-761-4002	Sequence 4002, Ap	276	56.6	5.7	50543	16	US-10-132-134-25	Sequence 25, Appl
204	63.2	6.4	9025608	15	US-10-156-761-1	Sequence 1, Appli	277	56.6	5.7	3225	18	US-10-437-963-82422	Sequence 82422, A
205	63	6.4	135005	18	US-10-723-860-2320	Sequence 2320, Ap	278	56.4	5.7	3957	16	US-10-200-562-193	Sequence 193, App
206	62.8	6.3	75216	15	US-10-080-170-646	Sequence 646, App	279	56.4	5.7	3957	16	US-10-237-551-193	Sequence 193, App
207	62.8	6.3	75216	18	US-10-080-170-646	Sequence 646, App	280	56.4	5.7	15738	16	US-10-329-079-46	Sequence 46, Appl
208	62.8	6.3	75216	18	US-10-468-356-646	Sequence 646, App	281	56.4	5.7	154746	10	US-09-827-688-8	Sequence 8, Appli
209	61.8	6.2	1128	15	US-10-156-761-2740	Sequence 2740, Ap	282	56.4	5.7	154746	10	US-09-827-688-8	Sequence 8, Appli
210	61.6	6.2	1079	17	US-10-424-599-98070	Sequence 98070, A	283	56.4	5.7	426	15	US-10-156-761-4164	Sequence 4164, Ap
211	61.6	6.2	2368	17	US-10-425-114-2674	Sequence 2674, A	284	56.2	5.7	426	15	US-10-156-761-4164	Sequence 4164, Ap
212	61.6	6.2	3362	18	US-10-425-115-173652	Sequence 173652, A	285	56.2	5.7	1143	17	US-10-107-431-222	Sequence 22, Appl
213	61.4	6.2	775	18	US-10-425-115-65597	Sequence 65597, A	286	56.2	5.7	1186	10	US-09-769-734-22	Sequence 22, Appl
214	61	6.2	2117	18	US-10-437-963-97603	Sequence 97603, A	287	56.2	5.7	48221	17	US-10-107-431-280	Sequence 280, App
215	60.6	6.1	2808	15	US-10-156-761-2021	Sequence 2021, Ap	288	56	5.7	411	15	US-10-156-761-5439	Sequence 5439, Ap
216	60.4	6.1	1544	18	US-10-437-963-72461	Sequence 72461, A	289	56	5.7	494	10	US-09-918-995-32147	Sequence 32147, A
217	60.4	6.1	2256646	18	US-10-470-565-1	Sequence 1, Appli	290	56	5.7	974	17	US-10-425-114-31148	Sequence 31148, A
218	60	6.1	729	9	US-09-938-842A-2400	Sequence 2400, Ap	291	56	5.7	1189	18	US-10-437-963-45522	Sequence 45522, A
219	60	6.1	729	11	US-09-938-842A-2400	Sequence 2400, Ap	292	56	5.7	1403	18	US-10-437-963-19360	Sequence 19360, A
220	60	6.1	966	18	US-10-739-930-382	Sequence 382, App	293	56	5.7	1473	17	US-10-282-122A-30078	Sequence 30078, A
221	60	6.1	982	9	US-09-452-239-31	Sequence 31, Appl	294	56	5.7	1658	18	US-10-646-664-6	Sequence 6, Appli
222	60	6.1	1143	17	US-10-282-122A-25877	Sequence 25877, A	295	56	5.7	2109	9	US-09-738-973-153	Sequence 153, App
223	59.8	6.0	1041	18	US-10-437-963-8597	Sequence 8597, Ap	296	56	5.7	2109	9	US-09-854-133-153	Sequence 153, App

297	56	5.7	2109	15	US-10-144-649A-153	Sequence 153, App	370	54.4	5.5	1873	18	US-10-425-115-90238	Sequence 90238, A
298	56	5.7	4257	9	US-09-825-288A-1	Sequence 1, Appl	371	54.4	5.5	2119	18	US-10-425-115-134714	Sequence 134714, A
299	56	5.7	4988	17	US-10-288-798-48	Sequence 48, Appl	372	54.4	5.5	2813	18	US-10-437-963-55796	Sequence 55796, A
300	56	5.7	4988	17	US-10-363-892-48	Sequence 48, Appl	373	54.2	5.5	742	18	US-10-425-115-181799	Sequence 181799, A
301	56	5.7	13862	10	US-09-764-891-5477	Sequence 5477, Ap	374	54.2	5.5	1617	17	US-10-425-114-32311	Sequence 32311, A
302	56	5.7	13862	10	US-09-764-891-10204	Sequence 10204, A	375	54.2	5.5	1969	18	US-10-437-963-71923	Sequence 71923, A
303	56	5.7	13862	10	US-10-203-428-1003	Sequence 1003, Ap	376	54.2	5.5	3351	18	US-10-425-115-151164	Sequence 151164, A
304	56	5.7	15559	18	US-10-646-664-1	Sequence 1, Appl	377	54.2	5.5	11058	15	US-10-156-761-3629	Sequence 3629, Ap
305	56	5.7	43058	9	US-09-954-456-292	Sequence 292, App	378	54.2	5.5	65140	18	US-10-203-295-1	Sequence 1, Appl
306	56	5.7	43058	9	US-09-954-456-292	Sequence 292, App	379	54.2	5.5	125401	18	US-10-203-295-35	Sequence 35, Appl
307	56	5.7	43058	9	US-09-880-107-3950	Sequence 3950, Ap	380	54	5.5	897	17	US-10-282-122A-11524	Sequence 11524, A
308	56	5.7	43058	19	US-10-843-641A-3319	Sequence 3319, Ap	381	54	5.5	1118	17	US-10-180-375-101	Sequence 101, App
309	56	5.7	43058	19	US-10-843-641A-3556	Sequence 3556, Ap	382	54	5.5	1118	17	US-10-183-687-117	Sequence 117, App
310	55.8	5.6	1152	15	US-10-259-165-201	Sequence 201, App	383	54	5.5	1391	18	US-10-437-963-86834	Sequence 86834, A
311	55.8	5.6	1209	18	US-10-437-963-84053	Sequence 84053, A	384	54	5.5	1527	15	US-10-156-761-6634	Sequence 6634, Ap
312	55.8	5.6	1275	15	US-10-156-761-5827	Sequence 5827, Ap	385	54	5.5	2670	18	US-10-437-963-82460	Sequence 82460, A
313	55.8	5.6	1662	18	US-10-437-963-7695	Sequence 7695, Ap	386	54	5.5	2997	15	US-10-156-761-7034	Sequence 7034, Ap
314	55.8	5.6	1926	15	US-10-294-804-3	Sequence 3, Appl	387	54	5.5	4530	17	US-10-302-172-881	Sequence 881, App
315	55.8	5.6	1926	15	US-10-194-046-3	Sequence 3, Appl	388	53.8	5.4	451	14	US-10-062-727-457	Sequence 457, App
316	55.8	5.6	8705	15	US-10-291-230-14	Sequence 14, Appl	389	53.8	5.4	658	18	US-10-767-701-4204	Sequence 4204, Ap
317	55.8	5.6	8705	15	US-10-291-249-14	Sequence 14, Appl	390	53.8	5.4	1320	15	US-10-156-761-5076	Sequence 5076, Ap
318	55.8	5.6	8705	17	US-10-273-678-16	Sequence 16, Appl	391	53.8	5.4	2082	18	US-10-746-167-67	Sequence 67, Appl
319	55.8	5.6	9482	19	US-10-888-961-4	Sequence 4, Appl	392	53.8	5.4	3150	15	US-10-156-761-1266	Sequence 1266, Ap
320	55.8	5.6	9600	16	US-10-278-751-1	Sequence 1, Appl	393	53.8	5.4	64492	17	US-10-378-083-1	Sequence 1, Appl
321	55.8	5.6	10233	16	US-10-050-898-283	Sequence 283, App	394	53.8	5.4	114793	15	US-10-148-806-3	Sequence 3, Appl
322	55.8	5.6	10285	16	US-10-050-903-283	Sequence 283, App	395	53.6	5.4	822	15	US-10-156-761-4587	Sequence 4587, Ap
323	55.8	5.6	10330	18	US-10-656-269-24	Sequence 24, Appl	396	53.6	5.4	885	18	US-10-437-963-60765	Sequence 60765, A
324	55.8	5.6	10477	18	US-10-656-269-22	Sequence 22, Appl	397	53.6	5.4	935	17	US-10-425-114-23310	Sequence 23310, A
325	55.8	5.6	10516	18	US-10-656-269-20	Sequence 20, Appl	398	53.6	5.4	958	18	US-10-425-115-42563	Sequence 42563, A
326	55.8	5.6	10561	18	US-10-656-269-18	Sequence 18, Appl	399	53.6	5.4	1164	15	US-10-156-761-6517	Sequence 6517, Ap
327	55.8	5.6	10615	18	US-10-656-269-45	Sequence 45, Appl	400	53.6	5.4	1664	15	US-10-437-963-66411	Sequence 66411, A
328	55.8	5.6	10774	18	US-10-656-269-23	Sequence 23, Appl	401	53.6	5.4	2673	15	US-10-156-761-2660	Sequence 2660, Ap
329	55.8	5.6	10921	18	US-10-656-269-21	Sequence 21, Appl	402	53.6	5.4	28499	19	US-10-741-600-17869	Sequence 17869, A
330	55.8	5.6	10961	18	US-10-656-269-19	Sequence 19, Appl	403	53.6	5.4	38734	10	US-09-373-658-30	Sequence 30, Appl
331	55.8	5.6	11006	18	US-10-656-269-17	Sequence 17, Appl	404	53.6	5.4	38734	11	US-09-989-687-30	Sequence 30, Appl
332	55.8	5.6	11059	18	US-10-656-269-16	Sequence 16, Appl	405	53.4	5.4	707	18	US-10-437-963-91406	Sequence 91406, A
333	55.8	5.6	11924	18	US-10-678-816-7	Sequence 6, Appl	406	53.4	5.4	837	18	US-10-425-115-97779	Sequence 97779, A
334	55.8	5.6	12242	18	US-10-678-816-6	Sequence 6, Appl	407	53.4	5.4	2402	13	US-10-425-115-164051	Sequence 164051, A
335	55.6	5.6	1281	15	US-10-156-761-2031	Sequence 4135, Ap	408	53.4	5.4	4176	13	US-10-098-841-34	Sequence 34, Appl
336	55.4	5.6	659	15	US-10-767-701-4135	Sequence 1727, Ap	409	53.4	5.4	8515	18	US-10-647-196-1	Sequence 1, Appl
337	55.4	5.6	1035	15	US-10-156-761-1727	Sequence 1, Appl	410	53.2	5.4	900	17	US-10-282-122A-14712	Sequence 14712, A
338	55.4	5.6	84428	17	US-10-229-1488-1	Sequence 1, Appl	411	53.2	5.4	972	17	US-10-424-599-133785	Sequence 133785, A
339	55.2	5.6	1161	17	US-10-425-114-30211	Sequence 30211, A	412	53.2	5.4	1400	18	US-10-437-963-19875	Sequence 19875, A
340	55.2	5.6	1182	15	US-10-156-761-1340	Sequence 1240, Ap	413	53.2	5.4	1431	18	US-10-437-963-73728	Sequence 73728, A
341	55.2	5.6	1203	17	US-10-425-114-13422	Sequence 13422, A	414	53.2	5.4	135638	16	US-10-314-657-1	Sequence 1, Appl
342	55.2	5.6	1344	17	US-10-425-114-30216	Sequence 30216, A	415	53	5.4	632	13	US-10-194-163-655	Sequence 655, App
343	55.2	5.6	1473	18	US-10-437-963-85114	Sequence 85114, A	416	53	5.4	797	17	US-10-424-599-78653	Sequence 78653, A
344	55.2	5.6	1685	17	US-10-183-687-149	Sequence 149, App	417	53	5.4	1068	15	US-10-156-761-5900	Sequence 5900, Ap
345	55.2	5.6	1887	17	US-10-282-122A-26004	Sequence 26004, A	418	53	5.4	1320	15	US-10-156-761-6285	Sequence 6285, Ap
346	55.2	5.6	21185	18	US-10-159-257A-2	Sequence 2, Appl	419	53	5.4	1695	17	US-10-369-493-40710	Sequence 40710, A
347	55.2	5.6	63158	16	US-10-293-198-1	Sequence 1, Appl	420	53	5.4	1444	17	US-10-425-115-149834	Sequence 149834, A
348	55	5.6	1875	18	US-10-437-963-33401	Sequence 33401, A	421	53	5.4	3444	17	US-10-369-493-40475	Sequence 40475, A
349	55	5.6	2259	18	US-10-723-860-2336	Sequence 2336, Ap	422	52.8	5.3	717	18	US-10-425-115-138006	Sequence 138006, A
350	55	5.6	53799	19	US-10-042-665A-3	Sequence 3, Appl	423	52.8	5.3	956	17	US-10-425-114-24149	Sequence 24149, A
351	54.8	5.5	594	15	US-10-174-693-105	Sequence 105, App	424	52.8	5.3	984	18	US-10-437-963-77477	Sequence 77477, A
352	54.8	5.5	607	15	US-10-174-693-23	Sequence 23, Appl	425	52.8	5.3	1027	18	US-10-739-930-4902	Sequence 4902, Ap
353	54.8	5.5	820	18	US-10-767-701-9492	Sequence 9492, Ap	426	52.8	5.3	1827	18	US-10-767-701-26823	Sequence 26823, A
354	54.8	5.5	1083	15	US-10-156-761-4116	Sequence 4116, Ap	427	52.8	5.3	2712	17	US-10-282-122A-26256	Sequence 26256, A
355	54.8	5.5	1188	18	US-10-437-963-65538	Sequence 65538, A	428	52.8	5.3	2715	17	US-10-282-122A-28396	Sequence 28396, A
356	54.8	5.5	1683	15	US-10-156-761-5824	Sequence 5824, Ap	429	52.6	5.3	3858	15	US-10-156-761-6773	Sequence 6773, Ap
357	54.6	5.5	1017	17	US-10-425-114-23250	Sequence 23250, A	430	52.6	5.3	447	17	US-10-260-238-74	Sequence 74, Appl
358	54.6	5.5	1221	17	US-10-369-493-41730	Sequence 41730, A	431	52.6	5.3	513	18	US-10-437-963-77477	Sequence 77477, A
359	54.6	5.5	1308	14	US-10-146-474-18	Sequence 18, Appl	432	52.6	5.3	584	18	US-10-767-701-7590	Sequence 7590, Ap
360	54.6	5.5	1308	17	US-10-301-764-18	Sequence 301, Ap	433	52.6	5.3	707	18	US-10-156-761-7048	Sequence 7048, Ap
361	54.6	5.5	1502	18	US-10-437-963-3321	Sequence 3321, Ap	434	52.6	5.3	1155	15	US-10-190-435-55	Sequence 55, Appl
362	54.6	5.5	1711	18	US-10-739-930-2421	Sequence 2421, Ap	435	52.6	5.3	1275	15	US-10-190-305A-79	Sequence 79, Appl
363	54.6	5.5	1950	18	US-10-437-963-11714	Sequence 11714, A	436	52.6	5.3	1368	17	US-10-282-122A-25876	Sequence 25876, A
364	54.6	5.5	2060	18	US-10-437-963-55219	Sequence 55219, A	437	52.6	5.3	1608	17	US-10-425-114-19193	Sequence 19193, A
365	54.6	5.5	158405	14	US-10-175-523-86	Sequence 86, Appl	438	52.6	5.3	2141	9	US-10-437-963-82757	Sequence 82757, A
366	54.4	5.5	752	18	US-10-437-963-37276	Sequence 37276, A	439	52.6	5.3	2561	13	US-09-976-740-48	Sequence 48, Appl
367	54.4	5.5	789	17	US-10-369-493-43079	Sequence 43079, A	440	52.6	5.3	2561	13	US-10-023-539-48	Sequence 48, Appl
368	54.4	5.5	1243	17	US-10-425-114-34784	Sequence 34784, A	441	52.6	5.3	2561	17	US-10-023-539-48	Sequence 48, Appl
369	54.4	5.5	1307	18	US-10-425-115-51013	Sequence 51013, A	442	52.6	5.3	2561	17	US-10-616-187-48	Sequence 48, Appl

c 443	52.6	5.3	2561	17	US-10-671-242-48	Sequence 48, Appl	516	51.8	5.2	2075	16	US-10-425-586-1	Sequence 1, Appli
444	52.6	5.3	3624	15	US-10-190-435-47	Sequence 47, Appl	517	51.8	5.2	2075	17	US-10-466-136-1	Sequence 1, Appli
445	52.6	5.3	3624	16	US-10-190-305A-41	Sequence 41, Appl	518	51.8	5.2	2145	17	US-10-282-122A-31855	Sequence 31855, A
446	52.4	5.3	867	15	US-10-156-761-2201	Sequence 2201, Ap	519	51.8	5.2	2322	18	US-10-739-930-2737	Sequence 2737, Ap
447	52.4	5.3	366	15	US-10-437-963-74149	Sequence 74149, A	520	51.8	5.2	2847	15	US-10-156-761-2404	Sequence 2404, Ap
c 448	52.4	5.3	1071	15	US-10-156-761-7131	Sequence 7131, Ap	521	51.8	5.2	4462	9	US-09-974-298-28	Sequence 28, Appli
449	52.4	5.3	1142	18	US-10-425-115-165350	Sequence 165350,	522	51.8	5.2	4469	9	US-09-796-008-1	Sequence 1, Appli
450	52.4	5.3	1388	18	US-10-427-701-14298	Sequence 14298, A	523	51.8	5.2	4469	9	US-10-133-937-42	Sequence 42, Appl
451	52.4	5.3	1518	15	US-10-156-761-2280	Sequence 2280, Ap	524	51.8	5.2	4469	17	US-10-172-118-857	Sequence 857, App
452	52.4	5.3	1339	18	US-10-425-115-129809	Sequence 129809,	525	51.8	5.2	4469	17	US-10-159-563-42	Sequence 42, Appl
453	52.4	5.3	1891	9	US-09-969-708-146	Sequence 146, App	526	51.8	5.2	4469	17	US-10-342-887-857	Sequence 857, App
454	52.4	5.3	1891	15	US-10-007-926A-234	Sequence 234, App	527	51.8	5.2	4469	18	US-10-786-720-15	Sequence 15, Appl
455	52.4	5.3	1891	18	US-10-684-422-210	Sequence 210, App	528	51.8	5.2	4469	18	US-10-788-732-21	Sequence 21, Appl
456	52.4	5.3	1891	19	US-10-843-641A-7617	Sequence 7617, Ap	529	51.8	5.2	4469	18	US-10-473-974-203	Sequence 203, App
457	52.4	5.3	3114	18	US-10-437-963-28971	Sequence 28971, A	530	51.8	5.2	4469	18	US-10-817-525-1	Sequence 1, Appli
458	52.4	5.3	5117	17	US-10-172-118-24	Sequence 24, Appl	c 531	51.6	5.2	786	15	US-10-156-761-4529	Sequence 4529, Ap
459	52.4	5.3	5117	17	US-10-343-887-24	Sequence 24, Appl	532	51.6	5.2	893	15	US-10-180-375-107	Sequence 107, App
460	52.4	5.3	5204	17	US-10-037-417-7	Sequence 7, Appli	533	51.6	5.2	893	17	US-10-183-687-123	Sequence 123, App
c 461	52.4	5.3	5403	17	US-10-112-944-583	Sequence 583, App	534	51.6	5.2	1177	18	US-10-437-963-12093	Sequence 12093, A
462	52.4	5.3	5640	15	US-10-037-270-41	Sequence 41, Appl	535	51.6	5.2	1242	17	US-10-282-122A-25883	Sequence 25883, A
463	52.4	5.3	5640	17	US-10-117-722-41	Sequence 41, Appl	536	51.6	5.2	2055	17	US-10-369-493-35729	Sequence 35729, A
464	52.4	5.3	8296	14	US-10-037-182-35	Sequence 35, Appl	537	51.6	5.2	2211	18	US-10-437-963-63253	Sequence 63253, A
465	52.4	5.3	11091	17	US-10-312-088-9	Sequence 9, Appli	538	51.6	5.2	2241	15	US-10-156-761-4107	Sequence 4107, Ap
466	52.4	5.3	11118	17	US-10-312-088-8	Sequence 8, Appli	539	51.6	5.2	2853	17	US-10-282-122A-13968	Sequence 13968, A
467	52.4	5.3	11238	15	US-10-205-032-15	Sequence 15, Appl	c 540	51.6	5.2	2865	18	US-10-109-048-1143	Sequence 1143, Ap
468	52.4	5.3	11350	14	US-10-037-182-1	Sequence 1, Appli	541	51.6	5.2	2973	15	US-10-156-761-2660	Sequence 2660, Ap
469	52.4	5.3	11367	17	US-10-312-352-58	Sequence 58, Appl	542	51.6	5.2	9369	16	US-10-200-562-190	Sequence 190, App
470	52.4	5.3	11640	17	US-10-112-944-103	Sequence 103, App	543	51.6	5.2	9369	16	US-10-237-551-190	Sequence 190, App
471	52.4	5.3	1420	15	US-10-156-761-2885	Sequence 2885, Ap	544	51.6	5.2	9369	16	US-10-237-551-190	Sequence 190, App
472	52.4	5.3	60196	15	US-10-205-032-1	Sequence 1, Appli	545	51.6	5.2	77294	19	US-10-729-802-1	Sequence 247, App
473	52.4	5.3	125746	15	US-10-156-761-15102	Sequence 15102, A	546	51.6	5.2	218802	19	US-10-897-508-1	Sequence 1, Appli
474	52.2	5.3	897	18	US-10-437-963-54305	Sequence 54305, A	547	51.4	5.2	673	18	US-10-425-115-165006	Sequence 165006,
475	52.2	5.3	1126	18	US-10-767-701-13291	Sequence 13291, A	548	51.4	5.2	1130	18	US-10-437-963-79440	Sequence 79440, A
476	52.2	5.3	1193	17	US-10-425-114-24011	Sequence 24011, A	549	51.4	5.2	1230	15	US-10-156-761-5404	Sequence 5404, Ap
477	52.2	5.3	1308	18	US-10-425-115-49576	Sequence 49576, A	550	51.4	5.2	1359	15	US-10-156-761-6586	Sequence 6586, Ap
c 478	52.2	5.3	1671	18	US-10-437-963-65581	Sequence 65581, A	551	51.4	5.2	1359	15	US-10-156-761-6587	Sequence 6587, Ap
479	52.2	5.3	1687	18	US-10-425-115-71979	Sequence 71979, A	552	51.4	5.2	1510	18	US-10-437-963-60807	Sequence 60807, A
480	52.2	5.3	1746	15	US-10-156-761-4388	Sequence 4388, Ap	553	51.4	5.2	1629	15	US-10-156-761-3330	Sequence 3330, Ap
481	52.2	5.3	2505	17	US-10-369-493-31754	Sequence 31754, A	554	51.4	5.2	2021	18	US-10-437-963-99040	Sequence 99040, A
482	52.2	5.3	2757	17	US-10-282-122A-26027	Sequence 26027, A	c 555	51.4	5.2	2031	18	US-10-437-963-81510	Sequence 81510, A
483	52.2	5.3	6297	16	US-10-132-134-37	Sequence 37, Appl	556	51.4	5.2	2307	17	US-10-282-122A-11169	Sequence 11169, A
484	52	5.3	1062	18	US-10-767-701-9233	Sequence 9233, Ap	557	51.4	5.2	2526	18	US-10-723-860-818	Sequence 818, App
485	52	5.3	1065	15	US-10-156-761-6270	Sequence 6270, Ap	558	51.4	5.2	2652	18	US-10-723-860-818	Sequence 818, App
486	52	5.3	1159	18	US-10-437-963-54428	Sequence 54428, A	559	51.4	5.2	4725	15	US-10-205-032-17	Sequence 17, Appl
487	52	5.3	1218	16	US-10-214-446-37	Sequence 37, Appl	560	51.4	5.2	6891	17	US-10-437-963-54940	Sequence 54940, A
488	52	5.3	1230	15	US-10-156-761-6139	Sequence 6139, Ap	561	51.4	5.2	7847	17	US-10-302-172-591	Sequence 591, App
489	52	5.3	1449	18	US-10-425-115-161558	Sequence 161558,	562	51.4	5.2	11817	15	US-10-156-761-2884	Sequence 2884, Ap
490	52	5.3	1459	10	US-10-437-963-26984	Sequence 26984, A	563	51.4	5.2	30000	11	US-09-980-217-2	Sequence 2, Appli
491	52	5.3	1491	10	US-09-899-575-99	Sequence 99, Appl	564	51.2	5.2	447	11	US-09-732-627A-4334	Sequence 4334, Ap
492	52	5.3	1556	17	US-10-425-114-19808	Sequence 19808, A	565	51.2	5.2	507	18	US-10-437-963-12967	Sequence 12967, A
493	52	5.3	1586	17	US-10-425-114-14339	Sequence 14339, A	566	51.2	5.2	522	15	US-10-156-761-3105	Sequence 3105, Ap
c 494	52	5.3	1707	15	US-10-156-761-4723	Sequence 4723, Ap	567	51.2	5.2	699	9	US-09-938-842A-1739	Sequence 1739, Ap
495	52	5.3	2763	15	US-10-156-761-1751	Sequence 1751, Ap	568	51.2	5.2	792	9	US-09-770-445-841	Sequence 841, App
496	52	5.3	3597	15	US-10-156-761-2534	Sequence 2534, Ap	c 569	51.2	5.2	699	11	US-09-938-842A-1739	Sequence 1739, Ap
497	51.8	5.2	672	15	US-10-156-761-1819	Sequence 1819, Ap	570	51.2	5.2	898	18	US-10-437-963-12968	Sequence 12968, A
498	51.8	5.2	918	15	US-10-156-761-6700	Sequence 6700, Ap	571	51.2	5.2	1002	15	US-10-156-761-2043	Sequence 2043, Ap
499	51.8	5.2	1227	17	US-10-282-122A-15076	Sequence 15076, A	572	51.2	5.2	1107	17	US-10-282-122A-14710	Sequence 14710, A
500	51.8	5.2	1253	13	US-10-087-192-1322	Sequence 1322, Ap	573	51.2	5.2	1134	15	US-10-156-761-3946	Sequence 3946, Ap
501	51.8	5.2	1344	15	US-10-156-761-1108	Sequence 1108, Ap	574	51.2	5.2	1188	15	US-10-156-761-421	Sequence 421, App
502	51.8	5.2	1347	17	US-10-369-493-43202	Sequence 43202, A	575	51.2	5.2	1267	18	US-10-425-115-15750	Sequence 15750, A
503	51.8	5.2	1593	15	US-10-156-761-5226	Sequence 5226, Ap	576	51.2	5.2	1290	18	US-10-739-930-2596	Sequence 2596, Ap
504	51.8	5.2	1645	17	US-10-425-114-32254	Sequence 32254, A	577	51.2	5.2	1493	18	US-10-739-930-2577	Sequence 2577, Ap
505	51.8	5.2	1645	17	US-10-425-114-30266	Sequence 30266, A	578	51.2	5.2	1536	15	US-10-156-761-7115	Sequence 7115, Ap
506	51.8	5.2	1659	17	US-10-369-493-39901	Sequence 39901, A	579	51.2	5.2	1557	18	US-10-437-963-89570	Sequence 89570, A
507	51.8	5.2	1677	17	US-10-369-493-39150	Sequence 39150, A	580	51.2	5.2	1637	18	US-10-437-963-73981	Sequence 73981, A
508	51.8	5.2	1777	15	US-10-369-493-39519	Sequence 39519, A	581	51.2	5.2	1683	15	US-10-205-032-3	Sequence 3, Appli
509	51.8	5.2	1704	18	US-10-739-930-2739	Sequence 2739, Ap	c 582	51.2	5.2	1841	18	US-10-437-963-89571	Sequence 89571, A
510	51.8	5.2	1779	15	US-10-156-761-1559	Sequence 1559, Ap	583	51.2	5.2	1959	18	US-10-739-930-3025	Sequence 3025, Ap
c 511	51.8	5.2	1796	18	US-10-437-963-43317	Sequence 43317, A	584	51.2	5.2	2034	9	US-09-815-242-8002	Sequence 8002, Ap
512	51.8	5.2	1803	18	US-10-425-115-133999	Sequence 133999,	585	51.2	5.2	2067	15	US-10-156-761-6391	Sequence 6391, Ap
513	51.8	5.2	1880	18	US-10-437-963-23751	Sequence 23751, A	586	51.2	5.2	10000	15	US-10-156-761-15103	Sequence 15103, A
514	51.8	5.2	1894	18	US-10-437-963-89370	Sequence 89370, A	587	51	5.2	687	15	US-10-156-761-2253	Sequence 2253, Ap
515	51.8	5.2	2075	16	US-10-138-434A-2	Sequence 2, Appli	588	51	5.2	694	18	US-10-425-115-101015	Sequence 101015,

589	51	5.2	894	18	US-10-739-930-2948	Sequence 2948, Ap	662	50.4	5.1	45055	17	US-10-107-431-277	Sequence 277, App
590	51	5.2	1008	18	US-10-437-963-12986	Sequence 16086, A	663	50.2	5.1	595	17	US-10-260-238-3262	Sequence 3262, Ap
591	51	5.2	1160	17	US-10-425-114-29979	Sequence 2979, Ap	664	50.2	5.1	740	18	US-10-437-963-67956	Sequence 67956, A
592	51	5.2	1203	18	US-10-425-115-1045	Sequence 1045, Ap	665	50.2	5.1	841	17	US-10-282-122A-14618	Sequence 14618, A
593	51	5.2	1218	15	US-10-156-761-6041	Sequence 6041, Ap	666	50.2	5.1	1002	15	US-10-156-761-696	Sequence 696, App
594	51	5.2	1497	17	US-10-282-122A-25509	Sequence 25509, A	667	50.2	5.1	1093	18	US-10-425-115-106454	Sequence 106454,
595	51	5.2	1503	17	US-10-260-238-1244	Sequence 1244, Ap	668	50.2	5.1	1266	18	US-10-437-963-1435	Sequence 1435, Ap
596	51	5.2	1632	16	US-10-132-350-39	Sequence 39, Appl	c 669	50.2	5.1	1426	18	US-10-437-963-59660	Sequence 59660, A
597	51	5.2	1755	17	US-10-369-493-32171	Sequence 32171, A	670	50.2	5.1	1856	15	US-10-156-761-5658	Sequence 5658, Ap
598	51	5.2	1803	16	US-10-132-350-37	Sequence 37, Appl	671	50.2	5.1	1896	15	US-10-437-963-61943	Sequence 61943, A
599	51	5.2	1878	18	US-10-437-963-42117	Sequence 42117, A	672	50.2	5.1	2056	18	US-10-437-963-16502	Sequence 16502, A
600	51	5.2	2220	15	US-10-156-761-5063	Sequence 5063, Ap	673	50.2	5.1	3032	17	US-10-437-963-16502	Sequence 16502, A
601	51	5.2	2266	18	US-10-425-115-130993	Sequence 130993, A	674	50.2	5.1	3039	17	US-10-369-493-42391	Sequence 42391, A
602	51	5.2	2370	15	US-10-156-761-4813	Sequence 4813, Ap	675	50.2	5.1	4826	9	US-09-772-304A-1	Sequence 1, Appl1
603	51	5.2	2561	9	US-09-976-740-48	Sequence 48, Appl	c 676	50.2	5.1	4826	18	US-10-717-381-1	Sequence 1, Appl1
604	51	5.2	2561	13	US-10-023-529-48	Sequence 48, Appl	c 677	50	5.1	390	9	US-09-960-352-14023	Sequence 14023, A
605	51	5.2	2561	13	US-10-023-523-48	Sequence 48, Appl	678	50	5.1	1020	17	US-10-437-963-98512	Sequence 98512, A
606	51	5.2	2561	17	US-10-616-187-48	Sequence 48, Appl	679	50	5.1	1057	17	US-10-425-114-24158	Sequence 24158, A
607	51	5.2	2561	17	US-10-671-242-48	Sequence 48, Appl	680	50	5.1	1213	18	US-10-425-115-122558	Sequence 122558,
608	51	5.2	2601	18	US-10-437-963-72883	Sequence 72883, A	681	50	5.1	1272	18	US-10-437-963-37456	Sequence 37456, A
609	51	5.2	2710	17	US-10-250-613-33	Sequence 33, Appl	682	50	5.1	1317	17	US-10-369-493-31645	Sequence 31645, A
610	51	5.2	2745	18	US-10-437-963-2941	Sequence 2941, Ap	683	50	5.1	1337	17	US-10-369-493-42992	Sequence 42992, A
611	51	5.2	3606	15	US-10-156-761-3063	Sequence 3063, Ap	c 684	50	5.1	1365	17	US-10-282-122A-13750	Sequence 13750, A
612	50.8	5.1	819	15	US-10-156-761-4765	Sequence 4765, Ap	685	50	5.1	1582	18	US-10-739-930-2333	Sequence 2333, Ap
613	50.8	5.1	1125	17	US-10-282-122A-31378	Sequence 31378, A	686	50	5.1	1806	16	US-10-328-079-38	Sequence 38, Appl
614	50.8	5.1	1155	15	US-10-193-002-12	Sequence 12, Appl	687	50	5.1	1806	17	US-10-328-027-29	Sequence 29, Appl
615	50.8	5.1	1155	15	US-10-084-843-12	Sequence 12, Appl	688	50	5.1	2148	17	US-10-156-761-6889	Sequence 6889, Ap
616	50.8	5.1	1173	17	US-10-260-238-706	Sequence 706, App	689	50	5.1	3012	18	US-10-369-493-42943	Sequence 42943, A
617	50.8	5.1	1188	15	US-10-156-761-421	Sequence 421, App	690	50	5.1	3135	15	US-10-437-963-78726	Sequence 78726, A
618	50.8	5.1	1230	18	US-10-437-963-96421	Sequence 96421, A	691	50	5.1	3374	18	US-10-156-761-2721	Sequence 2721, Ap
619	50.8	5.1	1317	9	US-09-815-242-4148	Sequence 4148, Ap	c 692	50	5.1	5061	18	US-10-437-963-10004	Sequence 10004, A
620	50.8	5.1	1317	9	US-10-282-122A-7337	Sequence 7337, Ap	c 693	50	5.1	10692	15	US-10-437-963-9832	Sequence 9832, Ap
621	50.8	5.1	1551	15	US-10-156-761-1622	Sequence 1622, Ap	694	50	5.1	13842	9	US-09-861-289-30	Sequence 30, Appl
622	50.8	5.1	1622	18	US-10-479-638-10	Sequence 10, Appl	695	50	5.1	13842	10	US-09-860-846-30	Sequence 30, Appl
623	50.8	5.1	2230	18	US-10-437-963-65821	Sequence 65821, A	696	50	5.1	13842	10	US-09-836-821-30	Sequence 30, Appl
624	50.8	5.1	5760	14	US-10-152-886-14	Sequence 14, Appl	697	50	5.1	13842	16	US-10-271-889-30	Sequence 30, Appl
c 625	50.8	5.1	100000	15	US-10-156-761-15103	Sequence 15103, A	699	50	5.1	15738	16	US-10-329-079-12	Sequence 12, Appl
626	50.6	5.1	908	9	US-09-452-239-15	Sequence 15, Appl	700	50	5.1	32329	17	US-10-374-903A-1	Sequence 1, Appl1
627	50.6	5.1	940	18	US-10-425-115-176490	Sequence 176490, A	701	50	5.1	36778	9	US-09-861-289-5	Sequence 5, Appl1
628	50.6	5.1	1031	15	US-10-437-963-36005	Sequence 36005, A	702	50	5.1	36778	9	US-09-860-846-5	Sequence 5, Appl1
629	50.6	5.1	1042	18	US-10-156-761-7418	Sequence 7418, Ap	703	50	5.1	36778	10	US-09-836-821-5	Sequence 5, Appl1
630	50.6	5.1	1371	17	US-10-282-122A-25436	Sequence 25436, A	704	50	5.1	36778	16	US-10-329-079-48	Sequence 48, Appl
631	50.6	5.1	1400	18	US-10-425-115-20597	Sequence 20597, A	705	50	5.1	37360	16	US-10-329-079-6	Sequence 6, Appl1
c 632	50.6	5.1	1449	18	US-10-437-963-64629	Sequence 64629, A	706	50	5.1	37948	10	US-09-988-384B-5	Sequence 5, Appl1
633	50.6	5.1	1695	15	US-10-156-761-3949	Sequence 3949, Ap	707	50	5.1	38506	10	US-09-793-708-19	Sequence 19, Appl
634	50.6	5.1	1848	18	US-10-437-963-22612	Sequence 22612, A	708	50	5.1	38506	15	US-10-201-365-1	Sequence 1, Appl1
635	50.6	5.1	2300	18	US-10-425-115-134362	Sequence 134362, A	709	50	5.1	38506	16	US-10-160-539-19	Sequence 19, Appl
c 636	50.6	5.1	2477	18	US-10-425-115-170055	Sequence 170055, A	710	50	5.1	38506	19	US-10-468-828-19	Sequence 19, Appl
637	50.6	5.1	2741	18	US-10-425-115-148395	Sequence 148395, A	711	49.8	5.0	856	9	US-09-823-245A-99	Sequence 99, Appl
638	50.6	5.1	3418	18	US-10-425-115-184346	Sequence 184346, A	712	49.8	5.0	880	17	US-10-425-114-32836	Sequence 32836, A
c 639	50.6	5.1	4123	18	US-10-425-115-184346	Sequence 184346, A	713	49.8	5.0	915	15	US-10-156-761-2013	Sequence 2013, Ap
640	50.6	5.1	4233	18	US-10-723-860-4143	Sequence 4143, Ap	714	49.8	5.0	940	17	US-10-425-114-35300	Sequence 35300, A
c 641	50.6	5.1	4244	18	US-10-723-860-8016	Sequence 8016, Ap	715	49.8	5.0	948	18	US-10-425-115-43218	Sequence 43218, A
c 642	50.4	5.1	599	17	US-10-260-238-239	Sequence 239, App	716	49.8	5.0	1227	15	US-10-156-761-6074	Sequence 6074, Ap
643	50.4	5.1	645	15	US-10-156-761-6059	Sequence 6059, Ap	717	49.8	5.0	1245	11	US-09-758-759-22	Sequence 22, Appl
c 644	50.4	5.1	662	18	US-10-437-963-74146	Sequence 74146, A	718	49.8	5.0	1272	17	US-10-107-431-32	Sequence 32, Appl
645	50.4	5.1	669	17	US-10-107-431-166	Sequence 166, App	719	49.8	5.0	1293	14	US-10-145-415-17	Sequence 17, Appl
646	50.4	5.1	777	18	US-10-425-115-83763	Sequence 83763, A	720	49.8	5.0	1374	17	US-10-282-122A-14455	Sequence 14455, A
647	50.4	5.1	838	18	US-10-425-115-127687	Sequence 127687, A	721	49.8	5.0	1410	18	US-10-437-963-97868	Sequence 97868, A
648	50.4	5.1	891	18	US-10-437-963-41595	Sequence 41595, A	722	49.8	5.0	1440	15	US-10-156-761-5216	Sequence 5216, Ap
649	50.4	5.1	1062	18	US-10-437-963-34793	Sequence 34793, A	723	49.8	5.0	1572	17	US-10-156-761-4159	Sequence 4159, Ap
650	50.4	5.1	1159	17	US-10-374-780A-879	Sequence 879, App	724	49.8	5.0	1581	17	US-10-464-368-113	Sequence 113, App
651	50.4	5.1	1454	18	US-10-425-115-68094	Sequence 68094, A	725	49.8	5.0	1594	18	US-10-437-963-42666	Sequence 42666, A
652	50.4	5.1	1587	15	US-10-156-761-5134	Sequence 5134, Ap	726	49.8	5.0	1791	15	US-10-156-761-2352	Sequence 2352, Ap
653	50.4	5.1	1848	15	US-10-156-761-3850	Sequence 3850, Ap	727	49.8	5.0	1814	14	US-10-060-036-182	Sequence 182, App
654	50.4	5.1	1910	18	US-10-437-963-23941	Sequence 23941, A	728	49.8	5.0	1837	19	US-10-278-698-240	Sequence 240, App
c 655	50.4	5.1	1951	18	US-10-437-963-31078	Sequence 31078, A	729	49.8	5.0	1837	19	US-10-278-698-241	Sequence 241, App
656	50.4	5.1	2082	15	US-10-156-761-6082	Sequence 6082, Ap	730	49.8	5.0	1837	19	US-10-278-698-754	Sequence 754, App
657	50.4	5.1	3048	15	US-10-156-761-3146	Sequence 3146, Ap	731	49.8	5.0	1837	19	US-10-278-698-755	Sequence 755, App
c 658	50.4	5.1	3456	18	US-10-437-963-50711	Sequence 50711, A	732	49.8	5.0	1929	9	US-09-761-534A-9	Sequence 9, Appl1
c 659	50.4	5.1	5003	18	US-10-437-963-18350	Sequence 18350, A	733	49.8	5.0	1929	19	US-10-885-523-9	Sequence 9, Appl1
660	50.4	5.1	6375	17	US-10-389-647-144	Sequence 144, App	734	49.8	5.0	2031	15	US-10-156-761-2451	Sequence 2451, Ap
661	50.4	5.1	14427	15	US-10-156-761-1540	Sequence 1540, Ap	734	49.8	5.0				



735	49.8	5.0	2115	15	US-10-156-761-5640	Sequence 5640, Ap	808	49.6	5.0	14023	19	US-10-741-600-17840	Sequence 17840, A
736	49.8	5.0	2136	18	US-10-437-963-49142	Sequence 49142, A	c 809	49.6	5.0	199130	19	US-10-741-600-17617	Sequence 17617, A
737	49.8	5.0	2220	10	US-09-873-367C-159	Sequence 159, App	810	49.4	5.0	426	18	US-10-437-963-99472	Sequence 99472, A
738	49.8	5.0	2320	19	US-10-843-641A-159	Sequence 159, App	811	49.4	5.0	843	15	US-10-156-761-1994	Sequence 1994, Ap
c 739	49.8	5.0	2335	18	US-10-437-963-11953	Sequence 11953, A	812	49.4	5.0	876	15	US-10-156-761-4743	Sequence 4743, Ap
740	49.8	5.0	2664	15	US-10-156-761-1241	Sequence 1241, Ap	813	49.4	5.0	951	15	US-10-259-165-313	Sequence 313, App
741	49.8	5.0	3066	15	US-10-156-761-1742	Sequence 1742, Ap	814	49.4	5.0	908	18	US-10-762-107-77	Sequence 77, Appl
742	49.8	5.0	3113	9	US-09-894-998-52	Sequence 52, Appl	c 815	49.4	5.0	1075	19	US-10-437-963-39562	Sequence 39562, A
743	49.8	5.0	3113	14	US-10-121-988-52	Sequence 52, Appl	816	49.4	5.0	1029	17	US-10-084-846A-87	Sequence 87, Appl
744	49.8	5.0	3113	16	US-10-200-562-52	Sequence 52, Appl	817	49.4	5.0	1173	17	US-10-282-122A-25963	Sequence 25963, A
745	49.8	5.0	3113	16	US-10-237-551-52	Sequence 52, Appl	818	49.4	5.0	1191	17	US-10-282-122A-15207	Sequence 15207, A
746	49.8	5.0	3345	9	US-09-894-998-49	Sequence 49, Appl	819	49.4	5.0	1281	15	US-10-156-761-2281	Sequence 2281, Ap
747	49.8	5.0	3345	14	US-10-121-988-49	Sequence 49, Appl	820	49.4	5.0	1385	17	US-10-425-114-26389	Sequence 26389, A
748	49.8	5.0	3345	16	US-10-200-562-49	Sequence 49, Appl	821	49.4	5.0	1401	18	US-10-437-963-95208	Sequence 95208, A
749	49.8	5.0	3345	16	US-10-200-562-189	Sequence 189, App	822	49.4	5.0	1557	17	US-10-425-114-18927	Sequence 18927, A
750	49.8	5.0	3345	16	US-10-237-551-49	Sequence 49, Appl	823	49.4	5.0	1587	17	US-10-282-122A-28573	Sequence 28573, A
751	49.8	5.0	3345	16	US-10-237-551-189	Sequence 189, App	824	49.4	5.0	1590	17	US-10-282-122A-26270	Sequence 26270, A
752	49.8	5.0	4323	17	US-10-282-122A-26577	Sequence 26577, A	c 825	49.4	5.0	1612	18	US-10-437-963-102480	Sequence 102480, A
c 753	49.8	5.0	37116	17	US-10-107-431-279	Sequence 279, App	826	49.4	5.0	1619	17	US-10-425-114-24202	Sequence 24202, A
754	49.8	5.0	65140	18	US-10-203-295-1	Sequence 1, Appli	827	49.4	5.0	1619	17	US-10-425-114-24326	Sequence 24326, A
755	49.8	5.0	125401	18	US-10-203-295-35	Sequence 35, Appl	828	49.4	5.0	1633	18	US-10-425-115-157740	Sequence 157740, A
756	49.6	5.0	242	9	US-09-823-876-781	Sequence 781, App	c 830	49.4	5.0	1697	17	US-10-425-114-29187	Sequence 29187, A
757	49.6	5.0	242	10	US-09-823-876-781	Sequence 781, App	831	49.4	5.0	1707	18	US-10-425-115-113441	Sequence 113441, A
c 758	49.6	5.0	746	17	US-10-425-114-12136	Sequence 12136, A	831	49.4	5.0	2091	14	US-10-121-988-78	Sequence 78, Appl
c 759	49.6	5.0	806	18	US-10-767-701-1614	Sequence 1614, Ap	832	49.4	5.0	2091	16	US-10-200-562-78	Sequence 78, Appl
c 760	49.6	5.0	876	17	US-10-425-115-55664	Sequence 55664, A	833	49.4	5.0	2091	16	US-10-237-551-78	Sequence 78, Appl
761	49.6	5.0	976	17	US-10-425-114-13780	Sequence 13780, A	834	49.4	5.0	2091	16	US-10-237-551-226	Sequence 226, App
762	49.6	5.0	978	15	US-10-156-761-6381	Sequence 6381, Ap	835	49.4	5.0	2118	14	US-10-121-988-87	Sequence 87, Appl
763	49.6	5.0	981	18	US-10-437-963-58326	Sequence 58326, A	836	49.4	5.0	2118	16	US-10-200-562-87	Sequence 87, Appl
c 765	49.6	5.0	1089	15	US-10-156-761-2655	Sequence 2655, Ap	837	49.4	5.0	2118	16	US-10-237-551-87	Sequence 87, Appl
c 766	49.6	5.0	1151	17	US-10-425-114-23539	Sequence 23539, A	838	49.4	5.0	2211	14	US-10-121-988-86	Sequence 86, Appl
767	49.6	5.0	1176	17	US-10-425-114-21556	Sequence 21556, A	839	49.4	5.0	2211	16	US-10-200-562-86	Sequence 86, Appl
768	49.6	5.0	1194	18	US-10-437-963-102262	Sequence 102262, A	840	49.4	5.0	2211	16	US-10-237-551-86	Sequence 86, Appl
769	49.6	5.0	1205	18	US-10-437-963-84924	Sequence 84924, A	c 841	49.4	5.0	2270	17	US-10-437-963-53336	Sequence 53336, A
770	49.6	5.0	1329	15	US-10-156-761-5851	Sequence 5851, Ap	842	49.4	5.0	2502	17	US-10-282-122A-17902	Sequence 17902, A
771	49.6	5.0	1404	17	US-10-282-122A-33594	Sequence 33594, A	843	49.4	5.0	2517	17	US-10-369-493-43222	Sequence 43222, A
772	49.6	5.0	1651	18	US-10-369-493-31750	Sequence 31750, A	844	49.4	5.0	3038	16	US-10-251-661-11	Sequence 11, Appl
773	49.6	5.0	1743	17	US-10-437-963-23386	Sequence 23386, A	845	49.4	5.0	3038	18	US-10-680-087-45	Sequence 45, Appl
774	49.6	5.0	1743	17	US-10-172-118-1387	Sequence 1387, Ap	846	49.4	5.0	3331	10	US-09-373-658-31	Sequence 31, Appl
775	49.6	5.0	1743	17	US-10-342-887-1387	Sequence 1387, Ap	847	49.4	5.0	3331	11	US-09-989-687-31	Sequence 31, Appl
776	49.6	5.0	1761	15	US-10-156-761-1503	Sequence 1503, Ap	848	49.4	5.0	3352	18	US-10-425-115-84048	Sequence 84048, A
777	49.6	5.0	1765	16	US-10-237-551-225	Sequence 225, App	c 849	49.4	5.0	3489	15	US-09-894-273-1	Sequence 1, Appli
c 778	49.6	5.0	1929	18	US-10-437-963-70663	Sequence 70663, A	850	49.4	5.0	3489	15	US-10-294-804-1	Sequence 1, Appli
c 779	49.6	5.0	1978	18	US-10-437-963-88743	Sequence 88743, A	c 851	49.4	5.0	3489	18	US-10-194-046-1	Sequence 1, Appli
780	49.6	5.0	2040	9	US-09-815-242-4027	Sequence 4027, Ap	852	49.4	5.0	4255	17	US-10-282-122A-14875	Sequence 14875, A
781	49.6	5.0	2040	17	US-10-282-122A-7316	Sequence 7316, Ap	853	49.4	5.0	4353	17	US-10-226-638A-15	Sequence 15, Appl
782	49.6	5.0	2059	18	US-10-437-963-59377	Sequence 59377, A	854	49.4	5.0	4353	19	US-10-762-107-73	Sequence 73, Appl
783	49.6	5.0	2065	18	US-10-437-963-31244	Sequence 31244, A	855	49.4	5.0	14061	17	US-10-093-463-73	Sequence 73, Appl
c 784	49.6	5.0	2218	17	US-10-108-260A-2174	Sequence 2174, Ap	c 856	49.4	5.0	30000	11	US-09-980-217-3	Sequence 3, Appli
c 785	49.6	5.0	2271	15	US-10-101-510-133	Sequence 133, App	857	49.4	5.0	32329	17	US-10-374-903A-1	Sequence 1, Appli
c 786	49.6	5.0	2487	15	US-10-208-823-135	Sequence 82369, A	858	49.4	5.0	59816	17	US-10-084-846A-1	Sequence 1, Appli
c 787	49.6	5.0	2487	17	US-10-172-118-1045	Sequence 135, App	c 859	49.4	5.0	59816	17	US-10-084-846A-2	Sequence 2, Appli
c 788	49.6	5.0	2487	17	US-10-342-887-1045	Sequence 1045, Ap	860	49.4	5.0	109519	11	US-09-758-759-1	Sequence 1, Appli
789	49.6	5.0	2700	15	US-10-156-761-7310	Sequence 7310, Ap	861	49.2	5.0	955	17	US-10-425-114-17203	Sequence 17203, A
790	49.6	5.0	2742	9	US-09-815-242-4163	Sequence 4163, Ap	862	49.2	5.0	972	17	US-10-369-493-32340	Sequence 32340, A
791	49.6	5.0	2742	17	US-10-282-122A-7408	Sequence 7408, Ap	863	49.2	5.0	975	18	US-10-425-115-150798	Sequence 150798, A
792	49.6	5.0	3459	17	US-10-369-493-31552	Sequence 31552, A	c 864	49.2	5.0	1004	17	US-10-332-859-324	Sequence 324, App
793	49.6	5.0	3729	17	US-10-671-403-86	Sequence 86, Appl	865	49.2	5.0	1051	18	US-10-425-115-173915	Sequence 173915, A
794	49.6	5.0	3729	17	US-10-671-419-86	Sequence 86, Appl	866	49.2	5.0	1155	18	US-10-437-963-94232	Sequence 94232, A
795	49.6	5.0	3729	17	US-10-670-844-86	Sequence 86, Appl	867	49.2	5.0	1296	18	US-10-437-963-82846	Sequence 82846, A
796	49.6	5.0	3729	17	US-10-671-138-86	Sequence 86, Appl	868	49.2	5.0	1317	15	US-10-156-761-3647	Sequence 3647, Ap
797	49.6	5.0	3729	17	US-10-673-104-86	Sequence 86, Appl	869	49.2	5.0	1357	18	US-10-437-963-18242	Sequence 18242, A
798	49.6	5.0	3729	17	US-10-673-638-86	Sequence 86, Appl	870	49.2	5.0	1493	17	US-10-425-114-3264	Sequence 3264, Ap
799	49.6	5.0	3729	17	US-10-673-127-86	Sequence 86, Appl	871	49.2	5.0	1587	15	US-10-156-761-4508	Sequence 4508, Ap
800	49.6	5.0	3729	18	US-10-673-119-86	Sequence 86, Appl	c 872	49.2	5.0	1602	9	US-09-833-790-417	Sequence 417, App
801	49.6	5.0	3729	18	US-10-671-207-86	Sequence 86, Appl	c 873	49.2	5.0	1602	16	US-10-293-582-15	Sequence 15, Appl
802	49.6	5.0	3729	18	US-10-671-119-86	Sequence 86, Appl	874	49.2	5.0	1602	17	US-10-761-169-5	Sequence 5, Appli
803	49.6	5.0	3729	19	US-10-673-120-86	Sequence 86, Appl	875	49.2	5.0	1613	17	US-10-425-114-3572	Sequence 3572, Ap
c 804	49.6	5.0	3942	15	US-10-156-761-5692	Sequence 86, Appl	876	49.2	5.0	1679	18	US-10-437-963-32154	Sequence 32154, A
c 805	49.6	5.0	5181	11	US-09-968-007A-802	Sequence 802, App	877	49.2	5.0	1908	15	US-10-156-761-260	Sequence 260, App
c 806	49.6	5.0	5181	19	US-10-843-641A-7272	Sequence 7272, Ap	878	49.2	5.0	2331	18	US-10-437-963-14511	Sequence 14511, A
807	49.6	5.0	12591	19	US-10-741-600-17855	Sequence 17855, A	879	49.2	5.0	2455	9	US-09-917-800A-1386	Sequence 1386, Ap
							880	49.2	5.0	2455	16	US-10-316-253-27	Sequence 27, Appl

881	49.2	5.0	2455	17	US-10-388-934-21	Sequence 21, Appl	954	48.8	4.9	4322	18	US-10-425-115-15092	Sequence 15092, A
882	49.2	5.0	2455	17	US-10-152-319A-1964	Sequence 1964, Ap	955	48.8	4.9	7897	17	US-10-359-120-161	Sequence 161, App
883	49.2	5.0	2607	16	US-10-247-671-13	Sequence 13, Appl	956	48.8	4.9	9166	17	US-10-359-120-168	Sequence 168, App
C 884	49.2	5.0	2717	17	US-10-723-860-8011	Sequence 8011, Ap	957	48.8	4.9	9167	17	US-10-359-120-171	Sequence 171, App
885	49.2	5.0	3540	17	US-10-369-493-32003	Sequence 32003, A	958	48.8	4.9	9169	17	US-10-359-120-169	Sequence 169, App
886	49.2	5.0	4161	15	US-10-156-761-5450	Sequence 5450, Ap	959	48.8	4.9	9170	17	US-10-359-120-166	Sequence 166, App
887	49.2	5.0	137560	18	US-10-481-111-1	Sequence 1, Appl	960	48.8	4.9	9189	17	US-10-359-120-159	Sequence 159, App
888	49.2	5.0	339	15	US-10-174-693-193	Sequence 193, App	961	48.8	4.9	9194	17	US-10-359-120-163	Sequence 163, App
889	49.2	5.0	717	17	US-10-282-122A-25697	Sequence 25697, A	962	48.8	4.9	9194	17	US-10-359-120-164	Sequence 164, App
C 891	49.2	5.0	1011	17	US-10-156-761-7058	Sequence 7058, Ap	963	48.8	4.9	9407	17	US-10-359-120-175	Sequence 175, App
892	49.2	5.0	1261	18	US-10-437-963-70724	Sequence 70724, A	964	48.8	4.9	9782	17	US-10-359-120-173	Sequence 173, App
893	49.2	5.0	1272	18	US-10-437-963-27235	Sequence 27235, A	965	48.8	4.9	9783	17	US-10-359-120-172	Sequence 172, App
894	49.2	5.0	1286	18	US-10-437-963-27235	Sequence 27235, A	966	48.8	4.9	9783	17	US-10-359-120-176	Sequence 176, App
895	49.2	5.0	1355	17	US-10-458-108-6	Sequence 6, Appl	967	48.8	4.9	9788	17	US-10-359-120-174	Sequence 174, App
896	49.2	5.0	1400	18	US-10-437-963-2506	Sequence 2506, Ap	968	48.8	4.9	9792	17	US-10-359-120-170	Sequence 170, App
897	49.2	5.0	1462	14	US-10-175-523-163	Sequence 163, App	969	48.8	4.9	10035	17	US-10-107-431-282	Sequence 282, App
C 898	49.2	5.0	1473	18	US-10-411-910A-261	Sequence 261, App	970	48.8	4.9	12411	17	US-10-359-120-165	Sequence 165, App
899	49.2	5.0	1614	9	US-09-976-740-45	Sequence 45, Appl	971	48.8	4.9	18435	15	US-10-156-761-412	Sequence 412, App
C 900	49.2	5.0	1614	13	US-10-023-523-45	Sequence 45, Appl	972	48.8	4.9	13538	16	US-10-314-657-1	Sequence 1, Appl
C 901	49.2	5.0	1614	17	US-10-616-187-45	Sequence 45, Appl	973	48.8	4.9	396	18	US-10-767-701-30763	Sequence 30763, A
C 902	49.2	5.0	1614	17	US-10-671-242-45	Sequence 45, Appl	974	48.6	4.9	528	9	US-09-452-239-33	Sequence 33, Appl
903	49.2	5.0	1797	18	US-10-437-963-28602	Sequence 28602, A	975	48.6	4.9	623	18	US-10-437-963-5272	Sequence 5272, Ap
904	49.2	5.0	1852	9	US-09-969-852-4	Sequence 4, Appl	976	48.6	4.9	668	18	US-10-767-701-11523	Sequence 11523, A
C 905	49.2	5.0	1891	17	US-10-310-151-280	Sequence 280, App	977	48.6	4.9	687	17	US-10-282-122A-26239	Sequence 26239, A
C 906	49.2	5.0	1946	18	US-10-437-963-22064	Sequence 22064, A	978	48.6	4.9	690	17	US-10-282-122A-28509	Sequence 28509, A
907	49.2	5.0	1974	18	US-10-437-963-87831	Sequence 87831, A	979	48.6	4.9	761	18	US-10-425-115-127921	Sequence 127921, A
908	49.2	5.0	2067	18	US-10-437-963-18405	Sequence 18405, A	980	48.6	4.9	796	18	US-10-767-701-7856	Sequence 7856, Ap
909	49.2	5.0	2143	17	US-10-425-114-23617	Sequence 23617, A	981	48.6	4.9	847	18	US-10-425-115-41717	Sequence 41717, A
C 910	49.2	5.0	2204	18	US-10-437-963-11022	Sequence 11022, A	982	48.6	4.9	934	17	US-10-425-114-17266	Sequence 17266, A
911	49.2	5.0	2239	17	US-10-425-114-52332	Sequence 5232, Ap	983	48.6	4.9	974	17	US-10-425-114-18881	Sequence 18881, A
912	49.2	5.0	2271	18	US-10-437-963-74809	Sequence 74809, A	984	48.6	4.9	1107	18	US-10-425-115-161174	Sequence 161174, A
C 913	49.2	5.0	2439	15	US-10-156-761-2569	Sequence 2569, Ap	985	48.6	4.9	1143	15	US-10-156-761-6453	Sequence 6453, Ap
914	49.2	5.0	2536	18	US-10-425-115-91117	Sequence 91117, A	986	48.6	4.9	1170	18	US-10-425-115-162747	Sequence 162747, A
C 915	49.2	5.0	2939	18	US-10-437-963-58050	Sequence 58050, A	987	48.6	4.9	1203	17	US-10-369-493-34414	Sequence 34414, A
C 916	49.2	5.0	12425	9	US-09-976-740-50	Sequence 50, Appl	988	48.6	4.9	1302	18	US-10-425-115-164928	Sequence 164928, A
C 917	49.2	5.0	12425	13	US-10-023-523-50	Sequence 50, Appl	989	48.6	4.9	1366	18	US-10-425-115-28293	Sequence 28293, A
C 918	49.2	5.0	12425	13	US-10-023-523-50	Sequence 50, Appl	990	48.6	4.9	1453	18	US-10-437-963-78719	Sequence 78719, A
C 919	49.2	5.0	12425	17	US-10-616-187-50	Sequence 50, Appl	991	48.6	4.9	1461	15	US-10-156-761-2205	Sequence 2205, Ap
C 920	49.2	5.0	12425	17	US-10-671-242-50	Sequence 50, Appl	992	48.6	4.9	1479	13	US-10-016-283-35	Sequence 35, Appl
C 921	49.2	5.0	77536	10	US-09-940-3168-1	Sequence 1, Appl	993	48.6	4.9	1533	18	US-09-814-353-20197	Sequence 20197, A
922	48.8	4.9	363	15	US-10-156-761-5224	Sequence 5224, Ap	994	48.6	4.9	1617	18	US-10-425-115-164014	Sequence 164014, A
C 923	48.8	4.9	389	18	US-10-425-115-178702	Sequence 178702, A	995	48.6	4.9	1685	17	US-10-425-114-27558	Sequence 27558, A
924	48.8	4.9	459	18	US-10-437-963-3398	Sequence 3398, Ap	996	48.6	4.9	1783	18	US-10-437-963-340	Sequence 340, App
925	48.8	4.9	513	15	US-10-156-761-5057	Sequence 5057, Ap	997	48.6	4.9	1839	11	US-09-758-759-150	Sequence 150, App
926	48.8	4.9	516	18	US-10-437-963-75898	Sequence 75898, A	998	48.6	4.9	1962	18	US-10-437-963-89753	Sequence 89753, A
927	48.8	4.9	602	18	US-10-425-115-17234	Sequence 17234, A	999	48.6	4.9	2040	9	US-09-874-923-5	Sequence 5, Appl
928	48.8	4.9	618	15	US-10-156-761-4061	Sequence 4061, Ap	1000	48.6	4.9	2040	9	US-09-991-496-5	Sequence 5, Appl
929	48.8	4.9	728	17	US-10-425-114-14002	Sequence 14002, A	1001	48.6	4.9	2040	16	US-10-098-732A-72	Sequence 72, Appl
930	48.8	4.9	827	17	US-10-425-114-18832	Sequence 18832, A	1002	48.6	4.9	2238	18	US-10-437-963-35019	Sequence 35019, A
931	48.8	4.9	828	15	US-10-156-761-1422	Sequence 1422, Ap	1003	48.6	4.9	2279	16	US-10-021-660-68	Sequence 68, Appl
932	48.8	4.9	933	15	US-10-156-761-1758	Sequence 1758, Ap	1004	48.6	4.9	2279	17	US-10-211-462-212	Sequence 212, App
933	48.8	4.9	1068	15	US-10-156-761-1861	Sequence 1861, Ap	1005	48.6	4.9	2577	18	US-10-332-413-9	Sequence 9, Appl
934	48.8	4.9	1085	17	US-10-425-114-3	Sequence 3, Appl	1006	48.6	4.9	2712	9	US-09-748-033-4	Sequence 4, Appl
935	48.8	4.9	1094	18	US-10-767-701-13435	Sequence 13435, A	1007	48.6	4.9	3298	17	US-10-362-247-4	Sequence 4, Appl
936	48.8	4.9	1125	17	US-10-425-114-14054	Sequence 14054, A	1008	48.6	4.9	3872	18	US-10-437-963-57556	Sequence 57556, A
C 937	48.8	4.9	1149	18	US-10-425-115-109968	Sequence 109968, A	1009	48.6	4.9	3975	15	US-10-156-761-4112	Sequence 4112, Ap
938	48.8	4.9	1164	18	US-10-767-701-12837	Sequence 12837, A	1010	48.6	4.9	5065	14	US-10-067-457-4	Sequence 4, Appl
939	48.8	4.9	1194	16	US-10-214-446-33	Sequence 33, Appl	1011	48.6	4.9	5499	17	US-10-276-774-973	Sequence 973, App
940	48.8	4.9	1224	17	US-10-425-114-21138	Sequence 21138, A	1012	48.4	4.9	562	15	US-10-174-693-53	Sequence 53, Appl
941	48.8	4.9	1272	17	US-10-107-431-262	Sequence 262, App	1013	48.4	4.9	642	15	US-10-156-761-6149	Sequence 6149, Ap
942	48.8	4.9	1290	18	US-10-767-701-9008	Sequence 9008, Ap	1014	48.4	4.9	651	15	US-10-156-761-6890	Sequence 6890, Ap
943	48.8	4.9	1335	15	US-10-156-761-7202	Sequence 7202, Ap	1015	48.4	4.9	800	18	US-10-425-115-25676	Sequence 25676, A
944	48.8	4.9	1392	15	US-10-156-761-4350	Sequence 4350, Ap	1016	48.4	4.9	819	18	US-10-425-115-151084	Sequence 151084, A
945	48.8	4.9	1455	17	US-10-425-114-31249	Sequence 31249, A	1017	48.4	4.9	1059	15	US-10-259-165-215	Sequence 215, App
946	48.8	4.9	1463	17	US-10-425-114-18406	Sequence 18406, A	1018	48.4	4.9	1164	17	US-10-425-114-21717	Sequence 21717, A
947	48.8	4.9	1743	18	US-10-425-115-85293	Sequence 85293, A	1019	48.4	4.9	1264	18	US-10-425-115-36748	Sequence 36748, A
948	48.8	4.9	2017	17	US-10-425-114-32728	Sequence 32728, A	1020	48.4	4.9	1335	18	US-10-437-963-27475	Sequence 27475, A
949	48.8	4.9	2135	18	US-10-425-115-169676	Sequence 169676, A	1021	48.4	4.9	1395	18	US-10-437-963-38959	Sequence 38959, A
C 950	48.8	4.9	2391	18	US-10-425-115-86864	Sequence 86864, A	1022	48.4	4.9	1558	17	US-10-425-114-1638	Sequence 1638, Ap
951	48.8	4.9	2671	18	US-10-425-115-158883	Sequence 158883, A	1023	48.4	4.9	1650	17	US-10-282-122A-25691	Sequence 25691, A
952	48.8	4.9	2771	18	US-10-425-115-167636	Sequence 167636, A	1024	48.4	4.9	1872	18	US-10-437-963-86467	Sequence 86467, A
953	48.8	4.9	3657	18	US-10-437-963-26197	Sequence 26197, A	1025	48.4	4.9	1794	18	US-10-437-963-78147	Sequence 78147, A
							1026	48.4	4.9	1809	18	US-10-437-963-86462	Sequence 86462, A

1027	48.4	4.9	2019	15	US-10-156-761-3693	Sequence 3693, Ap	1100	48.2	4.9	9579	16	US-10-132-134-11	Sequence 11, Appl
c1028	48.4	4.9	2523	17	US-10-282-122A-15228	Sequence 15228, A	1101	48.2	4.9	20922	10	US-09-942-025-14	Sequence 14, Appl
c1029	48.4	4.9	2865	18	US-10-437-963-96575	Sequence 96575, A	1102	48.2	4.9	27541	18	US-10-203-235-2	Sequence 2, Appl
1030	48.4	4.9	2892	15	US-10-156-761-3066	Sequence 3066, Ap	1103	48.2	4.9	27705	10	US-08-942-025-12	Sequence 12, Appl
1031	48.4	4.9	3377	17	US-10-437-963-92668	Sequence 92668, A	1104	48.2	4.9	52101	16	US-10-132-134-1	Sequence 1, Appl
1032	48.4	4.9	4751	17	US-10-311-795-5	Sequence 5, Appl	1105	48.2	4.9	67311	10	US-09-942-025-1	Sequence 1, Appl
1033	48.4	4.9	4833	17	US-10-282-122A-25605	Sequence 25605, A	1106	48.2	4.9	70383	15	US-10-283-247-3	Sequence 3, Appl
c1034	48.4	4.9	6779	18	US-10-437-963-29812	Sequence 29812, A	1107	48.2	4.9	86941	17	US-10-461-194-2	Sequence 2, Appl
c1035	48.4	4.9	24081	16	US-10-132-134-13	Sequence 13, Appl	1108	48	4.9	353	18	US-10-425-115-98452	Sequence 98452, A
1036	48.4	4.9	31263	17	US-10-282-122A-25447	Sequence 25447, A	1109	48	4.9	489	15	US-10-156-761-4741	Sequence 4741, Ap
c1037	48.4	4.9	52101	16	US-10-132-134-1	Sequence 1, Appl	1110	48	4.9	579	11	US-09-758-759-174	Sequence 174, App
1038	48.2	4.9	480	18	US-10-437-963-48143	Sequence 48143, A	1111	48	4.9	652	18	US-10-767-701-5497	Sequence 5497, Ap
c1039	48.2	4.9	553	18	US-10-425-115-82149	Sequence 82149, A	1112	48	4.9	712	18	US-10-363-345A-27449	Sequence 27449, A
1040	48.2	4.9	618	17	US-10-425-114-6672	Sequence 6672, Ap	1113	48	4.9	712	18	US-10-363-345A-27450	Sequence 27450, A
1041	48.2	4.9	729	18	US-10-425-115-154823	Sequence 154823, A	1114	48	4.9	712	18	US-10-363-483A-27449	Sequence 27449, A
1042	48.2	4.9	738	17	US-10-425-114-19698	Sequence 19698, A	1115	48	4.9	712	19	US-10-363-483A-27450	Sequence 27450, A
c1043	48.2	4.9	786	17	US-10-260-238-458	Sequence 458, App	1116	48	4.9	753	11	US-09-758-759-193	Sequence 193, App
1044	48.2	4.9	789	17	US-10-425-114-27917	Sequence 27917, A	1117	48	4.9	756	17	US-10-107-431-132	Sequence 132, App
1045	48.2	4.9	811	18	US-10-489-372-40	Sequence 40, Appl	1118	48	4.9	768	17	US-10-369-493-33233	Sequence 33233, A
1046	48.2	4.9	823	14	US-10-153-668-54	Sequence 54, Appl	1119	48	4.9	833	17	US-10-425-114-24992	Sequence 24992, A
1047	48.2	4.9	823	14	US-10-153-668-56	Sequence 56, Appl	1120	48	4.9	833	18	US-10-425-115-24687	Sequence 24687, A
1048	48.2	4.9	825	17	US-10-282-122A-25820	Sequence 25820, A	1121	48	4.9	888	18	US-10-437-963-98299	Sequence 98299, A
1049	48.2	4.9	852	18	US-10-437-963-89306	Sequence 89306, A	1122	48	4.9	954	15	US-10-156-761-4757	Sequence 4757, Ap
1050	48.2	4.9	861	15	US-10-156-761-3921	Sequence 3921, Ap	1123	48	4.9	1128	10	US-09-875-076-15	Sequence 875, Ap
1051	48.2	4.9	920	15	US-10-037-270-132	Sequence 132, App	1124	48	4.9	1128	10	US-09-875-252-17	Sequence 15, Appl
1052	48.2	4.9	920	17	US-10-117-722-132	Sequence 132, App	1125	48	4.9	1128	14	US-10-318-142-1	Sequence 1, Appl
c1053	48.2	4.9	930	17	US-10-282-122A-30550	Sequence 30550, A	1126	48	4.9	1128	15	US-10-225-567A-493	Sequence 493, App
1054	48.2	4.9	956	18	US-10-437-963-95323	Sequence 95323, A	1127	48	4.9	1128	15	US-10-272-983-15	Sequence 15, Appl
1055	48.2	4.9	969	9	US-09-789-836-3	Sequence 3, Appl	1128	48	4.9	1128	16	US-10-393-807-15	Sequence 15, Appl
1056	48.2	4.9	969	9	US-09-789-836-3	Sequence 3, Appl	1129	48	4.9	1128	17	US-10-417-820A-17	Sequence 17, Appl
1057	48.2	4.9	1038	9	US-09-789-831-3	Sequence 2, Appl	1130	48	4.9	1128	17	US-10-295-027-1121	Sequence 1121, Ap
1058	48.2	4.9	1038	10	US-09-789-831-2	Sequence 2, Appl	1131	48	4.9	1128	18	US-10-723-955-17	Sequence 17, Appl
1059	48.2	4.9	1038	16	US-10-251-661-9	Sequence 9, Appl	1132	48	4.9	1128	18	US-10-782-536-15	Sequence 15, Appl
1060	48.2	4.9	1038	17	US-10-410-888-3	Sequence 3, Appl	1133	48	4.9	1128	19	US-10-898-329-16	Sequence 16, Appl
1061	48.2	4.9	1038	17	US-10-159-563-166	Sequence 166, App	1134	48	4.9	1155	17	US-10-369-493-42888	Sequence 42888, A
1062	48.2	4.9	1038	18	US-10-415-325-22	Sequence 22, Appl	1135	48	4.9	1158	17	US-10-425-114-22632	Sequence 22632, A
1063	48.2	4.9	1042	10	US-09-789-831-17	Sequence 17, Appl	1136	48	4.9	1164	17	US-10-425-114-21171	Sequence 21171, A
1064	48.2	4.9	1059	17	US-10-389-647-304	Sequence 304, App	1137	48	4.9	1175	17	US-10-425-114-1930	Sequence 1930, Ap
1065	48.2	4.9	1151	18	US-10-425-115-175028	Sequence 175028, A	1138	48	4.9	1186	18	US-10-425-115-84443	Sequence 84443, A
1066	48.2	4.9	1215	15	US-10-156-761-2811	Sequence 2811, Ap	1139	48	4.9	1188	16	US-10-246-330-9	Sequence 9, Appl
1067	48.2	4.9	1336	19	US-10-488-056-9	Sequence 9, Appl	1140	48	4.9	1232	17	US-10-425-114-17219	Sequence 17219, A
1068	48.2	4.9	1347	15	US-10-156-761-6038	Sequence 6038, Ap	1141	48	4.9	1236	18	US-10-437-963-95996	Sequence 95996, A
1069	48.2	4.9	1566	18	US-10-817-483-30	Sequence 30, Appl	1142	48	4.9	1257	18	US-10-767-701-11943	Sequence 11943, A
1070	48.2	4.9	1638	18	US-10-437-963-82416	Sequence 82416, A	1143	48	4.9	1275	17	US-10-282-122A-25779	Sequence 25779, A
1071	48.2	4.9	1670	18	US-10-767-701-33989	Sequence 13989, A	1144	48	4.9	1297	18	US-10-425-115-14015	Sequence 14015, A
1072	48.2	4.9	1710	15	US-10-156-761-2318	Sequence 2318, Ap	1145	48	4.9	1313	17	US-10-425-114-33638	Sequence 33638, A
1073	48.2	4.9	1818	18	US-10-437-963-55757	Sequence 55757, A	1146	48	4.9	1392	15	US-10-156-761-2601	Sequence 2601, Ap
1074	48.2	4.9	1927	17	US-10-425-114-28744	Sequence 28744, A	1147	48	4.9	1437	17	US-10-369-493-42370	Sequence 42370, A
1075	48.2	4.9	1930	18	US-10-425-115-41313	Sequence 41313, A	1148	48	4.9	1533	18	US-10-425-115-161561	Sequence 161561, A
1076	48.2	4.9	1910	9	US-09-789-836-1	Sequence 1, Appl	1149	48	4.9	1593	18	US-10-425-115-60514	Sequence 60514, A
1077	48.2	4.9	1910	10	US-09-789-831-1	Sequence 1, Appl	1150	48	4.9	1644	18	US-10-437-963-97070	Sequence 97070, A
1078	48.2	4.9	1910	18	US-10-415-325-18	Sequence 18, Appl	1151	48	4.9	1677	17	US-10-369-493-43031	Sequence 43031, A
1079	48.2	4.9	1941	15	US-10-156-761-3418	Sequence 3418, Ap	1152	48	4.9	1782	17	US-10-282-122A-13824	Sequence 13824, A
1080	48.2	4.9	1975	10	US-09-972-607-10	Sequence 10, Appl	1153	48	4.9	1893	15	US-10-156-761-7478	Sequence 7478, Ap
1081	48.2	4.9	1975	17	US-10-628-841-10	Sequence 10, Appl	1154	48	4.9	2023	15	US-10-156-761-7068	Sequence 7068, Ap
1082	48.2	4.9	1987	17	US-10-425-114-20273	Sequence 20273, A	1155	48	4.9	2431	18	US-10-437-963-17818	Sequence 17818, A
1083	48.2	4.9	1994	10	US-09-972-607-3	Sequence 3, Appl	1156	48	4.9	2488	18	US-10-739-930-3708	Sequence 3708, Ap
1084	48.2	4.9	1994	17	US-09-851-673-1	Sequence 1, Appl	1157	48	4.9	2583	15	US-10-156-761-3378	Sequence 3378, Ap
1085	48.2	4.9	1994	17	US-10-628-841-3	Sequence 3, Appl	1158	48	4.9	3435	11	US-10-437-963-26695	Sequence 26695, A
1086	48.2	4.9	1997	18	US-10-425-115-111418	Sequence 111418, A	1159	48	4.9	3489	9	US-09-758-759-166	Sequence 166, App
1087	48.2	4.9	2007	18	US-10-761-370-1	Sequence 1, Appl	1160	48	4.9	3489	9	US-09-815-242-7731	Sequence 7731, Ap
1088	48.2	4.9	2034	18	US-10-761-370-2	Sequence 2, Appl	1161	48	4.9	3489	17	US-10-282-122A-30110	Sequence 30110, A
1089	48.2	4.9	2035	10	US-09-863-049A-3	Sequence 3, Appl	1162	48	4.9	3489	17	US-10-282-122A-30110	Sequence 30110, A
1090	48.2	4.9	2130	18	US-10-425-115-114288	Sequence 114288, A	1163	48	4.9	37116	17	US-10-107-431-279	Sequence 279, App
1091	48.2	4.9	2595	17	US-10-282-122A-14998	Sequence 14998, A	1164	48	4.9	43623	19	US-10-741-600-17818	Sequence 17818, A
c1092	48.2	4.9	3350	9	US-09-894-998-48	Sequence 48, Appl	1165	48	4.9	77294	19	US-10-729-802-1	Sequence 1, Appl
c1093	48.2	4.9	3350	14	US-10-121-988-48	Sequence 48, Appl	1166	48	4.9	487	17	US-10-374-780A-1253	Sequence 1253, Ap
c1094	48.2	4.9	3350	16	US-10-200-562-48	Sequence 48, Appl	1167	48	4.9	487	18	US-10-437-963-87078	Sequence 87078, A
c1095	48.2	4.9	3350	16	US-10-237-551-48	Sequence 48, Appl	1168	47.8	4.8	579	18	US-10-437-963-87078	Sequence 87078, A
c1096	48.2	4.9	4025	17	US-10-437-963-97674	Sequence 97674, A	1169	47.8	4.8	627	15	US-10-156-761-6579	Sequence 6579, Ap
c1097	48.2	4.9	4146	17	US-10-282-122A-28711	Sequence 28711, A	1170	47.8	4.8	702	18	US-10-437-963-14724	Sequence 14724, A
1098	48.2	4.9	4542	17	US-10-282-122A-28674	Sequence 28674, A	1171	47.8	4.8	717	17	US-10-425-114-18216	Sequence 18216, A
1099	48.2	4.9	6591	15	US-10-301-822-3	Sequence 3, Appl	1172	47.8	4.8	777	17	US-10-332-947-28	Sequence 28, Appl

1173	47.8	4.8	888	15	US-10-156-761-5898	Sequence 5898, Ap	1258	47.6	4.8	2305	17	US-10-387-336-80	Sequence 80, Appl
1174	47.8	4.8	982	17	US-10-767-701-8931	Sequence 8931, Ap	1259	47.6	4.8	2306	17	US-10-387-336-82	Sequence 82, Appl
1175	47.8	4.8	1029	17	US-10-282-122A-25590	Sequence 25590, A	1260	47.6	4.8	2337	17	US-10-282-122A-25485	Sequence 25485, A
1176	47.8	4.8	1037	17	US-10-425-114-23005	Sequence 23005, A	1261	47.6	4.8	2424	17	US-10-282-122A-15037	Sequence 15037, A
1177	47.8	4.8	1075	18	US-10-425-115-5563	Sequence 5563, Ap	1262	47.6	4.8	2457	15	US-10-190-435-44	Sequence 44, Appl
1178	47.8	4.8	1173	18	US-10-482-706-258	Sequence 258, App	1263	47.6	4.8	2457	15	US-10-190-305A-38	Sequence 38, Appl
1179	47.8	4.8	1179	17	US-10-425-114-14395	Sequence 14395, A	1264	47.6	4.8	2463	10	US-09-899-575-31	Sequence 31, Appl
1180	47.8	4.8	1191	18	US-10-425-115-79775	Sequence 79775, A	1265	47.6	4.8	2466	16	US-10-241-009-31	Sequence 31, Appl
1181	47.8	4.8	1287	17	US-10-282-122A-14756	Sequence 14756, A	1266	47.6	4.8	2466	16	US-10-190-434B-31	Sequence 31, Appl
1182	47.8	4.8	1329	18	US-10-437-963-32214	Sequence 32214, A	1267	47.6	4.8	2466	16	US-10-190-305A-33	Sequence 33, Appl
1183	47.8	4.8	1401	15	US-10-156-761-6097	Sequence 6097, Ap	1268	47.6	4.8	2481	9	US-09-894-998-35	Sequence 35, Appl
1184	47.8	4.8	1404	17	US-10-282-122A-25706	Sequence 25706, A	1269	47.6	4.8	2481	14	US-10-121-988-35	Sequence 35, Appl
1185	47.8	4.8	1428	18	US-10-437-963-48509	Sequence 48509, A	1270	47.6	4.8	2481	16	US-10-200-562-35	Sequence 35, Appl
1186	47.8	4.8	1471	18	US-10-425-115-82155	Sequence 82155, A	1271	47.6	4.8	2481	16	US-10-237-551-35	Sequence 35, Appl
1187	47.8	4.8	1527	17	US-10-282-122A-25749	Sequence 25749, A	1272	47.6	4.8	2552	17	US-10-369-493-42921	Sequence 42921, A
1188	47.8	4.8	1531	18	US-10-425-115-37426	Sequence 37426, A	1273	47.6	4.8	3066	14	US-10-121-988-152	Sequence 152, App
1189	47.8	4.8	1612	18	US-10-437-963-15030	Sequence 15030, A	1274	47.6	4.8	3066	16	US-10-200-562-152	Sequence 152, App
1190	47.8	4.8	1671	11	US-09-758-759-102	Sequence 102, App	1275	47.6	4.8	3066	16	US-10-237-551-152	Sequence 152, App
1191	47.8	4.8	1711	18	US-10-425-115-58741	Sequence 58741, A	1276	47.6	4.8	3090	17	US-10-369-493-40513	Sequence 40513, A
1192	47.8	4.8	1771	9	US-09-874-923-7	Sequence 7, Appl	1277	47.6	4.8	3783	16	US-10-316-253-96	Sequence 96, Appl
1193	47.8	4.8	1771	9	US-09-991-496-7	Sequence 7, Appl	1278	47.6	4.8	5780	17	US-10-336-472-19	Sequence 19, Appl
1194	47.8	4.8	2256	18	US-10-437-963-86656	Sequence 86656, A	1279	47.6	4.8	5802	14	US-10-152-886-84	Sequence 84, Appl
1195	47.8	4.8	2387	18	US-10-437-963-38072	Sequence 38072, A	1280	47.6	4.8	5886	18	US-10-798-037-3	Sequence 3, Appl
1196	47.8	4.8	2556	18	US-10-437-963-29317	Sequence 29317, A	1281	47.6	4.8	6008	17	US-10-336-472-21	Sequence 21, Appl
1197	47.8	4.8	2595	18	US-10-437-963-66971	Sequence 66971, A	1282	47.6	4.8	6008	18	US-10-717-597-197	Sequence 197, App
1198	47.8	4.8	3824	17	US-10-116-275-197	Sequence 197, App	1283	47.6	4.8	10692	15	US-10-156-761-414	Sequence 414, App
1199	47.8	4.8	3824	17	US-10-159-563-307	Sequence 307, App	1284	47.6	4.8	12801	18	US-10-798-037-5	Sequence 5, Appl
1200	47.8	4.8	3824	18	US-10-723-860-2600	Sequence 2600, Ap	1285	47.6	4.8	27541	18	US-10-203-295-2	Sequence 2, Appl
1201	47.8	4.8	3824	18	US-10-723-860-6734	Sequence 6734, Ap	1286	47.6	4.8	349	18	US-10-425-115-40892	Sequence 40892, A
1202	47.8	4.8	7201	18	US-10-600-790-20	Sequence 20, Appl	1287	47.6	4.8	414	15	US-10-259-165-779	Sequence 779, App
1203	47.8	4.8	7429	19	US-10-873-332-61	Sequence 61, Appl	1288	47.6	4.8	463	18	US-10-767-701-559	Sequence 559, App
1204	47.8	4.8	71989	9	US-09-727-889-2	Sequence 2, Appl	1289	47.6	4.8	497	18	US-10-425-115-51767	Sequence 51767, A
1205	47.8	4.8	71989	18	US-10-849-463-2	Sequence 2, Appl	1290	47.6	4.8	504	17	US-10-260-238-5853	Sequence 5853, Ap
1206	47.8	4.8	524	18	US-10-437-963-873	Sequence 873, App	1291	47.6	4.8	601	18	US-10-767-701-4418	Sequence 4418, Ap
1207	47.6	4.8	633	17	US-10-369-493-41491	Sequence 41491, A	1292	47.6	4.8	670	16	US-10-132-350-29	Sequence 29, Appl
1208	47.6	4.8	780	15	US-10-156-761-6288	Sequence 6288, Ap	1293	47.6	4.8	670	16	US-10-132-350-31	Sequence 31, Appl
1209	47.6	4.8	825	19	US-10-762-107-43	Sequence 43, Appl	1294	47.6	4.8	693	15	US-10-156-761-1183	Sequence 1183, Ap
1210	47.6	4.8	878	17	US-10-425-114-15378	Sequence 15378, A	1295	47.6	4.8	862	18	US-10-767-701-10425	Sequence 10425, Ap
1211	47.6	4.8	891	15	US-10-156-761-7285	Sequence 7285, Ap	1296	47.6	4.8	938	18	US-10-437-963-91705	Sequence 91705, A
1212	47.6	4.8	921	17	US-10-282-122A-7524	Sequence 7524, Ap	1297	47.6	4.8	951	18	US-10-437-963-86145	Sequence 86145, A
1213	47.6	4.8	967	18	US-10-425-115-66497	Sequence 66497, A	1298	47.6	4.8	996	15	US-10-156-761-7396	Sequence 7396, Ap
1214	47.6	4.8	968	17	US-10-425-114-19397	Sequence 19397, A	1299	47.6	4.8	1050	18	US-10-767-701-12642	Sequence 12642, A
1215	47.6	4.8	1026	17	US-10-259-194A-618	Sequence 618, App	1300	47.6	4.8	1195	18	US-10-425-115-172335	Sequence 172335
1216	47.6	4.8	1036	17	US-10-242-533A-53529	Sequence 53529, A	1301	47.6	4.8	1203	15	US-10-156-761-4664	Sequence 4664, Ap
1217	47.6	4.8	1036	17	US-10-085-783A-53529	Sequence 53529, A	1302	47.6	4.8	1236	18	US-10-425-115-73921	Sequence 73921, A
1218	47.6	4.8	1049	14	US-10-123-155-358	Sequence 358, App	1303	47.6	4.8	1345	17	US-10-425-114-24692	Sequence 24692, A
1219	47.6	4.8	1060	18	US-10-425-115-134347	Sequence 134347, A	1304	47.6	4.8	1404	17	US-10-282-122A-15189	Sequence 15189, A
1220	47.6	4.8	1110	15	US-10-156-761-4246	Sequence 4246, Ap	1305	47.6	4.8	1420	17	US-10-425-114-21968	Sequence 21968, A
1221	47.6	4.8	1176	17	US-10-369-493-40494	Sequence 40494, A	1306	47.6	4.8	1438	18	US-10-425-115-84149	Sequence 84149, A
1222	47.6	4.8	1203	17	US-10-282-122A-25722	Sequence 25722, A	1307	47.6	4.8	1443	15	US-10-156-761-3397	Sequence 3397, Ap
1223	47.6	4.8	1257	18	US-10-437-963-64185	Sequence 64185, A	1308	47.6	4.8	1468	18	US-10-425-115-115629	Sequence 115629, A
1224	47.6	4.8	1282	17	US-10-425-114-23644	Sequence 23644, A	1309	47.6	4.8	1649	18	US-10-437-963-89113	Sequence 89113, A
1225	47.6	4.8	1329	15	US-10-156-761-1297	Sequence 1297, Ap	1310	47.6	4.8	1672	18	US-10-437-963-81182	Sequence 81182, A
1226	47.6	4.8	1344	17	US-10-425-114-16346	Sequence 16346, A	1311	47.6	4.8	1695	18	US-10-437-963-76703	Sequence 76703, A
1227	47.6	4.8	1376	18	US-10-437-963-10544	Sequence 10544, A	1312	47.6	4.8	1723	18	US-10-437-963-11515	Sequence 11515, A
1228	47.6	4.8	1403	18	US-10-425-115-68130	Sequence 68130, A	1313	47.6	4.8	1734	17	US-10-282-122A-25721	Sequence 25721, A
1229	47.6	4.8	1410	17	US-10-369-493-42819	Sequence 42819, A	1314	47.6	4.8	1741	15	US-10-425-114-17536	Sequence 17536, A
1230	47.6	4.8	1469	17	US-10-425-114-31292	Sequence 31292, A	1315	47.6	4.8	1848	15	US-10-156-761-3041	Sequence 3041, Ap
1231	47.6	4.8	1522	17	US-10-369-493-31928	Sequence 31928, A	1316	47.6	4.8	1900	18	US-10-437-963-28228	Sequence 28228, A
1232	47.6	4.8	1644	18	US-10-425-115-14950	Sequence 14950, A	1317	47.6	4.8	1992	17	US-10-425-114-28230	Sequence 28230, A
1233	47.6	4.8	1661	18	US-10-437-963-12797	Sequence 12797, A	1318	47.6	4.8	2041	18	US-10-425-115-41669	Sequence 41669, A
1234	47.6	4.8	1699	17	US-10-425-114-17162	Sequence 17162, A	1319	47.6	4.8	2076	15	US-10-156-761-5585	Sequence 5585, Ap
1235	47.6	4.8	1713	18	US-10-324-967-33	Sequence 33, Appl	1320	47.6	4.8	2124	18	US-10-437-963-57642	Sequence 57642, A
1236	47.6	4.8	1956	15	US-10-156-761-5591	Sequence 5591, Ap	1321	47.6	4.8	2181	18	US-10-437-963-102020	Sequence 102020
1237	47.6	4.8	1970	17	US-10-425-114-22993	Sequence 22993, A	1322	47.6	4.8	2316	15	US-10-156-761-4416	Sequence 4416, Ap
1238	47.6	4.8	1971	16	US-10-190-435-49	Sequence 49, Appl	1323	47.6	4.8	2354	17	US-10-425-114-28070	Sequence 28070, A
1239	47.6	4.8	1971	16	US-10-241-009-38	Sequence 38, Appl	1324	47.6	4.8	2354	18	US-10-425-115-33746	Sequence 33746, A
1240	47.6	4.8	1971	16	US-10-190-434B-38	Sequence 38, Appl	1325	47.6	4.8	2354	18	US-10-715-872-155	Sequence 155, App
1241	47.6	4.8	1971	16	US-10-190-305A-48	Sequence 48, Appl	1326	47.6	4.8	2463	17	US-10-282-122A-13810	Sequence 13810, A
1242	47.6	4.8	1971	16	US-10-190-305A-54	Sequence 54, Appl	1327	47.6	4.8	2665	17	US-10-425-114-3437	Sequence 3437, Ap
1243	47.6	4.8	2078	19	US-10-488-056-20	Sequence 20, Appl	1328	47.6	4.8	2899	18	US-10-437-963-1877	Sequence 1877, Ap
1244	47.6	4.8	2111	18	US-10-437-963-3473	Sequence 3473, A	1329	47.6	4.8	2883	17	US-10-282-122A-11335	Sequence 11335, A
1245	47.6	4.8	2175	17	US-10-369-493-40571	Sequence 40571, A	1330	47.6	4.8	3629	16	US-10-289-757-9	Sequence 9, Appl

1331	47.4	4.8	3633	16	US-10-289-757-1330	Sequence 130, App	1404	47.2	4.8	3097	17	US-10-222-772-61	Sequence 61, Appl
1332	47.4	4.8	8244	17	US-10-402-842-3	Sequence 3, Appl	1405	47.2	4.8	3132	9	US-09-737-149-7	Sequence 7, Appl
1333	47.4	4.8	47988	17	US-10-402-842-1	Sequence 1, Appl	1406	47.2	4.8	3132	17	US-10-701-283-7	Sequence 7, Appl
1334	47.4	4.8	50937	10	US-09-808-880-1	Sequence 1, Appl	1407	47.2	4.8	3132	17	US-10-211-028-131	Sequence 131, App
c1335	47.4	4.8	50937	10	US-09-808-880-1	Sequence 1, Appl	1408	47.2	4.8	3639	16	US-10-241-009-33	Sequence 33, Appl
c1336	47.4	4.8	137560	18	US-10-481-112-1	Sequence 1, Appl	1409	47.2	4.8	3639	16	US-10-190-434B-33	Sequence 33, Appl
1337	47.2	4.8	564	18	US-10-437-963-72922	Sequence 72922, A	1410	47.2	4.8	3639	16	US-10-190-305A-35	Sequence 35, Appl
1338	47.2	4.8	619	18	US-10-425-115-183789	Sequence 183789, A	1411	47.2	4.8	3355	17	US-10-108-260A-804	Sequence 804, App
1339	47.2	4.8	852	17	US-10-282-122A-11557	Sequence 11557, A	1412	47.2	4.8	4319	17	US-10-387-336-6	Sequence 6, Appl
1340	47.2	4.8	867	18	US-10-425-115-105816	Sequence 105816, A	c1413	47.2	4.8	5676	19	US-10-042-665A-1	Sequence 1, Appl
1341	47.2	4.8	918	15	US-10-425-115-105816	Sequence 105816, A	1414	47.2	4.8	6402	19	US-10-486-706-322	Sequence 322, App
1342	47.2	4.8	962	18	US-10-767-701-9413	Sequence 9413, Ap	1415	47.2	4.8	11220	9	US-09-861-289-32	Sequence 32, Appl
1343	47.2	4.8	1011	18	US-10-425-115-135441	Sequence 135441, A	1416	47.2	4.8	11220	9	US-09-860-846-32	Sequence 32, Appl
1344	47.2	4.8	1014	15	US-10-156-761-5551	Sequence 5551, Ap	1417	47.2	4.8	11220	10	US-09-988-384B-32	Sequence 32, Appl
1345	47.2	4.8	1017	15	US-10-156-761-4338	Sequence 4338, Ap	1418	47.2	4.8	11220	10	US-09-836-821-32	Sequence 32, Appl
1346	47.2	4.8	1134	17	US-10-282-122A-14824	Sequence 14824, A	1419	47.2	4.8	11220	16	US-10-271-889-32	Sequence 32, Appl
1347	47.2	4.8	1152	15	US-10-156-761-1776	Sequence 1776, Ap	1420	47.2	4.8	23949	19	US-10-211-028-106	Sequence 106, App
c1348	47.2	4.8	1200	15	US-10-156-761-4546	Sequence 4546, Ap	1421	47.2	4.8	30000	11	US-09-980-217-1	Sequence 1, Appl
1349	47.2	4.8	1224	18	US-10-437-963-16908	Sequence 16908, A	c1422	47.2	4.8	53799	19	US-10-042-665A-3	Sequence 3, Appl
1350	47.2	4.8	1235	17	US-10-425-114-14166	Sequence 14166, A	1423	47	4.8	450	18	US-10-425-115-95875	Sequence 95875, A
1351	47.2	4.8	1237	18	US-10-425-115-137466	Sequence 137466, A	1424	47	4.8	536	17	US-10-338-110-119	Sequence 119, App
1352	47.2	4.8	1242	17	US-10-425-114-3643	Sequence 3643, Ap	c1425	47	4.8	546	18	US-10-425-115-77636	Sequence 77636, A
1353	47.2	4.8	1266	15	US-10-156-761-6436	Sequence 6436, Ap	1426	47	4.8	552	18	US-10-437-963-58537	Sequence 58537, A
1354	47.2	4.8	1314	17	US-10-425-115-119307	Sequence 119307, A	1427	47	4.8	647	17	US-10-425-114-16774	Sequence 16774, A
1355	47.2	4.8	1374	17	US-10-282-122A-11447	Sequence 11447, A	c1428	47	4.8	660	18	US-10-767-701-3246	Sequence 9246, Ap
1356	47.2	4.8	1382	18	US-10-425-115-120130	Sequence 120130, A	1429	47	4.8	675	17	US-10-282-122A-14648	Sequence 14648, A
1357	47.2	4.8	1386	17	US-10-363-493-42300	Sequence 42300, A	c1430	47	4.8	703	13	US-10-027-632-174146	Sequence 174146, A
1358	47.2	4.8	1395	17	US-10-282-122A-14398	Sequence 14398, A	c1431	47	4.8	703	17	US-10-027-632-174146	Sequence 174146, A
1359	47.2	4.8	1410	17	US-10-282-122A-25555	Sequence 25555, A	1432	47	4.8	758	9	US-09-902-331-5	Sequence 5, Appl
1360	47.2	4.8	1428	17	US-10-425-114-17352	Sequence 17352, A	1433	47	4.8	799	18	US-10-425-115-40891	Sequence 40891, A
1361	47.2	4.8	1431	15	US-10-156-761-7327	Sequence 7327, Ap	1434	47	4.8	851	18	US-10-425-115-38550	Sequence 38550, A
1362	47.2	4.8	1461	18	US-10-437-963-41312	Sequence 41312, A	1435	47	4.8	930	9	US-09-960-631A-4	Sequence 4, Appl
1363	47.2	4.8	1508	18	US-10-425-115-5536	Sequence 5536, Ap	1436	47	4.8	942	15	US-10-156-761-1702	Sequence 1702, Ap
1364	47.2	4.8	1513	17	US-10-425-114-33896	Sequence 33896, A	1437	47	4.8	1001	18	US-10-425-115-54065	Sequence 54065, A
c1365	47.2	4.8	1532	18	US-10-437-963-66895	Sequence 66895, A	1438	47	4.8	1120	17	US-10-294-445-22	Sequence 22, Appl
1366	47.2	4.8	1616	17	US-10-264-049-889	Sequence 889, App	1439	47	4.8	1245	15	US-10-156-761-2391	Sequence 2391, Ap
1367	47.2	4.8	1633	18	US-10-437-963-47476	Sequence 47476, A	1440	47	4.8	1293	17	US-10-107-431-46	Sequence 46, Appl
1368	47.2	4.8	1680	10	US-09-899-575-76	Sequence 76, Appl	1441	47	4.8	1354	17	US-10-264-049-523	Sequence 523, App
1369	47.2	4.8	1737	16	US-10-023-366-25063	Sequence 25063, A	1442	47	4.8	1536	17	US-10-282-122A-15096	Sequence 15096, A
c1370	47.2	4.8	1738	16	US-10-023-366-25470	Sequence 25470, A	1443	47	4.8	1701	18	US-10-425-115-168526	Sequence 168526, A
1371	47.2	4.8	1758	17	US-10-425-114-16348	Sequence 16348, A	1444	47	4.8	1713	15	US-10-156-761-2661	Sequence 2661, Ap
c1372	47.2	4.8	1896	17	US-10-381-779-16	Sequence 16, Appl	c1445	47	4.8	1714	18	US-10-739-930-1853	Sequence 1853, Ap
1373	47.2	4.8	1965	18	US-10-437-963-7490	Sequence 7490, Ap	c1446	47	4.8	1791	18	US-10-437-963-41437	Sequence 41437, A
c1374	47.2	4.8	1977	10	US-09-899-575-70	Sequence 70, Appl	1447	47	4.8	1881	18	US-10-437-963-61846	Sequence 61846, A
1375	47.2	4.8	1977	16	US-10-241-009-41	Sequence 41, Appl	1448	47	4.8	1968	17	US-10-282-122A-11496	Sequence 11496, A
1376	47.2	4.8	1977	16	US-10-190-434B-41	Sequence 41, Appl	1449	47	4.8	2013	15	US-10-156-761-1281	Sequence 1281, Ap
1377	47.2	4.8	1977	16	US-10-190-305A-51	Sequence 51, Appl	1450	47	4.8	2125	18	US-10-425-115-110021	Sequence 110021, A
1378	47.2	4.8	1989	16	US-10-241-009-47	Sequence 47, Appl	c1451	47	4.8	2335	19	US-10-734-049A-311	Sequence 311, App
1379	47.2	4.8	1989	16	US-10-190-434B-47	Sequence 47, Appl	1452	47	4.8	2848	17	US-10-425-114-30246	Sequence 30246, A
1380	47.2	4.8	2156	18	US-10-437-963-614	Sequence 614, App	1453	47	4.8	2890	17	US-10-425-114-32060	Sequence 32060, A
1381	47.2	4.8	2156	18	US-10-437-963-614	Sequence 614, App	c1454	47	4.8	3281	18	US-10-425-115-128924	Sequence 128924, A
1382	47.2	4.8	2145	16	US-10-241-009-35	Sequence 35, Appl	1455	47	4.8	80161	17	US-10-329-148A-1	Sequence 1, Appl
1383	47.2	4.8	2145	16	US-10-190-434B-35	Sequence 35, Appl	c1456	47	4.8	85692	17	US-10-461-194-1	Sequence 1, Appl
1384	47.2	4.8	2145	16	US-10-190-305A-43	Sequence 43, Appl	1457	46.8	4.7	296	15	US-10-174-693-195	Sequence 195, App
1385	47.2	4.8	2156	18	US-10-437-963-614	Sequence 614, App	1458	46.8	4.7	469	18	US-10-767-701-29716	Sequence 29716, A
1386	47.2	4.8	2312	17	US-10-387-336-84	Sequence 84, Appl	1459	46.8	4.7	527	18	US-10-425-115-97681	Sequence 97681, A
1387	47.2	4.8	2472	16	US-10-241-009-32	Sequence 32, Appl	c1460	46.8	4.7	528	18	US-10-437-963-18519	Sequence 18519, A
1388	47.2	4.8	2472	16	US-10-190-434B-32	Sequence 32, Appl	1461	46.8	4.7	564	18	US-10-437-963-76371	Sequence 76371, A
1389	47.2	4.8	2472	16	US-10-190-305A-34	Sequence 34, Appl	c1462	46.8	4.7	570	18	US-10-767-701-2473	Sequence 2473, Ap
1390	47.2	4.8	2475	18	US-10-437-963-82289	Sequence 82289, A	1463	46.8	4.7	588	18	US-10-437-963-7127	Sequence 29714, A
1391	47.2	4.8	2653	18	US-10-425-115-59271	Sequence 59271, A	1464	46.8	4.7	642	18	US-10-437-963-7127	Sequence 7127, Ap
1392	47.2	4.8	2691	10	US-09-934-070-9	Sequence 9, Appl	c1465	46.8	4.7	663	17	US-10-389-647-191	Sequence 191, App
1393	47.2	4.8	2691	17	US-10-222-772-9	Sequence 9, Appl	1466	46.8	4.7	768	9	US-09-938-842A-812	Sequence 812, App
1394	47.2	4.8	2706	17	US-10-416-793-1	Sequence 1, Appl	1467	46.8	4.7	768	11	US-09-938-842A-812	Sequence 812, App
c1395	47.2	4.8	2751	17	US-10-282-122A-26039	Sequence 26039, A	1468	46.8	4.7	801	11	US-09-894-273-3	Sequence 3, Appl
1396	47.2	4.8	2898	9	US-09-737-149-3	Sequence 3, Appl	1469	46.8	4.7	982	17	US-10-425-114-14294	Sequence 14294, A
1397	47.2	4.8	2898	9	US-09-737-149-3	Sequence 3, Appl	1470	46.8	4.7	984	17	US-10-282-122A-25620	Sequence 25620, A
1398	47.2	4.8	2916	9	US-09-737-149-5	Sequence 5, Appl	1471	46.8	4.7	1139	17	US-10-425-114-33569	Sequence 33569, A
1399	47.2	4.8	2916	9	US-09-737-149-5	Sequence 5, Appl	1472	46.8	4.7	1269	18	US-10-425-115-100962	Sequence 100962, A
1400	47.2	4.8	3015	16	US-09-899-575-62	Sequence 62, Appl	c1473	46.8	4.7	1345	18	US-10-425-115-33858	Sequence 93858, A
1401	47.2	4.8	3015	16	US-10-190-305A-44	Sequence 44, Appl	1474	46.8	4.7	1375	17	US-10-425-114-33375	Sequence 23375, A
1402	47.2	4.8	3096	10	US-09-934-070-5	Sequence 5, Appl	1475	46.8	4.7	1413	18	US-10-425-115-135998	Sequence 135998, A
1403	47.2	4.8	3096	17	US-10-222-772-5	Sequence 5, Appl	c1476	46.8	4.7	1464	17	US-10-282-122A-28163	Sequence 28163, A

1477	46.8	4.7	1695	18	US-10-437-963-51411	Sequence 51411, A
1478	46.8	4.7	1722	19	US-10-762-107-81	Sequence 81, Appl
c1479	46.8	4.7	1735	18	US-10-437-963-32738	Sequence 32738, A
c1480	46.8	4.7	1748	18	US-10-437-963-85706	Sequence 85706, A
1481	46.8	4.7	1773	18	US-10-437-963-90868	Sequence 90868, A
1482	46.8	4.7	1819	18	US-10-437-963-99823	Sequence 99823, A
1483	46.8	4.7	2013	17	US-10-369-493-31439	Sequence 31439, A
1484	46.8	4.7	2034	15	US-10-156-761-3529	Sequence 3529, Ap
1485	46.8	4.7	2151	17	US-10-425-114-24961	Sequence 24961, A
1486	46.8	4.7	2226	17	US-10-369-493-47118	Sequence 47118, A
1487	46.8	4.7	2274	15	US-10-156-761-5313	Sequence 5313, Ap
1488	46.8	4.7	2739	17	US-10-282-122A-25536	Sequence 25536, A
1489	46.8	4.7	3240	18	US-10-437-963-3533	Sequence 3533, Ap
1490	46.8	4.7	3972	15	US-10-156-761-5427	Sequence 5427, Ap
1491	46.8	4.7	4176	13	US-10-098-841-34	Sequence 34, Appl
1492	46.8	4.7	5862	16	US-10-132-134-15	Sequence 15, Appl
1493	46.8	4.7	10232	17	US-10-282-122A-25487	Sequence 25487, A
1494	46.8	4.7	25000	11	US-09-968-007A-215	Sequence 215, App
1495	46.8	4.7	25000	19	US-10-843-641A-6685	Sequence 6685, Ap
1499	46.6	4.7	462	18	US-10-437-963-204	Sequence 204, App
1500	46.6	4.7	487	18	US-10-425-115-7683	Sequence 7683, Ap

Search completed: April 19, 2005, 17:41:13

Job time : 718 secs

**THIS PAGE BLANK (USP10)**





101	56	5.7	1908	4	US-09-252-991A-14353	Sequence 14353, A	C 174	54.2	5.5	27707	4	US-09-902-540-1226	Sequence 1226, Ap
102	56	5.7	2109	3	US-09-370-838-153	Sequence 153, App	C 175	54	5.5	4530	4	US-09-799-451-881	Sequence 881, App
103	56	5.7	2109	3	US-09-854-133-153	Sequence 153, App	C 176	53.8	5.4	897	4	US-09-902-540-7777	Sequence 7777, Ap
104	56	5.7	2326	4	US-09-902-540-8346	Sequence 8346, Ap	C 177	53.8	5.4	1524	4	US-09-902-540-5671	Sequence 5671, Ap
105	56	5.7	4257	2	US-08-690-473-1	Sequence 1, Appl	C 178	53.8	5.4	2082	4	US-09-818-780-67	Sequence 67, Appl
106	56	5.7	4257	3	US-09-259-821A-1	Sequence 1, Appl	C 179	53.8	5.4	3813	4	US-09-902-540-7085	Sequence 7085, Ap
107	56	5.7	4257	3	US-08-843-659-1	Sequence 1, Appl	C 180	53.8	5.4	3815	4	US-09-902-540-634	Sequence 634, App
108	56	5.7	4257	4	US-09-825-288A-1	Sequence 1, Appl	C 181	53.8	5.4	6250	4	US-09-902-540-773	Sequence 773, App
109	56	5.7	4263	4	US-09-902-540-4659	Sequence 4659, Ap	C 182	53.8	5.4	44377	2	US-08-804-227C-7	Sequence 7, Appl
110	56	5.7	8738	4	US-09-902-540-873	Sequence 873, App	C 183	53.8	5.4	44377	2	US-08-804-198-1	Sequence 1, Appl
111	56	5.7	12001	1	US-08-458-568A-11	Sequence 11, Appl	C 184	53.8	5.4	50725	4	US-09-902-540-1271	Sequence 1271, Ap
112	56	5.7	22807	4	US-09-902-540-1214	Sequence 1214, Ap	C 185	53.8	5.4	114793	4	US-10-148-806-3	Sequence 3, Appl
113	56	5.7	29384	4	US-09-902-540-1229	Sequence 1229, Ap	C 186	53.6	5.4	14823	4	US-09-902-540-1087	Sequence 1087, Ap
114	55.8	5.6	639	4	US-09-902-540-6214	Sequence 6214, Ap	C 187	53.6	5.4	72704	4	US-09-902-540-1273	Sequence 1273, Ap
115	55.8	5.6	759	4	US-09-902-540-6214	Sequence 6214, Ap	C 188	53.4	5.4	969	4	US-09-902-540-7423	Sequence 7423, Ap
116	55.8	5.6	1266	3	US-09-249-585A-2	Sequence 3, Appl	C 189	53.4	5.4	1293	4	US-09-902-540-6161	Sequence 6161, Ap
117	55.8	5.6	1926	4	US-09-410-399-3	Sequence 3, Appl	C 190	53.4	5.4	1675	4	US-09-902-540-302	Sequence 302, App
118	55.8	5.6	2580	3	US-09-050-863-2	Sequence 2, Appl	C 191	53.4	5.4	2248	3	US-09-345-214-20	Sequence 20, Appl
119	55.8	5.6	2580	3	US-09-359-081-2	Sequence 2, Appl	C 192	53.4	5.4	2248	3	US-09-743-980-20	Sequence 20, Appl
120	55.8	5.6	5452	2	US-09-130-114-1	Sequence 1, Appl	C 193	53.4	5.4	2338	1	US-08-425-069-1	Sequence 1, Appl
121	55.8	5.6	8705	4	US-09-647-344A-14	Sequence 14, Appl	C 194	53.4	5.4	2338	2	US-08-317-8448-1	Sequence 1, Appl
122	55.8	5.6	9551	1	US-08-056-200-93	Sequence 93, Appl	C 195	53.4	5.4	6645	4	US-09-902-540-8819	Sequence 8819, Ap
123	55.8	5.6	9551	2	US-08-800-644-93	Sequence 93, Appl	C 196	53.4	5.4	7317	4	US-09-902-540-938	Sequence 938, App
124	55.8	5.6	9600	3	US-08-910-647-1	Sequence 1, Appl	C 197	53.4	5.4	10210	4	US-09-902-540-938	Sequence 938, App
125	55.8	5.6	9600	3	US-09-902-540-1041	Sequence 1, Appl	C 198	53.2	5.4	873	4	US-09-902-540-2517	Sequence 2517, Ap
126	55.8	5.6	10596	1	US-07-884-811-15	Sequence 15, Appl	C 199	53.2	5.4	1341	4	US-09-902-540-4938	Sequence 4938, Ap
127	55.8	5.6	10596	1	US-07-885-971-15	Sequence 15, Appl	C 200	53.2	5.4	1344	4	US-09-902-540-7558	Sequence 7558, Ap
128	55.8	5.6	10596	1	US-08-087-783A-15	Sequence 15, Appl	C 201	53.2	5.4	1575	4	US-09-902-540-6429	Sequence 6429, Ap
129	55.8	5.6	10596	1	US-08-194-088B-15	Sequence 15, Appl	C 202	53.2	5.4	1576	4	US-09-902-540-442	Sequence 442, App
130	55.8	5.6	10596	2	US-08-194-087-15	Sequence 15, Appl	C 203	53.2	5.4	6155	4	US-09-902-540-737	Sequence 737, App
131	55.8	5.6	10596	5	PCR-US93-04648-15	Sequence 15, Appl	C 204	53.2	5.4	30780	4	US-09-902-540-1243	Sequence 1243, Ap
132	55.8	5.6	16080	4	US-09-724-566A-48	Sequence 48, Appl	C 205	53	5.4	632	3	US-09-221-017B-655	Sequence 655, App
133	55.8	5.6	16080	4	US-09-471-669A-48	Sequence 48, Appl	C 206	52.8	5.3	591	4	US-09-902-540-9564	Sequence 9564, Ap
134	55.8	5.6	29103	4	US-09-902-540-1236	Sequence 1236, Ap	C 207	52.8	5.3	1071	4	US-09-902-540-4828	Sequence 4828, Ap
135	55.6	5.6	1164	4	US-09-902-540-5610	Sequence 5610, Ap	C 208	52.8	5.3	1080	4	US-09-902-540-5147	Sequence 5147, Ap
136	55.6	5.6	11812	4	US-09-902-540-1041	Sequence 1041, Ap	C 209	52.8	5.3	1236	1	US-08-440-856A-1	Sequence 1, Appl
137	55.4	5.6	774	4	US-09-252-991A-9665	Sequence 9665, Ap	C 210	52.8	5.3	26659	4	US-09-902-540-1237	Sequence 1237, Ap
138	55.4	5.6	3033	4	US-09-724-797-81	Sequence 81, Appl	C 211	52.8	5.3	29559	4	US-09-902-540-1254	Sequence 1254, Ap
139	55.2	5.6	1794	4	US-09-902-540-6985	Sequence 6985, Ap	C 212	52.6	5.3	888	4	US-09-902-540-7561	Sequence 7561, Ap
140	55.2	5.6	2010	4	US-09-902-540-9587	Sequence 9587, Ap	C 213	52.6	5.3	1446	4	US-09-902-540-8541	Sequence 8541, Ap
141	55.2	5.6	4042	4	US-09-902-540-609	Sequence 609, App	C 214	52.6	5.3	1458	4	US-09-902-540-5187	Sequence 5187, Ap
142	55.2	5.6	14807	4	US-09-902-540-1085	Sequence 1085, Ap	C 215	52.6	5.3	2561	4	US-09-616-289-48	Sequence 48, Appl
143	55	5.6	2358	4	US-09-902-540-2632	Sequence 2632, Ap	C 216	52.6	5.3	7295	4	US-09-902-540-924	Sequence 924, App
144	55	5.6	2559	4	US-09-657-013-40	Sequence 40, Appl	C 217	52.6	5.3	7713	4	US-09-902-540-900	Sequence 900, App
145	55	5.6	2559	4	US-09-949-016-1791	Sequence 1791, Ap	C 218	52.6	5.3	34199	4	US-09-902-540-1255	Sequence 1255, Ap
146	55	5.6	2567	4	US-09-949-016-567	Sequence 567, App	C 219	52.4	5.3	549	4	US-09-902-540-6777	Sequence 6777, Ap
147	55	5.6	17173	4	US-09-902-540-1122	Sequence 1122, Ap	C 220	52.4	5.3	591	4	US-09-902-540-6057	Sequence 6057, Ap
148	54.8	5.5	594	3	US-09-615-192A-105	Sequence 105, App	C 221	52.4	5.3	1591	4	US-09-902-540-250	Sequence 250, App
149	54.8	5.5	594	2	US-09-169-789-105	Sequence 105, App	C 222	52.4	5.3	3653	4	US-09-902-540-555	Sequence 555, App
150	54.8	5.5	607	2	US-08-975-316-23	Sequence 23, Appl	C 223	52.4	5.3	3978	3	US-08-726-214-1	Sequence 1, Appl
151	54.8	5.5	607	3	US-09-615-192A-23	Sequence 23, Appl	C 224	52.4	5.3	5640	4	US-09-620-312D-41	Sequence 41, Appl
152	54.8	5.5	607	4	US-09-169-789-23	Sequence 23, Appl	C 225	52.4	5.3	11220	4	US-09-949-016-5061	Sequence 5061, Ap
153	54.8	5.5	1350	4	US-09-902-540-8483	Sequence 8483, Ap	C 226	52.2	5.3	4296	4	US-09-902-540-3291	Sequence 3291, Ap
154	54.8	5.5	5673	4	US-09-902-540-8259	Sequence 8259, Ap	C 227	52.2	5.3	4455	4	US-09-902-540-7119	Sequence 7119, Ap
155	54.8	5.5	7513	4	US-09-902-540-892	Sequence 892, App	C 228	52.2	5.3	4458	4	US-09-902-540-650	Sequence 650, App
156	54.8	5.5	8704	4	US-09-902-540-854	Sequence 854, App	C 229	52.2	5.3	17727	4	US-09-902-540-1152	Sequence 1152, Ap
157	54.6	5.5	474	4	US-09-902-540-5898	Sequence 5898, Ap	C 230	52	5.3	693	4	US-09-902-540-9571	Sequence 9571, Ap
158	54.6	5.5	1257	4	US-09-902-540-8550	Sequence 8550, Ap	C 231	52	5.3	1152	4	US-09-902-540-5580	Sequence 5580, Ap
159	54.6	5.5	1358	4	US-09-902-540-166	Sequence 166, App	C 232	52	5.3	1209	4	US-09-902-540-147	Sequence 147, App
160	54.6	5.5	1308	3	US-08-937-067-18	Sequence 18, Appl	C 233	52	5.3	1248	4	US-09-252-991A-1681	Sequence 1681, Ap
161	54.6	5.5	2830	2	US-09-010-928B-1	Sequence 1, Appl	C 234	52	5.3	1302	4	US-09-252-991A-1437	Sequence 1437, Ap
162	54.6	5.5	3077	4	US-09-902-540-495	Sequence 495, App	C 235	52	5.3	1956	4	US-09-252-991A-1494	Sequence 1494, Ap
163	54.6	5.5	7562	4	US-09-902-540-902	Sequence 902, App	C 236	52	5.3	2586	4	US-09-902-540-5619	Sequence 5619, Ap
164	54.4	5.5	843	4	US-09-902-540-3428	Sequence 3428, Ap	C 237	52	5.3	1555	4	US-09-902-540-1096	Sequence 1096, Ap
165	54.4	5.5	2022	4	US-09-902-540-5510	Sequence 5510, Ap	C 238	52	5.3	4225	4	US-09-902-540-1269	Sequence 1269, Ap
166	54.4	5.5	2712	4	US-09-902-540-4301	Sequence 4301, Ap	C 239	51.8	5.2	498	4	US-09-252-991A-10580	Sequence 10580, A
167	54.4	5.5	18192	4	US-09-902-540-1162	Sequence 1162, Ap	C 240	51.8	5.2	561	4	US-09-252-991A-10684	Sequence 10684, A
168	54.4	5.5	41768	4	US-09-902-540-1266	Sequence 1266, Ap	C 241	51.8	5.2	1053	4	US-09-252-991A-10684	Sequence 6250, Ap
169	54.2	5.5	1374	4	US-09-902-540-4587	Sequence 4587, Ap	C 242	51.8	5.2	1149	4	US-09-902-540-6250	Sequence 3104, Ap
170	54.2	5.5	1689	4	US-09-902-540-3347	Sequence 3347, Ap	C 243	51.8	5.2	1233	4	US-09-252-991A-3104	Sequence 5243, Ap
171	54.2	5.5	1824	4	US-09-902-540-6709	Sequence 6709, Ap	C 244	51.8	5.2	1272	4	US-09-902-540-5243	Sequence 2867, Ap
172	54.2	5.5	4234	4	US-09-902-540-534	Sequence 534, App	C 245	51.8	5.2	1386	4	US-09-252-991A-2867	Sequence 9170, Ap
173	54.2	5.5	18537	4	US-09-902-540-1157	Sequence 1157, Ap	C 246	51.8	5.2	1581	4	US-09-902-540-9170	

C 247	51.8	5.2	1926	3	US-09-249-585A-4	Sequence 4, Appli	Sequence 4, Appli	320	50.4	5.1	1404	4	US-09-902-540-7362	Sequence 7362, Ap
C 248	51.8	5.2	1931	2	US-09-130-114-2	Sequence 2, Appli	Sequence 2, Appli	321	50.4	5.1	1818	4	US-09-902-540-5126	Sequence 5126, Ap
C 249	51.8	5.2	2075	4	US-09-087-031B-2	Sequence 2, Appli	Sequence 2, Appli	C 322	50.4	5.1	5121	4	US-09-902-540-704	Sequence 704, App
250	51.8	5.2	2075	4	US-09-546-043-1	Sequence 1, Appli	Sequence 1, Appli	323	50.4	5.1	23673	3	US-09-773-816-1	Sequence 1, Appli
251	51.8	5.2	2075	4	US-09-514-885-2	Sequence 2, Appli	Sequence 2, Appli	324	50.2	5.1	825	4	US-09-902-540-2941	Sequence 2941, Ap
252	51.8	5.2	2351	4	US-09-902-540-344	Sequence 344, App	Sequence 344, App	325	50.2	5.1	864	4	US-09-252-991A-10932	Sequence 10932, A
253	51.8	5.2	2469	4	US-09-949-016-428	Sequence 428, App	Sequence 428, App	326	50.2	5.1	930	4	US-09-902-540-3946	Sequence 3946, Ap
C 254	51.8	5.2	5097	4	US-09-902-540-5555	Sequence 5555, Ap	Sequence 5555, Ap	C 327	50.2	5.1	11587	4	US-09-902-540-3702	Sequence 3702, Ap
C 255	51.8	5.2	11612	4	US-09-902-540-981	Sequence 981, App	Sequence 981, App	C 328	50.2	5.1	2211	4	US-09-252-991A-11256	Sequence 11256, A
C 256	51.8	5.2	34316	4	US-09-902-540-1257	Sequence 1257, Ap	Sequence 1257, Ap	329	50.2	5.1	2289	4	US-09-252-991A-10995	Sequence 10995, A
C 257	51.8	5.2	41170	4	US-09-902-540-1267	Sequence 1267, Ap	Sequence 1267, Ap	330	50.2	5.1	2589	4	US-09-902-540-4601	Sequence 4601, Ap
C 258	51.6	5.2	591	4	US-09-902-540-4984	Sequence 1284, Ap	Sequence 1284, Ap	331	50.2	5.1	4826	4	US-09-772-304A-1	Sequence 1, Appli
C 259	51.6	5.2	1026	4	US-09-902-540-6694	Sequence 6694, Ap	Sequence 6694, Ap	C 332	50.2	5.1	12173	4	US-09-902-540-1022	Sequence 1022, Ap
C 260	51.6	5.2	1065	4	US-09-902-540-4327	Sequence 4327, Ap	Sequence 4327, Ap	C 333	50.2	5.1	21295	4	US-09-902-540-1194	Sequence 1194, Ap
C 261	51.6	5.2	1311	4	US-09-252-991A-14065	Sequence 14065, A	Sequence 14065, A	C 334	50.2	5.1	23417	4	US-09-902-540-1207	Sequence 1207, Ap
C 262	51.6	5.2	1581	4	US-09-902-540-3972	Sequence 3972, Ap	Sequence 3972, Ap	335	50.2	5.1	27490	4	US-09-902-540-1227	Sequence 1227, Ap
C 263	51.6	5.2	2850	4	US-09-252-991A-14205	Sequence 14205, A	Sequence 14205, A	336	50	5.1	636	4	US-09-902-540-4812	Sequence 4812, Ap
C 264	51.6	5.2	4353	4	US-09-902-540-529	Sequence 529, App	Sequence 529, App	337	50	5.1	888	4	US-09-311-021-155	Sequence 155, App
C 265	51.6	5.2	9369	4	US-10-237-551-190	Sequence 190, App	Sequence 190, App	338	50	5.1	1272	4	US-09-902-540-8789	Sequence 8789, Ap
C 266	51.6	5.2	9369	4	US-10-237-551-247	Sequence 247, App	Sequence 247, App	339	50	5.1	1365	4	US-09-902-540-5489	Sequence 5489, Ap
C 267	51.6	5.2	18324	4	US-09-902-540-1196	Sequence 1196, Ap	Sequence 1196, Ap	340	50	5.1	1579	4	US-09-902-540-4020	Sequence 4020, Ap
C 268	51.6	5.2	23951	4	US-09-902-540-1245	Sequence 1245, Ap	Sequence 1245, Ap	C 341	50	5.1	1619	4	US-09-902-540-331	Sequence 331, App
C 269	51.6	5.2	25733	4	US-09-902-540-1215	Sequence 1215, Ap	Sequence 1215, Ap	342	50	5.1	1695	4	US-09-902-540-4319	Sequence 4319, Ap
C 270	51.4	5.2	1368	4	US-09-902-540-9337	Sequence 9337, Ap	Sequence 9337, Ap	343	50	5.1	1702	4	US-09-902-540-8057	Sequence 8057, Ap
C 271	51.4	5.2	7847	4	US-09-799-451-591	Sequence 591, App	Sequence 591, App	344	50	5.1	2073	4	US-09-902-540-2661	Sequence 2661, Ap
C 272	51.4	5.2	8604	4	US-09-902-540-5331	Sequence 5331, Ap	Sequence 5331, Ap	345	50	5.1	2193	4	US-09-902-540-4585	Sequence 4585, Ap
C 273	51.4	5.2	10486	4	US-09-902-540-997	Sequence 997, App	Sequence 997, App	346	50	5.1	2190	4	US-09-902-540-8946	Sequence 8946, Ap
C 274	51.4	5.2	35399	4	US-09-902-540-1260	Sequence 1260, Ap	Sequence 1260, Ap	C 347	50	5.1	2319	4	US-09-902-540-2035	Sequence 2035, Ap
C 275	51.2	5.2	762	4	US-09-902-540-5117	Sequence 5117, Ap	Sequence 5117, Ap	348	50	5.1	2699	4	US-09-902-540-6501	Sequence 6501, Ap
C 276	51.2	5.2	1395	4	US-09-902-540-3473	Sequence 3473, Ap	Sequence 3473, Ap	349	50	5.1	2700	4	US-09-902-540-467	Sequence 467, App
C 277	51.2	5.2	2277	1	US-08-676-967-5	Sequence 5, Appli	Sequence 5, Appli	350	50	5.1	2733	4	US-09-902-540-3104	Sequence 3104, Ap
C 278	51.2	5.2	2277	1	US-08-676-974-5	Sequence 5, Appli	Sequence 5, Appli	351	50	5.1	7160	4	US-09-902-540-821	Sequence 821, App
C 279	51.2	5.2	2277	2	US-09-098-487-5	Sequence 5, Appli	Sequence 5, Appli	C 352	50	5.1	8967	4	US-09-902-540-954	Sequence 954, App
C 280	51.2	5.2	2757	4	US-09-902-540-5701	Sequence 5701, Ap	Sequence 5701, Ap	353	50	5.1	10096	4	US-09-902-540-935	Sequence 935, App
C 281	51.2	5.2	3699	4	US-09-902-540-3731	Sequence 3731, Ap	Sequence 3731, Ap	C 354	50	5.1	12730	4	US-09-105-537-30	Sequence 30, Appl
C 282	51.2	5.2	17188	4	US-09-902-540-1166	Sequence 1166, Ap	Sequence 1166, Ap	355	50	5.1	13842	3	US-09-105-537-30	Sequence 30, Appl
C 283	51.2	5.2	19112	4	US-09-902-540-1181	Sequence 1181, Ap	Sequence 1181, Ap	356	50	5.1	15499	4	US-09-902-540-1140	Sequence 1140, Ap
C 284	51.2	5.2	28058	4	US-09-902-540-1252	Sequence 1252, Ap	Sequence 1252, Ap	C 357	50	5.1	19068	4	US-09-902-540-1123	Sequence 1123, Ap
C 285	51.2	5.2	50725	4	US-09-902-540-1271	Sequence 1271, Ap	Sequence 1271, Ap	C 358	50	5.1	26533	4	US-09-902-540-1199	Sequence 1199, Ap
C 286	51	5.2	501	4	US-09-252-991A-11947	Sequence 11947, A	Sequence 11947, A	359	50	5.1	36778	3	US-09-105-537-5	Sequence 5, Appli
C 287	51	5.2	600	4	US-09-902-540-4489	Sequence 4489, Ap	Sequence 4489, Ap	360	50	5.1	38506	4	US-09-320-878-19	Sequence 19, Appl
C 288	51	5.2	1341	4	US-09-902-540-6300	Sequence 6300, Ap	Sequence 6300, Ap	361	50	5.1	38506	4	US-09-141-908-1	Sequence 1, Appli
C 289	51	5.2	1344	4	US-09-902-540-381	Sequence 381, App	Sequence 381, App	362	50	5.1	38506	4	US-09-657-440-19	Sequence 19, Appl
C 290	51	5.2	1500	4	US-09-252-991A-11907	Sequence 11907, A	Sequence 11907, A	C 363	50	5.1	229354	4	US-09-705-400-64	Sequence 64, Appl
C 291	51	5.2	2118	4	US-09-902-540-3960	Sequence 3960, Ap	Sequence 3960, Ap	364	49.8	5.0	1644	4	US-09-902-540-4613	Sequence 4613, Ap
C 292	51	5.2	2561	4	US-09-616-289-48	Sequence 48, Appl	Sequence 48, Appl	365	49.8	5.0	3003	4	US-09-252-991A-14790	Sequence 14790, A
C 293	51	5.2	3381	4	US-09-902-540-7493	Sequence 7493, Ap	Sequence 7493, Ap	366	49.8	5.0	3113	4	US-09-894-988A-52	Sequence 52, Appl
C 294	51	5.2	6269	4	US-09-902-540-726	Sequence 726, App	Sequence 726, App	367	49.8	5.0	3113	4	US-10-237-551-52	Sequence 52, Appl
C 295	51	5.2	8438	1	US-07-945-283-1	Sequence 1, Appli	Sequence 1, Appli	368	49.8	5.0	3132	4	US-09-252-991A-14540	Sequence 14540, A
C 296	51	5.2	10593	4	US-09-902-540-1030	Sequence 1030, Ap	Sequence 1030, Ap	369	49.8	5.0	3147	2	US-08-781-802-7	Sequence 7, Appli
C 297	51	5.2	18324	4	US-09-902-540-1196	Sequence 1196, Ap	Sequence 1196, Ap	370	49.8	5.0	3147	3	US-08-694-078-7	Sequence 7, Appli
C 298	50.8	5.1	741	4	US-09-724-797-73	Sequence 73, Appl	Sequence 73, Appl	371	49.8	5.0	3147	3	US-09-058-260-7	Sequence 7, Appli
C 299	50.8	5.1	1047	4	US-09-902-540-9236	Sequence 9236, Ap	Sequence 9236, Ap	372	49.8	5.0	3345	4	US-09-894-988A-49	Sequence 49, Appl
C 300	50.8	5.1	1155	3	US-08-818-112-12	Sequence 12, Appl	Sequence 12, Appl	373	49.8	5.0	3345	4	US-10-237-551-49	Sequence 49, Appl
C 301	50.8	5.1	1155	3	US-09-056-556-12	Sequence 12, Appl	Sequence 12, Appl	374	49.8	5.0	3345	4	US-10-237-551-189	Sequence 189, App
C 302	50.8	5.1	1155	3	US-09-072-596-12	Sequence 12, Appl	Sequence 12, Appl	C 375	49.8	5.0	3411	4	US-09-252-991A-14823	Sequence 14823, A
C 303	50.8	5.1	1155	3	US-09-072-596-12	Sequence 12, Appl	Sequence 12, Appl	376	49.8	5.0	9521	4	US-09-902-540-953	Sequence 953, App
C 304	50.8	5.1	1155	4	US-09-072-967-12	Sequence 12, Appl	Sequence 12, Appl	C 377	49.8	5.0	27490	4	US-09-902-540-1227	Sequence 1227, Ap
C 305	50.8	5.1	1380	4	US-09-902-540-3259	Sequence 3259, Ap	Sequence 3259, Ap	C 378	49.6	5.0	678	4	US-09-252-991A-2221	Sequence 2221, Ap
C 306	50.8	5.1	1850	4	US-09-902-540-3982	Sequence 3982, Ap	Sequence 3982, Ap	C 379	49.6	5.0	753	4	US-09-252-991A-2382	Sequence 2382, Ap
C 307	50.8	5.1	2032	4	US-09-902-540-8077	Sequence 8077, Ap	Sequence 8077, Ap	C 380	49.6	5.0	789	4	US-09-902-540-7266	Sequence 7266, Ap
C 308	50.8	5.1	7811	4	US-09-902-540-824	Sequence 824, App	Sequence 824, App	381	49.6	5.0	831	4	US-09-902-540-5618	Sequence 5618, Ap
C 309	50.8	5.1	9818	4	US-09-902-540-987	Sequence 987, App	Sequence 987, App	382	49.6	5.0	831	4	US-09-902-540-8404	Sequence 8404, Ap
C 310	50.8	5.1	19954	4	US-09-902-540-1150	Sequence 1150, Ap	Sequence 1150, Ap	383	49.6	5.0	867	4	US-09-902-540-7887	Sequence 7887, Ap
C 311	50.8	5.1	20232	4	US-09-902-540-1197	Sequence 1197, Ap	Sequence 1197, Ap	384	49.6	5.0	1137	4	US-09-902-540-3757	Sequence 3757, Ap
C 312	50.8	5.1	72704	4	US-09-902-540-1273	Sequence 1273, Ap	Sequence 1273, Ap	385	49.6	5.0	1743	4	US-09-949-016-945	Sequence 945, App
C 313	50.6	5.1	508	3	US-09-452-239-15	Sequence 15, Appl	Sequence 15, Appl	C 386	49.6	5.0	1743	4	US-09-949-016-2709	Sequence 2709, Ap
C 314	50.6	5.1	1011	4	US-09-902-540-5491	Sequence 5491, Ap	Sequence 5491, Ap	387	49.6	5.0	1752	4	US-09-902-540-8626	Sequence 8626, Ap
C 315	50.6	5.1	1521	4	US-09-902-540-7472	Sequence 7472, Ap	Sequence 7472, Ap	C 388	49.6	5.0	1765	4	US-10-237-551-225	Sequence 225, App
C 316	50.6	5.1	2448	4	US-09-902-540-5509	Sequence 5509, Ap	Sequence 5509, Ap	389	49.6	5.0	1929	4	US-09-902-540-9129	Sequence 9129, Ap
C 317	50.6	5.1	3588	4	US-09-902-540-4681	Sequence 4681, Ap	Sequence 4681, Ap	390	49.6	5.0	2814	4	US-09-252-991A-2537	Sequence 2537, Ap
C 318	50.6	5.1	14467	4	US-09-902-540-1058	Sequence 1058, Ap	Sequence 1058, Ap	391	49.6	5.0	4324	4	US-09-902-540-684	Sequence 684, App
C 319	50.6	5.1	24754	4	US-09-902-540-1230	Sequence 1230, Ap	Sequence 1230, Ap	392	49.6	5.0	5743	4	US-09-949-016-12687	Sequence 12687, A

C 393	49.6	5.0	5743	4	US-09-949-016-14451	Sequence 14451, A	C 466	49	5.0	77536	4	US-09-940-316B-1	Sequence 1, Appli
C 394	49.6	5.0	5808	4	US-09-902-540-794	Sequence 794, App	467	48.8	4.9	531	4	US-09-902-540-7089	Sequence 7089, Ap
C 395	49.6	5.0	5973	4	US-09-902-540-3951	Sequence 3951, Ap	468	48.8	4.9	543	4	US-09-902-540-5931	Sequence 5931, Ap
C 396	49.6	5.0	7561	4	US-09-902-540-882	Sequence 882, App	469	48.8	4.9	852	4	US-09-252-991A-7607	Sequence 7607, Ap
C 397	49.6	5.0	7661	4	US-09-902-540-912	Sequence 912, App	470	48.8	4.9	852	4	US-09-902-540-5894	Sequence 5894, Ap
C 398	49.6	5.0	10216	4	US-09-902-540-976	Sequence 976, App	C 471	48.8	4.9	1083	4	US-09-252-991A-8817	Sequence 8817, Ap
C 399	49.6	5.0	11612	4	US-09-902-540-981	Sequence 981, App	472	48.8	4.9	1194	4	US-09-902-540-4954	Sequence 4954, Ap
C 400	49.6	5.0	17897	4	US-09-902-540-1182	Sequence 1182, Ap	473	48.8	4.9	1227	4	US-09-252-991A-9232	Sequence 9232, Ap
C 401	49.6	5.0	22156	4	US-09-902-540-1195	Sequence 1195, Ap	474	48.8	4.9	1296	4	US-09-252-991A-9150	Sequence 9150, Ap
C 402	49.6	5.0	134890	4	US-09-949-016-15602	Sequence 15602, A	475	48.8	4.9	1403	4	US-09-902-540-163	Sequence 163, App
C 403	49.4	5.0	552	4	US-09-902-540-3608	Sequence 3608, Ap	476	48.8	4.9	1415	4	US-09-902-540-5962	Sequence 5962, Ap
C 404	49.4	5.0	1419	4	US-09-252-991A-152	Sequence 152, App	477	48.8	4.9	1495	4	US-09-902-540-203	Sequence 203, App
C 405	49.4	5.0	1692	4	US-09-252-991A-157	Sequence 157, App	478	48.8	4.9	1542	4	US-09-902-540-5690	Sequence 5690, Ap
C 406	49.4	5.0	1698	4	US-09-252-991A-186	Sequence 186, App	479	48.8	4.9	1782	4	US-09-902-540-5356	Sequence 5356, Ap
C 407	49.4	5.0	2091	4	US-10-237-551-78	Sequence 78, Appl	480	48.8	4.9	2232	4	US-09-252-991A-11756	Sequence 11756, A
C 408	49.4	5.0	2091	4	US-10-237-551-226	Sequence 226, App	C 481	48.8	4.9	2274	4	US-09-252-991A-11609	Sequence 11609, A
C 409	49.4	5.0	2118	4	US-10-237-551-87	Sequence 87, Appl	482	48.8	4.9	2613	4	US-09-252-991A-11836	Sequence 11836, A
C 410	49.4	5.0	2211	4	US-10-237-551-86	Sequence 86, Appl	C 483	48.8	4.9	2715	4	US-09-252-991A-8715	Sequence 8715, A
C 411	49.4	5.0	2214	3	US-08-864-038A-1	Sequence 1, Appli	C 484	48.8	4.9	4992	4	US-09-902-540-635	Sequence 635, App
C 412	49.4	5.0	2244	4	US-09-902-540-3217	Sequence 3217, Ap	C 485	48.8	4.9	8829	4	US-09-902-540-2387	Sequence 2387, Ap
C 413	49.4	5.0	2745	1	US-08-363-255-1	Sequence 1, Appli	C 486	48.8	4.9	15644	4	US-09-902-540-1133	Sequence 1133, Ap
C 414	49.4	5.0	2745	1	US-08-363-255-13	Sequence 13, Appl	C 487	48.8	4.9	17315	4	US-09-902-540-1103	Sequence 1103, Ap
C 415	49.4	5.0	2754	4	US-09-902-540-5587	Sequence 5587, Ap	C 488	48.8	4.9	18848	4	US-09-902-540-1174	Sequence 1174, Ap
C 416	49.4	5.0	3331	3	US-08-864-038A-2	Sequence 2, Appli	C 489	48.8	4.9	27219	4	US-09-902-540-1244	Sequence 1244, Ap
C 417	49.4	5.0	3331	3	US-08-864-038A-4	Sequence 4, Appli	C 490	48.8	4.9	34662	4	US-09-902-540-1261	Sequence 1261, Ap
C 418	49.4	5.0	3489	2	US-08-728-123A-1	Sequence 1, Appli	C 491	48.6	4.9	528	3	US-09-453-239-33	Sequence 33, Appl
C 419	49.4	5.0	3489	3	US-09-298-568-1	Sequence 1, Appli	C 492	48.6	4.9	1278	4	US-09-902-540-8457	Sequence 8457, Ap
C 420	49.4	5.0	3489	4	US-09-410-399-1	Sequence 1, Appli	C 493	48.6	4.9	1320	4	US-09-724-797-85	Sequence 85, Appl
C 421	49.4	5.0	3489	4	US-09-894-273-1	Sequence 1, Appli	C 494	48.6	4.9	1410	4	US-09-902-540-3735	Sequence 3735, Ap
C 422	49.4	5.0	8144	4	US-09-902-540-820	Sequence 820, Appl	C 495	48.6	4.9	1479	4	US-08-644-271-31	Sequence 31, Appl
C 423	49.4	5.0	17726	4	US-09-902-540-1148	Sequence 1148, Ap	C 496	48.6	4.9	1479	3	US-09-077-955-35	Sequence 35, Appl
C 424	49.4	5.0	20113	4	US-09-902-540-1173	Sequence 1173, Ap	C 497	48.6	4.9	1575	4	US-09-252-991A-11212	Sequence 11212, A
C 425	49.4	5.0	32207	2	US-08-770-379-20	Sequence 20, Appl	C 498	48.6	4.9	1620	4	US-09-252-991A-11146	Sequence 11146, A
C 426	49.4	5.0	32207	3	US-08-757-669A-20	Sequence 20, Appl	C 499	48.6	4.9	1893	4	US-09-902-540-4291	Sequence 4291, Ap
C 427	49.4	5.0	41927	3	US-09-230-371A-20	Sequence 20, Appl	C 500	48.6	4.9	2040	2	US-08-533-669A-5	Sequence 5, Appli
C 428	49.4	5.0	789	4	US-09-902-540-1268	Sequence 1268, Ap	C 501	48.6	4.9	2040	3	US-09-183-861-5	Sequence 5, Appli
C 429	49.2	5.0	789	4	US-09-252-991A-15913	Sequence 15913, A	C 502	48.6	4.9	2040	3	US-09-022-765-5	Sequence 5, Appli
C 430	49.2	5.0	795	4	US-09-252-991A-11852	Sequence 11852, A	C 503	48.6	4.9	2040	4	US-09-551-974A-5	Sequence 5, Appli
C 431	49.2	5.0	861	4	US-09-902-540-188	Sequence 188, App	C 504	48.6	4.9	2040	4	US-09-565-501A-5	Sequence 5, Appli
C 432	49.2	5.0	888	4	US-09-252-991A-16512	Sequence 16512, A	C 505	48.6	4.9	2040	4	US-09-639-206A-5	Sequence 5, Appli
C 433	49.2	5.0	1221	4	US-09-252-991A-11531	Sequence 11531, A	C 506	48.6	4.9	2040	4	US-08-874-923-5	Sequence 5, Appli
C 434	49.2	5.0	1263	4	US-09-252-991A-13467	Sequence 13467, A	C 507	48.6	4.9	2040	4	US-08-798-841-5	Sequence 5, Appli
C 435	49.2	5.0	1263	4	US-09-252-991A-13658	Sequence 13658, A	C 508	48.6	4.9	2274	4	US-09-902-540-4081	Sequence 4081, Ap
C 436	49.2	5.0	1512	4	US-09-252-991A-16092	Sequence 16092, A	C 509	48.6	4.9	2472	4	US-09-252-991A-11043	Sequence 11043, A
C 437	49.2	5.0	1521	4	US-09-252-991A-15778	Sequence 15778, A	C 510	48.6	4.9	2712	3	US-09-025-691-4	Sequence 4, Appli
C 438	49.2	5.0	1569	4	US-09-252-991A-15857	Sequence 15857, A	C 511	48.6	4.9	4276	4	US-09-949-016-4900	Sequence 4900, Ap
C 439	49.2	5.0	2133	4	US-09-902-540-8854	Sequence 8854, Ap	C 512	48.6	4.9	5065	4	US-09-949-016-744	Sequence 744, App
C 440	49.2	5.0	2401	4	US-09-902-540-15991	Sequence 15991, A	C 513	48.6	4.9	7190	4	US-09-902-540-843	Sequence 843, App
C 441	49.2	5.0	2481	4	US-09-902-540-1867	Sequence 1867, Ap	C 514	48.6	4.9	7686	4	US-09-949-016-13489	Sequence 13489, A
C 442	49.2	5.0	2541	4	US-09-902-540-8123	Sequence 8123, Ap	C 515	48.6	4.9	8590	4	US-09-902-540-889	Sequence 889, App
C 443	49.2	5.0	3218	3	US-09-593-589-3	Sequence 3, Appli	C 516	48.6	4.9	20113	4	US-09-902-540-1173	Sequence 1173, Ap
C 444	49.2	5.0	7325	4	US-09-949-016-13839	Sequence 13839, A	C 517	48.6	4.9	20250	4	US-09-902-540-1213	Sequence 1213, Ap
C 445	49.2	5.0	7846	4	US-09-902-540-830	Sequence 830, App	C 518	48.6	4.9	23847	4	US-09-902-540-1177	Sequence 1177, Ap
C 446	49.2	5.0	9993	4	US-09-902-540-942	Sequence 942, App	C 519	48.6	4.9	24602	4	US-09-902-540-1202	Sequence 1202, Ap
C 447	49	5.0	399	3	US-09-615-192A-193	Sequence 193, App	C 520	48.6	4.9	50453	4	US-09-949-016-15642	Sequence 15642, A
C 448	49	5.0	678	4	US-09-902-540-6290	Sequence 6290, Ap	C 521	48.6	4.9	152142	4	US-09-949-016-12486	Sequence 12486, A
C 449	49	5.0	843	4	US-09-724-797-33	Sequence 33, Appl	C 522	48.6	4.9	152132	4	US-09-949-016-13845	Sequence 13845, A
C 450	49	5.0	1011	4	US-09-902-540-3362	Sequence 3362, Ap	C 523	48.6	4.9	152145	4	US-09-949-016-12371	Sequence 12371, A
C 451	49	5.0	1355	3	US-08-415-655-14	Sequence 14, Appl	C 524	48.4	4.9	562	2	US-08-973-316-53	Sequence 53, Appl
C 452	49	5.0	1614	4	US-09-616-289-45	Sequence 45, Appl	C 525	48.4	4.9	562	3	US-09-615-192A-53	Sequence 53, Appl
C 453	49	5.0	1731	4	US-09-902-540-6944	Sequence 6944, Ap	C 526	48.4	4.9	562	4	US-09-169-789-53	Sequence 53, Appl
C 454	49	5.0	1811	4	US-09-902-540-375	Sequence 375, App	C 527	48.4	4.9	756	1	US-08-642-255-50	Sequence 50, Appl
C 455	49	5.0	1899	4	US-09-902-540-4564	Sequence 4564, Ap	C 528	48.4	4.9	1116	4	US-09-902-540-2568	Sequence 2568, Ap
C 456	49	5.0	3270	4	US-09-902-540-4814	Sequence 4814, Ap	C 529	48.4	4.9	1350	4	US-09-902-540-5339	Sequence 5339, Ap
C 457	49	5.0	3810	4	US-09-902-540-3021	Sequence 3021, Ap	C 530	48.4	4.9	1351	4	US-09-902-540-1192	Sequence 1192, App
C 458	49	5.0	3812	4	US-09-902-540-641	Sequence 641, App	C 531	48.4	4.9	1407	4	US-09-902-540-4833	Sequence 4833, Ap
C 459	49	5.0	4587	4	US-09-902-540-600	Sequence 600, App	C 532	48.4	4.9	1935	4	US-09-902-540-7710	Sequence 7710, Ap
C 460	49	5.0	6935	4	US-09-902-540-865	Sequence 865, App	C 533	48.4	4.9	6611	4	US-09-902-540-762	Sequence 762, App
C 461	49	5.0	9125	4	US-09-902-540-959	Sequence 959, App	C 534	48.4	4.9	6975	4	US-09-902-540-2386	Sequence 2386, Ap
C 462	49	5.0	12425	4	US-09-616-289-50	Sequence 50, Appl	C 535	48.4	4.9	13706	4	US-09-902-540-1124	Sequence 1124, Ap
C 463	49	5.0	17125	4	US-09-902-540-1158	Sequence 1158, Ap	C 536	48.4	4.9	13855	4	US-09-902-540-1117	Sequence 1117, Ap
C 464	49	5.0	24905	4	US-09-902-540-1225	Sequence 1225, Ap	C 537	48.2	4.9	822	4	US-09-252-991A-11707	Sequence 11707, A
C 465	49	5.0	77536	4	US-09-410-551B-1	Sequence 1, Appli	C 538	48.2	4.9	920	4	US-09-620-312D-132	Sequence 132, App

539	48.2	4.9	957	4	US-09-902-540-4213	Sequence 4213, Ap	612	47.8	4.8	1771	4	US-09-551-974A-7	Sequence 7, Appli
540	48.2	4.9	1035	1	US-07-601-094-30	Sequence 30, Appl	613	47.8	4.8	1771	4	US-09-565-501A-7	Sequence 7, Appli
541	48.2	4.9	1035	1	US-08-012-735-30	Sequence 30, Appl	614	47.8	4.8	1771	4	US-09-639-206A-7	Sequence 7, Appli
542	48.2	4.9	1306	4	US-09-902-540-8937	Sequence 8937, Ap	615	47.8	4.8	1771	4	US-09-874-923-7	Sequence 7, Appli
543	48.2	4.9	1701	4	US-09-949-016-1139	Sequence 1139, Ap	616	47.8	4.8	1771	4	US-08-798-841-7	Sequence 7, Appli
544	48.2	4.9	1701	4	US-09-949-016-2634	Sequence 2634, Ap	617	47.8	4.8	1962	4	US-09-252-991A-16037	Sequence 16037, A
545	48.2	4.9	1910	3	US-09-593-711A-3	Sequence 3, Appli	618	47.8	4.8	2526	4	US-09-252-991A-18563	Sequence 18563, A
546	48.2	4.9	1914	1	US-07-601-094-1	Sequence 1, Appli	619	47.8	4.8	2526	4	US-09-902-540-2500	Sequence 2500, Ap
547	48.2	4.9	1914	1	US-08-012-735-1	Sequence 1, Appli	620	47.8	4.8	3126	4	US-09-252-991A-9066	Sequence 9066, Ap
548	48.2	4.9	2009	4	US-09-646-403-1	Sequence 1, Appli	621	47.8	4.8	4410	4	US-09-902-540-673	Sequence 673, App
549	48.2	4.9	2023	3	US-09-491-522-6	Sequence 6, Appli	622	47.8	4.8	4524	2	US-08-845-998-7	Sequence 7, Appli
550	48.2	4.9	2034	4	US-09-646-403-2	Sequence 2, Appli	623	47.8	4.8	4524	3	US-09-206-537-7	Sequence 7, Appli
551	48.2	4.9	2035	4	US-09-863-049B-3	Sequence 3, Appli	624	47.8	4.8	4524	3	US-09-430-854-7	Sequence 7, Appli
552	48.2	4.9	2450	3	US-09-491-522-2	Sequence 2, Appli	625	47.8	4.8	4991	4	US-09-902-540-719	Sequence 719, App
553	48.2	4.9	3350	4	US-09-894-998A-48	Sequence 48, Appl	626	47.8	4.8	5121	4	US-09-252-991A-15189	Sequence 15189, A
554	48.2	4.9	3350	4	US-10-237-551-48	Sequence 48, Appl	627	47.8	4.8	6327	4	US-09-252-991A-14931	Sequence 14931, A
555	48.2	4.9	3636	4	US-09-949-016-5530	Sequence 5530, Ap	628	47.8	4.8	10871	4	US-09-902-540-1025	Sequence 1025, Ap
556	48.2	4.9	4761	4	US-09-902-540-739	Sequence 739, App	629	47.8	4.8	12950	4	US-09-902-540-1036	Sequence 1036, Ap
557	48.2	4.9	6692	3	US-09-491-522-1	Sequence 1, Appli	630	47.8	4.8	15338	4	US-09-902-540-1121	Sequence 1121, Ap
558	48.2	4.9	17639	4	US-09-902-540-1153	Sequence 1153, Ap	631	47.8	4.8	15782	4	US-09-902-540-1094	Sequence 1094, Ap
559	48.2	4.9	21330	4	US-09-902-540-1209	Sequence 1209, Ap	632	47.8	4.8	16833	4	US-09-902-540-1112	Sequence 1112, Ap
560	48	4.9	465	4	US-09-252-991A-2233	Sequence 2233, Ap	633	47.8	4.8	24459	4	US-09-902-540-5004	Sequence 5004, Ap
561	48	4.9	561	4	US-09-902-540-3942	Sequence 3942, Ap	634	47.8	4.8	32241	4	US-09-902-540-1247	Sequence 1247, Ap
562	48	4.9	822	4	US-09-252-991A-7080	Sequence 7080, Ap	635	47.8	4.8	71989	3	US-09-443-501A-2	Sequence 2, Appli
563	48	4.9	822	4	US-09-252-991A-2447	Sequence 2447, Ap	636	47.6	4.8	687	4	US-09-902-540-6345	Sequence 6345, Ap
564	48	4.9	933	4	US-09-902-540-6632	Sequence 6632, Ap	637	47.6	4.8	720	4	US-09-902-540-7501	Sequence 7501, Ap
565	48	4.9	1071	4	US-09-252-991A-1635	Sequence 1635, Ap	638	47.6	4.8	924	4	US-09-902-540-3612	Sequence 3612, Ap
566	48	4.9	1128	4	US-09-622-439-1	Sequence 1, Appli	639	47.6	4.8	930	4	US-09-252-991A-15663	Sequence 15663, A
567	48	4.9	1128	4	US-10-318-142-1	Sequence 1, Appli	640	47.6	4.8	1248	4	US-09-252-991A-2635	Sequence 2635, Ap
568	48	4.9	1161	4	US-09-902-540-3053	Sequence 3053, Ap	641	47.6	4.8	1278	4	US-09-252-991A-3896	Sequence 3896, Ap
569	48	4.9	1341	4	US-09-902-540-5533	Sequence 5533, Ap	642	47.6	4.8	1365	4	US-09-902-540-6352	Sequence 6352, Ap
570	48	4.9	1359	4	US-09-252-991A-2528	Sequence 2528, Ap	643	47.6	4.8	1646	4	US-09-902-540-402	Sequence 402, App
571	48	4.9	1473	4	US-09-252-991A-2391	Sequence 2391, Ap	644	47.6	4.8	1667	4	US-09-902-540-407	Sequence 407, App
572	48	4.9	1677	4	US-09-902-540-7773	Sequence 7773, Ap	645	47.6	4.8	1971	4	US-09-252-991A-2197	Sequence 2197, App
573	48	4.9	1695	4	US-09-252-991A-1686	Sequence 1686, Ap	646	47.6	4.8	1977	4	US-09-252-991A-3924	Sequence 3924, Ap
574	48	4.9	1701	4	US-09-902-540-9608	Sequence 9608, Ap	647	47.6	4.8	2091	4	US-09-252-991A-4016	Sequence 4016, Ap
575	48	4.9	1740	4	US-09-252-991A-1492	Sequence 1492, Ap	648	47.6	4.8	2211	4	US-09-252-991A-2477	Sequence 2477, Ap
576	48	4.9	1806	4	US-09-252-991A-1534	Sequence 1534, Ap	649	47.6	4.8	2305	4	US-09-475-515-82	Sequence 82, Appl
577	48	4.9	1929	4	US-09-252-991A-7017	Sequence 7017, Ap	650	47.6	4.8	2306	4	US-09-475-515-82	Sequence 82, Appl
578	48	4.9	1947	4	US-09-252-991A-7111	Sequence 7111, Ap	651	47.6	4.8	2481	4	US-09-894-998A-35	Sequence 35, Appl
579	48	4.9	2230	4	US-09-902-540-6807	Sequence 6807, Ap	652	47.6	4.8	2481	4	US-10-237-551-35	Sequence 35, Appl
580	48	4.9	2253	4	US-09-252-991A-7191	Sequence 7191, Ap	653	47.6	4.8	2670	4	US-09-902-540-8525	Sequence 8525, Ap
581	48	4.9	2403	4	US-09-252-991A-7253	Sequence 7253, Ap	654	47.6	4.8	3066	4	US-10-237-551-152	Sequence 152, App
582	48	4.9	2490	4	US-09-252-991A-7447	Sequence 7447, Ap	655	47.6	4.8	3390	4	US-09-902-540-6647	Sequence 6647, Ap
583	48	4.9	3492	4	US-09-949-016-837	Sequence 837, App	656	47.6	4.8	3393	4	US-09-902-540-514	Sequence 514, App
584	48	4.9	4800	4	US-09-902-540-562	Sequence 562, App	657	47.6	4.8	5001	4	US-09-902-540-8618	Sequence 8618, App
585	48	4.9	6250	4	US-09-902-540-773	Sequence 773, App	658	47.6	4.8	5481	4	US-09-902-540-7351	Sequence 7351, Ap
586	48	4.9	6713	4	US-09-902-540-793	Sequence 793, App	659	47.6	4.8	5618	4	US-09-902-540-728	Sequence 728, App
587	48	4.9	9165	4	US-09-902-540-1050	Sequence 1050, Ap	660	47.6	4.8	6008	4	US-09-949-016-5058	Sequence 5058, Ap
588	48	4.9	12194	4	US-09-902-540-1091	Sequence 1091, Ap	661	47.6	4.8	6402	4	US-09-902-540-702	Sequence 702, App
589	48	4.9	15482	4	US-09-902-540-1067	Sequence 1067, Ap	662	47.6	4.8	9321	4	US-09-902-540-898	Sequence 898, App
590	48	4.9	22431	4	US-09-949-016-14099	Sequence 14099, A	663	47.6	4.8	9960	3	US-08-822-586-46	Sequence 46, Appl
591	48	4.9	24509	4	US-09-949-016-12612	Sequence 12612, A	664	47.6	4.8	13299	4	US-09-902-540-968	Sequence 968, App
592	48	4.9	24509	4	US-09-949-016-13687	Sequence 13687, A	665	47.6	4.8	14158	4	US-09-902-540-1069	Sequence 1069, Ap
593	48	4.9	33529	3	US-09-144-085-3	Sequence 3, Appli	666	47.4	4.8	411	4	US-09-902-540-5862	Sequence 5862, Ap
594	48	4.9	41170	4	US-09-902-540-1267	Sequence 1267, Ap	667	47.4	4.8	789	4	US-09-902-540-3137	Sequence 3137, Ap
595	47.8	4.8	309	4	US-09-252-991A-6725	Sequence 6725, Ap	668	47.4	4.8	918	4	US-09-252-991A-8762	Sequence 8762, Ap
596	47.8	4.8	468	4	US-09-902-540-2625	Sequence 2625, Ap	669	47.4	4.8	948	4	US-09-252-991A-9192	Sequence 9192, Ap
597	47.8	4.8	482	4	US-09-902-540-7213	Sequence 7213, Ap	670	47.4	4.8	954	4	US-09-252-991A-5807	Sequence 5807, Ap
598	47.8	4.8	801	4	US-09-252-991A-15941	Sequence 15941, A	671	47.4	4.8	1023	4	US-09-902-540-3025	Sequence 3025, Ap
599	47.8	4.8	819	4	US-09-252-991A-14581	Sequence 14581, A	672	47.4	4.8	1116	4	US-09-252-991A-10924	Sequence 10924, A
600	47.8	4.8	896	4	US-09-902-540-7446	Sequence 7446, Ap	673	47.4	4.8	1149	4	US-09-252-991A-8983	Sequence 8983, Ap
601	47.8	4.8	966	4	US-09-252-991A-6895	Sequence 6895, Ap	674	47.4	4.8	1209	4	US-09-252-991A-11138	Sequence 11138, A
602	47.8	4.8	1218	4	US-09-252-991A-16453	Sequence 16453, A	675	47.4	4.8	1245	4	US-09-902-540-4829	Sequence 4829, Ap
603	47.8	4.8	1485	4	US-09-252-991A-6815	Sequence 6815, Ap	676	47.4	4.8	1248	4	US-09-724-797-23	Sequence 23, Appl
604	47.8	4.8	1509	4	US-09-252-991A-6930	Sequence 6930, Ap	677	47.4	4.8	1251	4	US-09-252-991A-5844	Sequence 5844, Ap
605	47.8	4.8	1652	4	US-09-902-540-9646	Sequence 9646, Ap	678	47.4	4.8	1332	4	US-09-902-540-9176	Sequence 9176, Ap
606	47.8	4.8	1671	4	US-09-902-540-4098	Sequence 4098, Ap	679	47.4	4.8	1413	4	US-09-902-540-5411	Sequence 5411, Ap
607	47.8	4.8	1708	4	US-09-902-540-5058	Sequence 5058, Ap	680	47.4	4.8	1650	4	US-09-252-991A-3338	Sequence 3338, Ap
608	47.8	4.8	1771	2	US-08-533-669A-7	Sequence 7, Appli	681	47.4	4.8	1812	4	US-09-902-540-2482	Sequence 2482, Ap
609	47.8	4.8	1771	2	US-08-511-872-1	Sequence 1, Appli	682	47.4	4.8	1869	4	US-09-252-991A-3331	Sequence 3331, Ap
610	47.8	4.8	1771	3	US-09-183-861-7	Sequence 7, Appli	683	47.4	4.8	1881	4	US-09-252-991A-11264	Sequence 11264, A
611	47.8	4.8	1771	3	US-09-022-765-7	Sequence 7, Appli	684	47.4	4.8	1977	4	US-09-902-540-7785	Sequence 7785, Ap

685	47.4	4.8	1986	4	US-09-252-991A-5767	Sequence 5767, Ap	758	47	4.8	4377	3	US-08-911-853-28	Sequence 28, Appl
686	47.4	4.8	2283	4	US-09-252-991A-3298	Sequence 3298, Ap	759	47	4.8	4377	3	US-09-479-409-28	Sequence 28, Appl
687	47.4	4.8	2583	4	US-09-252-991A-9110	Sequence 9110, Ap	760	47	4.8	4377	3	US-09-479-453-28	Sequence 28, Appl
688	47.4	4.8	2634	1	US-08-196-218-31	Sequence 31, Appl	761	47	4.8	13434	4	US-09-902-540-1003	Sequence 1003, Ap
689	47.4	4.8	2634	1	US-08-681-953-31	Sequence 31, Appl	762	47	4.8	18469	4	US-09-902-540-1200	Sequence 1200, Ap
690	47.4	4.8	3073	4	US-09-302-540-643	Sequence 643, App	763	47	4.8	24986	4	US-09-902-540-1205	Sequence 1200, Ap
691	47.4	4.8	3099	4	US-09-302-540-5065	Sequence 5065, Ap	764	47	4.8	26659	4	US-09-902-540-1237	Sequence 1237, Ap
692	47.4	4.8	3333	4	US-09-302-540-1965	Sequence 1965, Ap	765	47	4.8	80161	3	US-09-036-987A-1	Sequence 1, Appli
693	47.4	4.8	5175	4	US-09-302-540-774	Sequence 774, App	766	47	4.8	80161	3	US-09-370-700-1	Sequence 1, Appli
694	47.4	4.8	8820	4	US-09-302-540-974	Sequence 974, App	767	47	4.8	80161	3	US-09-603-207-1	Sequence 1, Appli
695	47.4	4.8	17938	4	US-09-302-540-1111	Sequence 1111, Ap	768	46.8	4.7	296	3	US-09-615-192A-195	Sequence 195, App
696	47.4	4.8	19598	4	US-09-302-540-1143	Sequence 1143, Ap	769	46.8	4.7	687	4	US-09-902-540-7361	Sequence 7361, Ap
697	47.4	4.8	28194	4	US-09-302-540-1143	Sequence 1143, Ap	770	46.8	4.7	792	4	US-09-252-991A-4971	Sequence 4971, Ap
698	47.4	4.8	34953	4	US-09-302-540-1250	Sequence 1250, Ap	771	46.8	4.7	801	2	US-08-770-379-16	Sequence 16, Appl
699	47.4	4.8	50937	3	US-09-302-540-1263	Sequence 1263, Ap	772	46.8	4.7	801	3	US-08-757-669A-16	Sequence 16, Appl
700	47.4	4.8	50937	3	US-09-428-517-1	Sequence 1, Appli	773	46.8	4.7	801	3	US-09-298-568-3	Sequence 3, Appli
701	47.4	4.8	767677	4	US-09-428-517-1	Sequence 1, Appli	774	46.8	4.7	801	3	US-09-230-371A-16	Sequence 16, Appl
702	47.4	4.8	767677	4	US-09-949-016-12147	Sequence 12147, A	775	46.8	4.7	801	4	US-09-894-273-3	Sequence 3, Appli
703	47.2	4.8	519	4	US-09-949-016-17361	Sequence 17361, A	776	46.8	4.7	1071	4	US-09-252-991A-4955	Sequence 4955, Ap
704	47.2	4.8	714	4	US-09-302-540-6955	Sequence 6955, Ap	777	46.8	4.7	1131	4	US-09-252-991A-4994	Sequence 4994, Ap
705	47.2	4.8	864	4	US-09-252-991A-16021	Sequence 16021, A	778	46.8	4.7	1315	4	US-09-252-991A-4984	Sequence 4984, Ap
706	47.2	4.8	888	3	US-09-302-540-8350	Sequence 8350, Ap	779	46.8	4.7	2592	4	US-09-902-540-3407	Sequence 3407, Ap
707	47.2	4.8	888	4	US-08-765-907A-2	Sequence 2, Appli	780	46.8	4.7	2811	4	US-09-902-540-2406	Sequence 2406, Ap
708	47.2	4.8	897	4	US-09-987-614A-2	Sequence 2, Appli	781	46.8	4.7	2962	4	US-09-902-540-6991	Sequence 6991, Ap
709	47.2	4.8	897	4	US-09-302-540-2413	Sequence 2413, Ap	782	46.8	4.7	3171	4	US-09-252-991A-7591	Sequence 7591, Ap
710	47.2	4.8	1110	4	US-09-252-991A-970	Sequence 970, App	783	46.8	4.7	3210	4	US-09-252-991A-7962	Sequence 7962, Ap
711	47.2	4.8	1194	4	US-09-724-797-25	Sequence 1014, Ap	784	46.8	4.7	4632	4	US-09-902-540-8368	Sequence 8368, Ap
712	47.2	4.8	1231	4	US-09-302-540-3596	Sequence 3596, Ap	785	46.8	4.7	4873	4	US-09-902-540-610	Sequence 610, App
713	47.2	4.8	1275	4	US-09-252-991A-1080	Sequence 1080, Ap	786	46.8	4.7	10182	4	US-09-902-540-1049	Sequence 1049, Ap
714	47.2	4.8	1335	4	US-09-302-540-5111	Sequence 5111, Ap	787	46.8	4.7	17654	4	US-09-902-540-1161	Sequence 1161, Ap
715	47.2	4.8	1347	4	US-09-724-797-43	Sequence 43, Appl	788	46.6	4.7	270	4	US-09-252-991A-14378	Sequence 14378, A
716	47.2	4.8	1818	4	US-09-302-540-4685	Sequence 4685, Ap	789	46.6	4.7	489	4	US-09-252-991A-452	Sequence 452, App
717	47.2	4.8	1869	4	US-09-302-540-8930	Sequence 8930, Ap	790	46.6	4.7	741	4	US-09-902-540-8930	Sequence 8930, Ap
718	47.2	4.8	1902	4	US-09-302-540-8930	Sequence 8930, Ap	791	46.6	4.7	777	4	US-09-252-991A-12568	Sequence 12568, A
719	47.2	4.8	1944	4	US-09-302-540-8758	Sequence 8758, Ap	792	46.6	4.7	780	4	US-09-902-540-5800	Sequence 5800, Ap
720	47.2	4.8	2065	4	US-09-252-991A-16245	Sequence 16245, A	793	46.6	4.7	786	4	US-09-252-991A-13239	Sequence 13239, A
721	47.2	4.8	2133	4	US-09-302-540-7188	Sequence 7188, Ap	794	46.6	4.7	932	4	US-09-902-540-8519	Sequence 8519, Ap
722	47.2	4.8	2112	4	US-09-475-515-84	Sequence 84, Appl	795	46.6	4.7	981	4	US-09-252-991A-431	Sequence 431, App
723	47.2	4.8	2406	4	US-09-302-540-5545	Sequence 5545, Ap	796	46.6	4.7	1032	4	US-09-252-991A-10487	Sequence 10487, A
724	47.2	4.8	2808	4	US-09-252-991A-16466	Sequence 16466, A	797	46.6	4.7	1062	4	US-09-902-540-6426	Sequence 6426, Ap
725	47.2	4.8	2862	4	US-09-252-991A-10659	Sequence 10659, A	798	46.6	4.7	1206	4	US-09-252-991A-6751	Sequence 6751, Ap
726	47.2	4.8	2888	3	US-08-765-907A-1	Sequence 1, Appli	799	46.6	4.7	1320	4	US-09-902-540-3165	Sequence 3165, Ap
727	47.2	4.8	2888	4	US-09-987-614A-1	Sequence 1, Appli	800	46.6	4.7	1380	4	US-09-902-540-7649	Sequence 7649, Ap
728	47.2	4.8	2910	4	US-09-252-991A-10414	Sequence 10414, A	801	46.6	4.7	1530	4	US-09-252-991A-3550	Sequence 3550, Ap
729	47.2	4.8	3111	4	US-09-252-991A-10504	Sequence 10504, A	802	46.6	4.7	1770	4	US-09-252-991A-6874	Sequence 6874, Ap
730	47.2	4.8	3135	4	US-09-252-991A-5922	Sequence 5922, Ap	803	46.6	4.7	1947	4	US-09-902-540-7504	Sequence 7504, Ap
731	47.2	4.8	4319	4	US-09-475-515-6	Sequence 6, Appli	804	46.6	4.7	2247	4	US-09-252-991A-3557	Sequence 3557, Ap
732	47.2	4.8	4604	4	US-09-302-540-602	Sequence 602, App	805	46.6	4.7	2295	4	US-09-902-540-3294	Sequence 3294, Ap
733	47.2	4.8	5033	4	US-09-302-540-670	Sequence 670, App	806	46.6	4.7	2325	4	US-09-902-540-7287	Sequence 7287, Ap
734	47.2	4.8	5051	4	US-09-302-540-667	Sequence 667, App	807	46.6	4.7	2632	4	US-09-902-540-6888	Sequence 688, App
735	47.2	4.8	9556	4	US-09-302-540-929	Sequence 929, App	808	46.6	4.7	4487	4	US-09-902-540-6888	Sequence 688, App
736	47.2	4.8	9992	4	US-09-902-540-952	Sequence 952, App	809	46.6	4.7	5411	4	US-09-902-540-8809	Sequence 8809, Ap
737	47.2	4.8	11220	3	US-09-105-537-32	Sequence 32, Appl	810	46.6	4.7	5618	4	US-09-902-540-7828	Sequence 728, App
738	47.2	4.8	11812	4	US-09-302-540-1041	Sequence 1041, Ap	811	46.6	4.7	6594	4	US-09-902-540-752	Sequence 752, App
739	47.2	4.8	16782	4	US-09-302-540-1105	Sequence 1105, Ap	812	46.6	4.7	7419	4	US-09-252-991A-481	Sequence 481, App
740	47.2	4.8	28058	4	US-09-302-540-1252	Sequence 1252, Ap	813	46.6	4.7	7449	4	US-09-252-991A-396	Sequence 396, App
741	47	4.8	441	4	US-09-252-991A-14658	Sequence 14658, A	814	46.6	4.7	8310	4	US-09-902-540-1001	Sequence 1001, Ap
742	47	4.8	758	4	US-09-302-331B-5	Sequence 5, Appli	815	46.6	4.7	8765	4	US-09-902-540-939	Sequence 939, App
743	47	4.8	936	4	US-09-902-540-4133	Sequence 4133, Ap	816	46.6	4.7	8765	4	US-09-902-540-939	Sequence 939, App
744	47	4.8	1260	4	US-09-252-991A-14526	Sequence 14526, A	817	46.6	4.7	9880	4	US-09-902-540-936	Sequence 936, App
745	47	4.8	1260	4	US-09-252-991A-14838	Sequence 14838, A	818	46.6	4.7	16350	4	US-09-902-540-1144	Sequence 1144, Ap
746	47	4.8	1320	2	US-08-461-775-8	Sequence 8, Appli	819	46.6	4.7	19862	4	US-09-902-540-1198	Sequence 1198, Ap
747	47	4.8	1320	3	US-09-031-606-8	Sequence 8, Appli	820	46.4	4.7	475	4	US-09-902-540-6044	Sequence 6044, Ap
748	47	4.8	1416	3	US-08-911-853-3	Sequence 3, Appli	821	46.4	4.7	525	4	US-09-902-540-6280	Sequence 6280, Ap
749	47	4.8	1416	3	US-09-479-409-3	Sequence 3, Appli	822	46.4	4.7	819	4	US-09-902-540-8196	Sequence 8196, Ap
750	47	4.8	1416	3	US-09-479-453-3	Sequence 3, Appli	823	46.4	4.7	876	4	US-09-902-540-5288	Sequence 5288, Ap
751	47	4.8	1620	2	US-08-461-775-10	Sequence 10, Appl	824	46.4	4.7	9871	3	US-09-252-991A-14299	Sequence 14299, A
752	47	4.8	1620	3	US-09-031-606-10	Sequence 10, Appl	825	46.4	4.7	1072	3	US-09-088-549-2	Sequence 2, Appli
753	47	4.8	1707	4	US-09-724-797-15	Sequence 15, Appl	826	46.4	4.7	1263	4	US-09-252-991A-14349	Sequence 14349, A
754	47	4.8	2223	4	US-09-302-540-3967	Sequence 3967, Ap	827	46.4	4.7	1296	4	US-09-902-540-4063	Sequence 4063, Ap
755	47	4.8	2724	4	US-09-902-540-1968	Sequence 1968, Ap	828	46.4	4.7	1551	4	US-09-902-540-9008	Sequence 9008, Ap
756	47	4.8	2745	4	US-09-902-540-4835	Sequence 4835, Ap	829	46.4	4.7	1553	4	US-09-902-540-245	Sequence 245, App
757	47	4.8	2946	4	US-09-902-540-2504	Sequence 2504, Ap	830	46.4	4.7	1644	4	US-09-902-540-371	Sequence 371, App



831	46.4	4.7	2187	4	US-09-902-540-9583	Sequence 9583, Ap	C 904	46	4.7	11358	4	US-09-902-540-1075	Sequence 1075, Ap
832	46.4	4.7	2186	4	US-09-902-540-6529	Sequence 6529, Ap	C 905	46	4.7	12323	4	US-09-949-016-16703	Sequence 16703, A
833	46.4	4.7	2235	4	US-09-252-991A-14374	Sequence 14374, A	906	46	4.7	17228	4	US-09-902-540-11703	Sequence 1170, Ap
834	46.4	4.7	3147	4	US-09-902-540-476	Sequence 476, App	907	46	4.7	17612	3	US-08-911-853-29	Sequence 29, Appl
835	46.4	4.7	3768	4	US-09-902-540-5368	Sequence 5368, Ap	908	46	4.7	17612	3	US-09-479-409-29	Sequence 29, Appl
836	46.4	4.7	11566	4	US-09-902-540-1088	Sequence 1088, Ap	909	46	4.7	17612	3	US-09-479-453-29	Sequence 29, Appl
837	46.4	4.7	12849	4	US-09-902-540-963	Sequence 963, App	C 910	46	4.7	19394	4	US-09-902-540-1172	Sequence 1172, Ap
838	46.4	4.7	21511	4	US-09-902-540-1201	Sequence 1201, Ap	C 911	46	4.7	19954	4	US-09-902-540-1150	Sequence 1150, Ap
839	46.4	4.7	30783	4	US-09-902-540-1258	Sequence 1258, Ap	C 912	46	4.7	34552	4	US-09-902-540-1262	Sequence 1262, Ap
840	46.4	4.7	41927	4	US-09-902-540-1268	Sequence 1268, Ap	C 913	46	4.7	41768	4	US-09-902-540-1266	Sequence 1266, Ap
841	46.2	4.7	432	1	US-08-642-255-48	Sequence 48, Appl	914	45.8	4.6	549	4	US-09-902-540-5246	Sequence 5246, Ap
842	46.2	4.7	465	4	US-09-902-540-6929	Sequence 6929, Ap	915	45.8	4.6	557	4	US-09-252-991A-4833	Sequence 4833, Ap
843	46.2	4.7	822	4	US-08-893-737-227	Sequence 227, App	C 916	45.8	4.6	774	3	US-08-956-307B-12	Sequence 12, Appl
844	46.2	4.7	1050	4	US-09-902-540-3534	Sequence 3534, Ap	917	45.8	4.6	778	3	US-08-956-307B-11	Sequence 11, Appl
845	46.2	4.7	1086	4	US-09-902-540-5546	Sequence 5546, Ap	C 918	45.8	4.6	960	4	US-09-534-229C-8	Sequence 8, Appl
846	46.2	4.7	1362	4	US-09-724-797-31	Sequence 31, Appl	919	45.8	4.6	1140	4	US-09-902-540-2965	Sequence 2965, Ap
847	46.2	4.7	1396	4	US-09-902-540-2306	Sequence 2306, Ap	920	45.8	4.6	1245	4	US-09-252-991A-13463	Sequence 13463, A
848	46.2	4.7	1401	4	US-09-902-540-6962	Sequence 6962, Ap	921	45.8	4.6	1284	4	US-09-902-540-8320	Sequence 8320, Ap
849	46.2	4.7	1458	4	US-09-902-540-9498	Sequence 9498, Ap	C 922	45.8	4.6	1323	4	US-09-902-540-2671	Sequence 2671, Ap
850	46.2	4.7	1476	4	US-09-902-540-6774	Sequence 6774, Ap	C 923	45.8	4.6	1401	4	US-09-252-991A-4911	Sequence 4911, Ap
851	46.2	4.7	1509	4	US-09-724-797-89	Sequence 89, Appl	C 924	45.8	4.6	1434	4	US-09-902-540-5292	Sequence 5292, Ap
852	46.2	4.7	1590	4	US-09-902-540-3116	Sequence 3116, Ap	C 925	45.8	4.6	1569	4	US-09-252-991A-13880	Sequence 13880, A
853	46.2	4.7	2334	4	US-09-902-540-7862	Sequence 7862, Ap	926	45.8	4.6	1628	4	US-09-902-540-9218	Sequence 9218, Ap
854	46.2	4.7	2976	4	US-09-902-540-554	Sequence 554, App	927	45.8	4.6	1651	4	US-09-902-540-6097	Sequence 6097, Ap
855	46.2	4.7	3102	4	US-09-252-991A-4429	Sequence 4429, Ap	928	45.8	4.6	1652	4	US-09-902-540-273	Sequence 273, App
856	46.2	4.7	4050	4	US-09-902-540-604	Sequence 604, App	929	45.8	4.6	1802	4	US-09-949-016-1604	Sequence 1604, Ap
857	46.2	4.7	4320	4	US-09-902-540-577	Sequence 577, App	930	45.8	4.6	2259	4	US-09-252-991A-13556	Sequence 13556, A
858	46.2	4.7	4320	4	US-09-902-540-6854	Sequence 6854, Ap	931	45.8	4.6	2625	4	US-09-902-540-8554	Sequence 8554, Ap
859	46.2	4.7	5132	4	US-09-902-540-597	Sequence 597, App	932	45.8	4.6	2847	4	US-09-902-540-7588	Sequence 7588, Ap
860	46.2	4.7	8614	4	US-09-902-540-787	Sequence 787, App	933	45.8	4.6	4107	4	US-09-902-540-2552	Sequence 2552, Ap
861	46.2	4.7	13256	4	US-09-902-540-1006	Sequence 1006, Ap	934	45.8	4.6	4217	4	US-09-902-540-9677	Sequence 9677, Ap
862	46.2	4.7	14101	4	US-09-902-540-1080	Sequence 1080, Ap	935	45.8	4.6	4835	4	US-09-902-540-627	Sequence 627, App
863	46.2	4.7	18538	4	US-09-902-540-1169	Sequence 1169, Ap	936	45.8	4.6	5661	3	US-08-938-105-2	Sequence 2, Appl
864	46.2	4.7	18809	4	US-09-902-540-1141	Sequence 1141, Ap	937	45.8	4.6	5802	4	US-09-949-016-13346	Sequence 13346, A
865	46.2	4.7	30001	1	US-08-125-468-1	Sequence 1, Appl	938	45.8	4.6	6637	4	US-09-902-540-850	Sequence 850, App
866	46.2	4.7	30001	2	US-08-474-933-1	Sequence 1, Appl	939	45.8	4.6	7404	4	US-09-902-540-3115	Sequence 3115, Ap
867	46.2	4.7	35000	4	US-09-266-965-76	Sequence 76, Appl	C 940	45.8	4.6	7562	4	US-09-902-540-902	Sequence 902, App
868	46	4.7	528	4	US-09-902-540-9054	Sequence 9054, Ap	941	45.8	4.6	7704	4	US-09-902-540-743	Sequence 743, App
869	46	4.7	606	4	US-09-252-991A-2567	Sequence 2567, Ap	942	45.8	4.6	13637	4	US-09-902-540-1097	Sequence 1097, Ap
870	46	4.7	609	4	US-09-252-991A-9531	Sequence 9531, Ap	943	45.8	4.6	14462	4	US-09-902-540-1090	Sequence 1090, Ap
871	46	4.7	765	4	US-09-902-540-3589	Sequence 3589, Ap	944	45.8	4.6	14462	4	US-09-902-540-9997	Sequence 9997, Ap
872	46	4.7	906	4	US-09-252-991A-1329	Sequence 1329, Ap	C 945	45.8	4.6	15377	4	US-09-902-540-1116	Sequence 1116, Ap
873	46	4.7	936	4	US-09-902-540-7713	Sequence 7713, Ap	C 946	45.8	4.6	16541	4	US-09-902-540-1165	Sequence 1165, Ap
874	46	4.7	942	4	US-09-902-540-6941	Sequence 6941, Ap	C 947	45.8	4.6	17245	4	US-09-902-540-1073	Sequence 1073, Ap
875	46	4.7	1023	4	US-09-252-991A-1283	Sequence 1283, Ap	948	45.8	4.6	17622	4	US-09-902-540-1125	Sequence 1125, Ap
876	46	4.7	1023	4	US-09-902-540-4306	Sequence 4306, Ap	C 949	45.8	4.6	25686	4	US-09-902-540-1246	Sequence 1246, Ap
877	46	4.7	1044	1	US-07-975-526-3	Sequence 3, Appl	C 950	45.8	4.6	34316	4	US-09-902-540-1157	Sequence 1257, Ap
878	46	4.7	1044	3	US-07-974-409C-425	Sequence 425, App	951	45.8	4.6	43280	2	US-08-804-227C-1	Sequence 1, Appl
879	46	4.7	1077	4	US-09-252-991A-7892	Sequence 7892, Ap	952	45.6	4.6	450	4	US-09-902-540-3155	Sequence 3155, Ap
880	46	4.7	1080	4	US-09-252-991A-1187	Sequence 1187, Ap	C 953	45.6	4.6	747	4	US-09-252-991A-14108	Sequence 14108, A
881	46	4.7	1095	4	US-09-902-540-5522	Sequence 5522, Ap	954	45.6	4.6	765	4	US-09-902-540-5240	Sequence 5240, Ap
882	46	4.7	1112	3	US-09-434-288-9	Sequence 9, Appl	955	45.6	4.6	777	4	US-09-902-540-2656	Sequence 2656, Ap
883	46	4.7	1143	4	US-09-902-540-7593	Sequence 7593, Ap	956	45.6	4.6	900	4	US-09-252-991A-1017	Sequence 1017, Ap
884	46	4.7	1167	4	US-09-902-540-9338	Sequence 9338, Ap	C 957	45.6	4.6	924	4	US-09-252-991A-1483	Sequence 1483, Ap
885	46	4.7	1263	4	US-09-902-540-6477	Sequence 6477, Ap	C 958	45.6	4.6	1035	4	US-09-252-991A-14017	Sequence 14017, A
886	46	4.7	1266	4	US-09-252-991A-10804	Sequence 10804, A	959	45.6	4.6	1131	4	US-09-902-540-2616	Sequence 2616, Ap
887	46	4.7	1275	4	US-09-252-991A-2484	Sequence 2484, Ap	960	45.6	4.6	1200	4	US-09-787-292-4	Sequence 4, Appl
888	46	4.7	1317	4	US-09-902-540-9439	Sequence 9439, Ap	961	45.6	4.6	1209	6	5352575-4	Patent No. 5352575
889	46	4.7	1371	4	US-09-252-991A-9717	Sequence 9717, Ap	962	45.6	4.6	1209	6	5352575-4	Patent No. 5352575
890	46	4.7	1383	4	US-09-252-991A-2350	Sequence 2350, Ap	963	45.6	4.6	1213	3	US-09-232-468A-7	Sequence 7, Appl
891	46	4.7	1443	4	US-09-252-991A-10228	Sequence 10228, A	964	45.6	4.6	1213	3	US-09-784-984B-6	Sequence 6, Appl
892	46	4.7	1458	4	US-09-902-540-3540	Sequence 3540, Ap	965	45.6	4.6	1242	4	US-09-902-540-5044	Sequence 5044, Ap
893	46	4.7	1481	4	US-09-902-540-10345	Sequence 10345, A	966	45.6	4.6	1251	4	US-09-902-540-8793	Sequence 8793, Ap
894	46	4.7	1935	4	US-09-620-312D-236	Sequence 236, App	967	45.6	4.6	1365	4	US-09-252-991A-14122	Sequence 14122, A
895	46	4.7	1987	4	US-09-902-540-3186	Sequence 3186, Ap	C 968	45.6	4.6	1458	4	US-09-252-991A-1112	Sequence 1112, Ap
896	46	4.7	2400	1	US-08-967-513-1	Sequence 1, Appl	969	45.6	4.6	1461	4	US-09-252-991A-972	Sequence 972, App
897	46	4.7	2400	2	US-08-687-645B-1	Sequence 1, Appl	970	45.6	4.6	1485	4	US-09-902-540-9444	Sequence 9444, Ap
898	46	4.7	3597	4	US-09-902-540-5402	Sequence 5402, Ap	971	45.6	4.6	1500	4	US-09-902-540-8297	Sequence 8297, Ap
899	46	4.7	3603	4	US-09-902-540-3266	Sequence 3266, Ap	972	45.6	4.6	1505	1	US-07-915-246-1	Sequence 1, Appl
900	46	4.7	4402	4	US-09-902-540-742	Sequence 742, App	973	45.6	4.6	1545	4	US-09-902-540-2849	Sequence 2849, Ap
901	46	4.7	6083	4	US-09-902-540-763	Sequence 763, App	974	45.6	4.6	1581	4	US-09-902-540-9170	Sequence 9170, Ap
902	46	4.7	10013	4	US-09-949-016-16474	Sequence 16474, A	975	45.6	4.6	1588	4	US-09-490-291-7	Sequence 7, Appl
903	46	4.7	10424	4	US-09-902-540-1015	Sequence 1015, Ap	976	45.6	4.6	1623	4	US-09-902-540-9607	Sequence 9607, Ap



977	45.6	4.6	1663	4	US-09-398-522-108	Sequence 108, Appl	ci1050	45.4	4.6	28172	4	US-09-902-540-1321	Sequence 1221, Ap
c 978	45.6	4.6	1768	4	US-09-485-529-13	Sequence 13, Appl	1051	45.4	4.6	32278	4	US-09-949-016-14575	Sequence 14575, A
979	45.6	4.6	2124	4	US-09-266-965-44	Sequence 44, Appl	ci1052	45.2	4.6	357	3	US-08-556-9788-93	Sequence 83, Appl
c 980	45.6	4.6	2125	4	US-09-485-529-14	Sequence 14, Appl	ci1053	45.2	4.6	447	4	US-09-252-991A-4677	Sequence 4677, Ap
981	45.6	4.6	2178	4	US-09-302-540-7409	Sequence 7409, Ap	ci1054	45.2	4.6	504	4	US-09-252-991A-4720	Sequence 4720, A
982	45.6	4.6	2282	4	US-09-922-445-50	Sequence 50, Appl	ci1055	45.2	4.6	522	4	US-09-252-991A-12264	Sequence 12264, A
c 983	45.6	4.6	3681	4	US-09-581-105-1	Sequence 1, Appl	ci1056	45.2	4.6	702	4	US-09-253-991A-4703	Sequence 4703, Ap
984	45.6	4.6	4095	4	US-09-252-991A-10309	Sequence 10309, A	ci1057	45.2	4.6	711	4	US-09-902-540-6903	Sequence 6903, Ap
985	45.6	4.6	4164	4	US-09-902-540-4661	Sequence 4661, Ap	1058	45.2	4.6	807	4	US-09-252-991A-12392	Sequence 12392, A
986	45.6	4.6	4233	4	US-09-551-974A-99	Sequence 99, Appl	1059	45.2	4.6	867	4	US-09-902-540-3225	Sequence 3225, Ap
987	45.6	4.6	4233	4	US-09-565-501A-99	Sequence 99, Appl	1060	45.2	4.6	888	4	US-09-252-991A-7041	Sequence 7041, Ap
988	45.6	4.6	4233	4	US-09-639-206A-99	Sequence 99, Appl	ci1061	45.2	4.6	897	4	US-09-252-991A-8854	Sequence 8854, A
989	45.6	4.6	4233	4	US-09-874-923-99	Sequence 99, Appl	1062	45.2	4.6	1026	4	US-09-253-991A-12295	Sequence 12295, A
990	45.6	4.6	4563	4	US-09-252-991A-930	Sequence 930, Appl	1063	45.2	4.6	1095	4	US-09-252-991A-6626	Sequence 6626, Ap
991	45.6	4.6	4917	4	US-09-551-974A-100	Sequence 100, Appl	1064	45.2	4.6	1095	4	US-09-902-540-7052	Sequence 7052, Ap
992	45.6	4.6	4917	4	US-09-565-501A-100	Sequence 100, Appl	1065	45.2	4.6	1242	4	US-09-902-540-2362	Sequence 2362, Ap
993	45.6	4.6	4917	4	US-09-639-206A-100	Sequence 100, Appl	1066	45.2	4.6	1278	4	US-09-902-540-7241	Sequence 7241, Ap
994	45.6	4.6	4917	4	US-09-874-923-100	Sequence 100, Appl	1067	45.2	4.6	1416	4	US-09-902-540-9491	Sequence 9491, Ap
995	45.6	4.6	4929	4	US-09-551-974A-98	Sequence 98, Appl	ci1068	45.2	4.6	1419	4	US-09-253-991A-10421	Sequence 10421, A
996	45.6	4.6	4929	4	US-09-565-501A-98	Sequence 98, Appl	1069	45.2	4.6	1491	4	US-09-902-540-7572	Sequence 7572, A
997	45.6	4.6	4929	4	US-09-639-206A-98	Sequence 98, Appl	1070	45.2	4.6	1494	4	US-09-902-540-8469	Sequence 8469, Ap
998	45.6	4.6	4929	4	US-09-874-923-98	Sequence 98, Appl	1071	45.2	4.6	1602	4	US-09-252-991A-5989	Sequence 5989, Ap
c 999	45.6	4.6	6119	4	US-09-902-540-713	Sequence 713, Appl	ci1072	45.2	4.6	1695	4	US-09-252-991A-10319	Sequence 10319, A
1000	45.6	4.6	6935	4	US-09-902-540-865	Sequence 865, Appl	1073	45.2	4.6	1967	4	US-09-902-540-2665	Sequence 2665, Ap
c1001	45.6	4.6	7950	4	US-09-902-540-934	Sequence 934, Appl	1074	45.2	4.6	2028	4	US-09-902-540-7226	Sequence 7226, Ap
1002	45.6	4.6	8241	4	US-09-902-540-798	Sequence 798, Appl	1075	45.2	4.6	2316	4	US-09-949-016-870	Sequence 870, Appl
c1003	45.6	4.6	13631	4	US-09-902-540-1092	Sequence 1092, Appl	1076	45.2	4.6	2316	4	US-09-949-016-1945	Sequence 1945, Ap
1004	45.6	4.6	13904	4	US-09-902-540-1076	Sequence 1076, Appl	1077	45.2	4.6	2363	4	US-09-818-780-22	Sequence 22, Appl
1005	45.6	4.6	15132	4	US-09-902-540-1137	Sequence 1137, Appl	1078	45.2	4.6	2376	4	US-09-252-991A-10741	Sequence 10741, A
1006	45.6	4.6	15338	4	US-09-902-540-1121	Sequence 1121, Appl	1079	45.2	4.6	2379	4	US-09-252-991A-9205	Sequence 9205, Ap
1007	45.6	4.6	16350	4	US-09-902-540-1144	Sequence 1144, Appl	1080	45.2	4.6	2844	4	US-09-253-991A-4764	Sequence 4764, Ap
c1008	45.6	4.6	30135	4	US-09-902-540-1249	Sequence 1249, Appl	ci1081	45.2	4.6	3084	4	US-09-252-991A-6639	Sequence 6639, Ap
c1009	45.4	4.6	468	4	US-09-252-991A-3528	Sequence 3528, Appl	1082	45.2	4.6	3273	4	US-09-252-991A-6578	Sequence 6578, Ap
1010	45.4	4.6	538	1	US-10-095-946-13	Sequence 13, Appl	ci1083	45.2	4.6	3402	4	US-09-902-540-4967	Sequence 4967, Ap
1011	45.4	4.6	538	1	US-09-183-959-13	Sequence 13, Appl	1084	45.2	4.6	4169	4	US-09-902-540-590	Sequence 590, Appl
1012	45.4	4.6	538	4	US-09-535-315-13	Sequence 13, Appl	ci1085	45.2	4.6	4377	4	US-09-902-540-676	Sequence 676, Appl
1013	45.4	4.6	601	4	US-09-949-016-55209	Sequence 55209, A	1086	45.2	4.6	4387	4	US-09-902-540-679	Sequence 679, Appl
1014	45.4	4.6	845	4	US-09-347-650-1	Sequence 1, Appl	1087	45.2	4.6	4521	4	US-09-902-540-3633	Sequence 3633, Ap
1015	45.4	4.6	897	4	US-09-902-540-7143	Sequence 7143, Appl	1088	45.2	4.6	6201	4	US-09-902-540-740	Sequence 740, Appl
1016	45.4	4.6	954	3	US-08-911-853-24	Sequence 24, Appl	1089	45.2	4.6	6380	4	US-09-902-540-891	Sequence 891, Appl
1017	45.4	4.6	954	3	US-09-479-403-24	Sequence 24, Appl	ci1090	45.2	4.6	13466	4	US-09-902-540-11007	Sequence 11007, Ap
1018	45.4	4.6	954	3	US-09-479-453-24	Sequence 24, Appl	ci1091	45.2	4.6	15447	4	US-09-902-540-11100	Sequence 11100, Ap
1019	45.4	4.6	975	4	US-09-489-039A-791	Sequence 791, Appl	1092	45.2	4.6	16448	4	US-09-902-540-9686	Sequence 9686, Ap
1020	45.4	4.6	1059	4	US-09-902-540-5064	Sequence 5064, Appl	ci1093	45.2	4.6	16450	4	US-09-902-540-1098	Sequence 1098, Ap
1021	45.4	4.6	1170	4	US-09-902-540-7350	Sequence 7350, Appl	ci1094	45.2	4.6	17726	4	US-09-902-540-1148	Sequence 1148, Ap
1022	45.4	4.6	1449	4	US-09-252-991A-3558	Sequence 3558, Appl	1095	45.2	4.6	19289	4	US-09-902-540-1175	Sequence 1175, Ap
1023	45.4	4.6	1548	2	US-08-762-106-5	Sequence 5, Appl	1096	45.2	4.6	26896	4	US-09-949-016-16800	Sequence 16800, A
1024	45.4	4.6	1548	3	US-09-320-774-5	Sequence 5, Appl	ci1097	45.2	4.6	30001	1	US-08-125-468-1	Sequence 1, Appl
1025	45.4	4.6	1572	4	US-09-252-991A-3270	Sequence 3270, Appl	ci1098	45.2	4.6	30001	2	US-08-474-933-1	Sequence 1, Appl
1026	45.4	4.6	1581	2	US-08-762-106-6	Sequence 6, Appl	1099	45	4.6	582	4	US-09-252-991A-6152	Sequence 6152, Ap
1027	45.4	4.6	1581	3	US-09-320-774-6	Sequence 6, Appl	1100	45	4.6	732	4	US-09-902-540-5323	Sequence 5323, Ap
1028	45.4	4.6	1698	4	US-09-252-991A-3551	Sequence 3551, Appl	1101	45	4.6	801	4	US-09-902-540-4823	Sequence 4823, Ap
1029	45.4	4.6	1843	1	US-07-918-023-1	Sequence 1, Appl	1102	45	4.6	804	3	US-09-813-453B-38	Sequence 38, Appl
1030	45.4	4.6	1965	4	US-09-252-991A-3234	Sequence 3234, Appl	1103	45	4.6	820	4	US-09-150-900-48	Sequence 48, Appl
1031	45.4	4.6	2148	4	US-09-902-540-5682	Sequence 5682, Appl	1104	45	4.6	855	4	US-09-902-540-2898	Sequence 2898, Ap
c1032	45.4	4.6	2167	2	US-08-461-775-9	Sequence 9, Appl	1105	45	4.6	879	4	US-09-902-540-7823	Sequence 7823, Ap
ci1033	45.4	4.6	2167	3	US-09-031-608-9	Sequence 9, Appl	1106	45	4.6	987	4	US-09-902-540-6321	Sequence 6321, Ap
ci1034	45.4	4.6	2196	4	US-09-252-991A-3536	Sequence 3536, Appl	1107	45	4.6	1161	4	US-09-902-540-3273	Sequence 3273, Ap
1035	45.4	4.6	2286	4	US-09-902-540-2486	Sequence 2486, Appl	1108	45	4.6	1187	1	US-08-440-856A-2	Sequence 2, Appl
ci1036	45.4	4.6	2325	4	US-09-252-991A-3413	Sequence 3413, Appl	1109	45	4.6	1206	4	US-09-585-173B-43	Sequence 43, Appl
1037	45.4	4.6	2571	4	US-09-984-880-1	Sequence 1, Appl	1110	45	4.6	1377	4	US-09-902-540-7709	Sequence 7709, Ap
1038	45.4	4.6	2571	4	US-10-277-032-1	Sequence 1, Appl	1111	45	4.6	1413	4	US-09-252-991A-6071	Sequence 6071, Ap
1039	45.4	4.6	2643	4	US-09-902-540-2841	Sequence 2841, Appl	1112	45	4.6	1455	4	US-09-902-540-3393	Sequence 3393, Ap
ci1040	45.4	4.6	2668	2	US-08-461-775-11	Sequence 11, Appl	1113	45	4.6	1458	4	US-09-902-540-6238	Sequence 6238, Ap
ci1041	45.4	4.6	2668	3	US-09-031-606-11	Sequence 11, Appl	ci1114	45	4.6	1491	4	US-09-252-991A-6232	Sequence 6232, Ap
1042	45.4	4.6	2973	4	US-09-902-540-4476	Sequence 4476, Appl	1115	45	4.6	1506	4	US-09-252-991A-6228	Sequence 6228, Ap
ci1043	45.4	4.6	3999	4	US-09-902-540-655	Sequence 655, Appl	1116	45	4.6	1690	4	US-09-620-312D-69	Sequence 69, Appl
1044	45.4	4.6	4180	4	US-09-814-918A-93	Sequence 93, Appl	ci1117	45	4.6	1713	4	US-09-902-540-6981	Sequence 6981, Ap
ci1045	45.4	4.6	5515	4	US-09-902-540-701	Sequence 701, Appl	ci1118	45	4.6	1743	4	US-09-949-016-945	Sequence 945, Appl
1046	45.4	4.6	5523	4	US-09-902-540-3952	Sequence 3952, Appl	ci1119	45	4.6	1743	4	US-09-949-016-2709	Sequence 2709, Ap
ci1047	45.4	4.6	16047	4	US-09-902-540-1136	Sequence 1136, Appl	ci1120	45	4.6	1803	4	US-09-902-540-339	Sequence 339, Appl
1048	45.4	4.6	19979	4	US-09-949-016-12309	Sequence 12309, A	ci1121	45	4.6	1843	4	US-09-902-540-389	Sequence 389, Appl
1049	45.4	4.6	19980	4	US-09-949-016-13533	Sequence 13533, A	1122	45	4.6	1845	4	US-09-902-540-7160	Sequence 7160, Ap

1123	45	4.6	3192	4	US-09-302-540-4843	Sequence 4843, Ap	1196	44.6	4.5	462	4	US-09-302-540-4652	Sequence 4652, Ap
1124	45	4.6	3651	2	US-08-790-374-1	Sequence 1, Appl1	1197	44.6	4.5	642	4	US-09-302-540-8653	Sequence 8653, Ap
1125	45	4.6	4135	4	US-09-302-540-9587	Sequence 9587, Ap	1198	44.6	4.5	813	4	US-09-302-540-9587	Sequence 9587, Ap
1126	45	4.6	4494	4	US-09-302-540-659	Sequence 659, App	1199	44.6	4.5	822	4	US-09-302-540-9235	Sequence 9235, Ap
1127	45	4.6	4862	4	US-09-302-540-608	Sequence 608, App	1200	44.6	4.5	837	4	US-09-302-540-9235	Sequence 9235, Ap
1128	45	4.6	5743	4	US-09-302-540-12687	Sequence 12687, A	1201	44.6	4.5	867	4	US-09-302-540-7100	Sequence 7100, Ap
1129	45	4.6	5743	4	US-09-302-540-12687	Sequence 12687, A	1202	44.6	4.5	897	4	US-09-302-540-7100	Sequence 7100, Ap
1130	45	4.6	6260	4	US-09-302-540-781	Sequence 781, App	1203	44.6	4.5	1080	4	US-09-302-540-5177	Sequence 5177, Ap
1131	45	4.6	7280	4	US-09-302-540-827	Sequence 827, App	1204	44.6	4.5	1236	4	US-09-302-540-8061	Sequence 8061, Ap
1132	45	4.6	7812	3	US-09-368-590-1	Sequence 1, Appl1	1205	44.6	4.5	1260	4	US-09-302-540-4016	Sequence 4016, Ap
1133	45	4.6	8604	4	US-09-302-540-916	Sequence 916, App	1206	44.6	4.5	1272	4	US-09-302-540-14082	Sequence 14082, A
1134	45	4.6	8756	4	US-09-302-540-1438	Sequence 1438, Ap	1207	44.6	4.5	1329	4	US-09-302-540-14036	Sequence 14036, A
1135	45	4.6	8914	4	US-09-302-540-915	Sequence 915, App	1208	44.6	4.5	1334	4	US-09-302-540-4356	Sequence 4356, Ap
1136	45	4.6	16437	4	US-09-302-540-1160	Sequence 1160, Ap	1209	44.6	4.5	1545	4	US-09-302-540-5060	Sequence 5060, Ap
1137	45	4.6	16924	4	US-09-302-540-1178	Sequence 1178, Ap	1210	44.6	4.5	1578	4	US-09-302-540-5060	Sequence 5060, Ap
1138	45	4.6	21758	4	US-09-302-540-1238	Sequence 1238, Ap	1211	44.6	4.5	1587	4	US-09-302-540-16504	Sequence 16504, A
1139	45	4.6	23187	4	US-09-499-522-1	Sequence 1, Appl1	1212	44.6	4.5	1620	4	US-09-302-540-14186	Sequence 14186, A
1140	45	4.6	35614	4	US-09-302-540-1259	Sequence 1259, Ap	1213	44.6	4.5	1623	4	US-09-302-540-5431	Sequence 5431, Ap
1141	44.8	4.5	591	4	US-09-302-540-9199	Sequence 9199, Ap	1214	44.6	4.5	1629	4	US-09-302-540-9163	Sequence 9163, Ap
1142	44.8	4.5	660	4	US-09-302-540-3995	Sequence 3995, Ap	1215	44.6	4.5	1638	4	US-09-302-540-3216	Sequence 3216, Ap
1143	44.8	4.5	753	4	US-09-302-540-6830	Sequence 6830, Ap	1216	44.6	4.5	2005	4	US-09-302-540-9101	Sequence 9101, Ap
1144	44.8	4.5	753	4	US-09-302-540-6830	Sequence 6830, Ap	1217	44.6	4.5	2070	4	US-09-302-540-9101	Sequence 9101, Ap
1145	44.8	4.5	783	4	US-09-302-540-9609	Sequence 9609, Ap	1218	44.6	4.5	2154	4	US-09-302-540-453	Sequence 453, App
1146	44.8	4.5	858	4	US-09-302-540-8452	Sequence 8452, Ap	1219	44.6	4.5	2163	4	US-09-302-540-2947	Sequence 2947, Ap
1147	44.8	4.5	948	4	US-09-302-540-8298	Sequence 8298, Ap	1220	44.6	4.5	2178	4	US-09-302-540-6462	Sequence 6462, Ap
1148	44.8	4.5	965	4	US-09-302-540-14810	Sequence 14810, A	1221	44.6	4.5	2205	4	US-09-302-540-4101	Sequence 4101, Ap
1149	44.8	4.5	1062	4	US-09-302-540-6043	Sequence 6043, Ap	1222	44.6	4.5	2214	4	US-09-302-540-9199	Sequence 9199, Ap
1150	44.8	4.5	1068	4	US-09-302-540-244	Sequence 244, App	1223	44.6	4.5	2387	4	US-09-302-540-453	Sequence 453, App
1151	44.8	4.5	1095	4	US-09-302-540-4983	Sequence 4983, Ap	1224	44.6	4.5	2556	4	US-09-302-540-8202	Sequence 8202, Ap
1152	44.8	4.5	1110	4	US-09-302-540-8388	Sequence 8388, Ap	1225	44.6	4.5	2564	4	US-09-302-540-8202	Sequence 8202, Ap
1153	44.8	4.5	1131	4	US-09-302-540-8486	Sequence 8486, Ap	1226	44.6	4.5	3453	4	US-09-302-540-8100	Sequence 8100, Ap
1154	44.8	4.5	1162	2	US-08-726-306A-52	Sequence 52, Appl	1227	44.6	4.5	3456	4	US-09-302-540-1309	Sequence 1309, Ap
1155	44.8	4.5	1257	4	US-09-302-540-8931	Sequence 8931, Ap	1228	44.6	4.5	3978	4	US-09-302-540-965-19	Sequence 965-19, Appl
1156	44.8	4.5	1275	4	US-09-302-540-3545	Sequence 3545, Ap	1229	44.6	4.5	4591	4	US-09-302-540-3369	Sequence 3369, Ap
1157	44.8	4.5	1320	4	US-09-302-540-7598	Sequence 7598, Ap	1230	44.6	4.5	4591	4	US-09-302-540-646	Sequence 646, App
1158	44.8	4.5	1341	4	US-09-302-540-7598	Sequence 7598, Ap	1231	44.6	4.5	4874	4	US-09-302-540-771	Sequence 771, App
1159	44.8	4.5	1365	3	US-09-319-892-1	Sequence 1, Appl1	1232	44.6	4.5	5275	3	US-09-302-540-934-28	Sequence 934-28, Appl
1160	44.8	4.5	1428	4	US-09-302-540-14802	Sequence 14802, A	1233	44.6	4.5	9039	4	US-09-302-540-983	Sequence 983, App
1161	44.8	4.5	1479	4	US-09-302-540-7414	Sequence 7414, Ap	1234	44.6	4.5	9676	4	US-09-302-540-16629	Sequence 16629, A
1162	44.8	4.5	1485	4	US-09-302-540-7202	Sequence 7202, Ap	1235	44.6	4.5	10280	4	US-09-302-540-980	Sequence 980, App
1163	44.8	4.5	1515	4	US-09-302-540-6108	Sequence 6108, Ap	1236	44.6	4.5	12173	4	US-09-302-540-1022	Sequence 1022, Ap
1164	44.8	4.5	1519	4	US-09-302-540-279	Sequence 279, App	1237	44.6	4.5	12249	4	US-09-302-540-1022	Sequence 1022, Ap
1165	44.8	4.5	1658	4	US-09-302-540-14950	Sequence 14950, A	1238	44.6	4.5	17125	4	US-09-302-540-1158	Sequence 1158, Ap
1166	44.8	4.5	1684	4	US-09-302-540-8051	Sequence 8051, Ap	1239	44.6	4.5	17173	4	US-09-302-540-1158	Sequence 1158, Ap
1167	44.8	4.5	1899	4	US-09-302-540-6781	Sequence 6781, Ap	1240	44.6	4.5	18331	4	US-09-302-540-1158	Sequence 1158, Ap
1168	44.8	4.5	1895	4	US-09-302-540-9209	Sequence 9209, Ap	1241	44.6	4.5	23694	4	US-09-302-540-1216	Sequence 1216, Ap
1169	44.8	4.5	2016	4	US-09-302-540-4303	Sequence 4303, Ap	1242	44.6	4.5	23738	4	US-09-302-540-1203	Sequence 1203, Ap
1170	44.8	4.5	2028	4	US-09-302-540-7091	Sequence 7091, Ap	1243	44.6	4.5	28320	4	US-09-302-540-1222	Sequence 1222, Ap
1171	44.8	4.5	2064	4	US-09-302-540-9616	Sequence 9616, Ap	1244	44.6	4.5	29559	4	US-09-302-540-1254	Sequence 1254, Ap
1172	44.8	4.5	2136	4	US-09-302-540-5582	Sequence 5582, Ap	1245	44.6	4.5	47818	4	US-09-302-540-12324	Sequence 12324, A
1173	44.8	4.5	2211	4	US-09-302-540-5403	Sequence 5403, Ap	1246	44.6	4.5	48480	4	US-09-302-540-15166	Sequence 15166, A
1174	44.8	4.5	2235	4	US-09-302-540-7032	Sequence 7032, Ap	1247	44.6	4.5	76165	4	US-09-302-540-12288	Sequence 12288, A
1175	44.8	4.5	2316	4	US-09-302-540-3869	Sequence 3869, Ap	1248	44.6	4.5	76165	4	US-09-302-540-14005	Sequence 14005, A
1176	44.8	4.5	3036	4	US-09-302-540-4040	Sequence 4040, Ap	1249	44.6	4.5	465	4	US-09-302-540-1459	Sequence 1459, Ap
1177	44.8	4.5	3078	3	US-09-418-817-9	Sequence 9, Appl1	1250	44.4	4.5	546	4	US-09-302-540-5427	Sequence 5427, Ap
1178	44.8	4.5	3162	4	US-09-302-540-9569	Sequence 9569, Ap	1251	44.4	4.5	720	4	US-09-302-540-14268	Sequence 14268, A
1179	44.8	4.5	3225	4	US-09-302-540-3099	Sequence 3099, Ap	1252	44.4	4.5	750	4	US-09-302-540-5834	Sequence 5834, Ap
1180	44.8	4.5	3793	4	US-09-302-540-4846	Sequence 4846, Ap	1253	44.4	4.5	756	4	US-09-302-540-15229	Sequence 15229, A
1181	44.8	4.5	5064	4	US-09-774-528-224	Sequence 224, App	1254	44.4	4.5	819	4	US-09-302-540-15235	Sequence 15235, A
1182	44.8	4.5	5097	4	US-09-302-540-745	Sequence 745, App	1255	44.4	4.5	1077	4	US-09-302-540-1917	Sequence 1917, Ap
1183	44.8	4.5	5245	4	US-09-302-540-714	Sequence 714, App	1256	44.4	4.5	1089	4	US-09-302-540-9317	Sequence 9317, Ap
1184	44.8	4.5	5893	4	US-09-302-540-5001	Sequence 5001, Ap	1257	44.4	4.5	1116	4	US-09-302-540-9445	Sequence 9445, A
1185	44.8	4.5	6217	3	US-09-418-817-1	Sequence 1, Appl1	1258	44.4	4.5	1161	4	US-09-302-540-10489	Sequence 10489, A
1186	44.8	4.5	6569	4	US-09-302-540-17534	Sequence 17534, A	1259	44.4	4.5	1305	4	US-09-302-540-11607	Sequence 11607, A
1187	44.8	4.5	8832	4	US-09-302-540-984	Sequence 984, App	1260	44.4	4.5	1317	4	US-09-302-540-11762	Sequence 11762, A
1188	44.8	4.5	10301	4	US-09-302-540-985	Sequence 985, App	1261	44.4	4.5	1317	4	US-09-302-540-3356	Sequence 3356, Ap
1189	44.8	4.5	11282	4	US-09-302-540-1039	Sequence 1039, Ap	1262	44.4	4.5	1395	4	US-09-302-540-3185	Sequence 3185, Ap
1190	44.8	4.5	12865	4	US-09-302-540-1048	Sequence 1048, Ap	1263	44.4	4.5	1512	4	US-09-302-540-1551	Sequence 1551, Ap
1191	44.8	4.5	14330	4	US-09-302-540-1009	Sequence 1009, Ap	1264	44.4	4.5	1600	3	US-09-302-540-288-10	Sequence 10, Appl
1192	44.8	4.5	17592	4	US-09-302-540-1138	Sequence 1138, Ap	1265	44.4	4.5	1608	4	US-09-302-540-7945	Sequence 7945, Ap
1193	44.8	4.5	21143	4	US-09-302-540-1191	Sequence 1191, Ap	1266	44.4	4.5	1677	4	US-09-302-540-1816	Sequence 1816, Ap
1194	44.8	4.5	61158	4	US-09-302-540-15041	Sequence 15041, A	1267	44.4	4.5	1731	2	US-08-466-583-1	Sequence 1, Appl1
1195	44.8	4.5	75431	4	US-09-302-540-15122	Sequence 15122, A	1268	44.4	4.5	1731	4	US-08-365-427-1	Sequence 1, Appl1

1269	44.4	4.5	1731	5	PCT-US95-07820-1	Sequence 1, Appli	1342	44.2	4.5	1629	4	US-09-902-540-8462	Sequence 8462, Ap
1270	44.4	4.5	1878	4	US-09-489-039A-2045	Sequence 2045, Ap	c1343	44.2	4.5	1632	4	US-09-252-991A-3859	Sequence 3859, Ap
c1271	44.4	4.5	2073	4	US-09-252-991A-10279	Sequence 10279, A	1344	44.2	4.5	1716	4	US-09-252-991A-15268	Sequence 15268, A
1272	44.4	4.5	2176	6	5320958-1	Patent No. 5320958	1345	44.2	4.5	1740	4	US-09-252-991A-13753	Sequence 13753, A
1273	44.4	4.5	2176	6	5320958-1	Patent No. 5320958	1346	44.2	4.5	1779	4	US-09-902-540-3312	Sequence 3312, Ap
1274	44.4	4.5	2256	4	US-09-902-540-2730	Sequence 2730, Ap	1347	44.2	4.5	1835	3	US-09-417-704-2	Sequence 2, Appli
1275	44.4	4.5	2325	4	US-09-252-991A-218	Sequence 218, Ap	c1348	44.2	4.5	1848	4	US-09-252-991A-15408	Sequence 15408, A
1276	44.4	4.5	2352	4	US-09-902-540-4536	Sequence 4536, Ap	c1349	44.2	4.5	2040	4	US-09-252-991A-12316	Sequence 12316, A
1277	44.4	4.5	2352	4	US-09-902-540-4536	Sequence 4536, Ap	1350	44.2	4.5	2187	4	US-09-902-540-3500	Sequence 3500, Ap
1278	44.4	4.5	2330	4	US-09-252-991A-15188	Sequence 15188, A	1351	44.2	4.5	2483	1	US-08-464-340A-3	Sequence 3, Appli
c1279	44.4	4.5	2772	4	US-09-252-991A-10577	Sequence 10577, A	1352	44.2	4.5	2483	5	PCT-US94-08449A-3	Sequence 3, Appli
c1280	44.4	4.5	2784	4	US-09-252-991A-194	Sequence 194, App	c1353	44.2	4.5	2725	4	US-09-902-540-537	Sequence 527, App
1281	44.4	4.5	2946	4	US-09-252-991A-227	Sequence 227, App	1354	44.2	4.5	2751	4	US-09-252-991A-14671	Sequence 14671, A
1282	44.4	4.5	3186	4	US-09-949-016-1250	Sequence 1250, Ap	c1355	44.2	4.5	2872	3	US-09-327-487A-2	Sequence 2, Appli
1283	44.4	4.5	3384	4	US-09-902-540-3780	Sequence 3780, Ap	c1356	44.2	4.5	3201	4	US-09-252-991A-14959	Sequence 14959, A
c1284	44.4	4.5	3392	4	US-09-902-540-3089	Sequence 3089, Ap	c1357	44.2	4.5	3255	4	US-09-252-991A-10617	Sequence 10617, A
c1285	44.4	4.5	3603	4	US-09-252-991A-14443	Sequence 14443, A	1358	44.2	4.5	3375	4	US-09-252-991A-10239	Sequence 10239, A
1286	44.4	4.5	4267	3	US-08-949-155-51	Sequence 51, Appl	c1359	44.2	4.5	3402	4	US-09-252-991A-14791	Sequence 14791, A
c1287	44.4	4.5	4267	3	US-08-919-964-51	Sequence 51, Appl	c1360	44.2	4.5	3783	4	US-09-902-540-4846	Sequence 4846, Ap
1288	44.4	4.5	5663	4	US-09-902-540-839	Sequence 839, App	1361	44.2	4.5	3841	4	US-09-902-540-607	Sequence 607, App
c1289	44.4	4.5	6377	4	US-09-902-540-802	Sequence 802, App	c1362	44.2	4.5	4689	3	US-09-105-537-34	Sequence 34, Appl
c1290	44.4	4.5	7865	4	US-09-949-016-13537	Sequence 13537, A	c1363	44.2	4.5	5467	4	US-09-902-540-703	Sequence 703, App
c1291	44.4	4.5	10835	4	US-09-902-540-1031	Sequence 1031, Ap	c1364	44.2	4.5	6012	4	US-09-902-540-808	Sequence 808, App
c1292	44.4	4.5	11992	4	US-09-902-540-995	Sequence 995, App	1365	44.2	4.5	7012	4	US-09-902-540-890	Sequence 890, App
1293	44.4	4.5	15689	4	US-09-902-540-1129	Sequence 1129, Ap	c1366	44.2	4.5	7518	4	US-09-902-540-870	Sequence 870, App
1294	44.4	4.5	15789	4	US-09-902-540-1139	Sequence 1139, Ap	1367	44.2	4.5	7680	4	US-09-902-540-8948	Sequence 8948, Ap
c1295	44.4	4.5	18917	4	US-09-949-016-13129	Sequence 13129, A	c1368	44.2	4.5	8532	4	US-09-902-540-927	Sequence 927, App
c1296	44.4	4.5	18917	4	US-09-949-016-13130	Sequence 13130, A	c1369	44.2	4.5	8563	4	US-09-902-540-3318	Sequence 3318, Ap
c1297	44.4	4.5	18917	4	US-09-949-016-13131	Sequence 13131, A	c1370	44.2	4.5	11476	4	US-09-902-540-955	Sequence 955, App
c1298	44.4	4.5	23233	4	US-09-902-540-1184	Sequence 1184, Ap	c1371	44.2	4.5	11922	4	US-09-902-540-1063	Sequence 1063, Ap
1299	44.4	4.5	25497	4	US-09-902-540-1224	Sequence 1224, Ap	c1372	44.2	4.5	13842	3	US-09-105-537-30	Sequence 30, Appl
c1300	44.4	4.5	34953	4	US-09-902-540-1263	Sequence 1263, Ap	1373	44.2	4.5	13551	4	US-09-902-540-1154	Sequence 1154, Ap
c1301	44.4	4.5	670889	4	US-09-949-016-150505	Sequence 12505, A	c1374	44.2	4.5	18471	4	US-09-902-540-1167	Sequence 1167, Ap
c1302	44.4	4.5	670890	4	US-09-949-016-15207	Sequence 14207, A	1375	44.2	4.5	20235	1	US-07-642-734C-3	Sequence 3, Appli
1303	44.2	4.5	483	4	US-09-252-991A-15272	Sequence 15272, A	c1376	44.2	4.5	20235	3	US-08-439-009A-3	Sequence 3, Appli
1304	44.2	4.5	594	4	US-09-252-991A-3950	Sequence 3950, Ap	c1377	44.2	4.5	21010	4	US-09-902-540-1188	Sequence 1188, Ap
1305	44.2	4.5	627	4	US-09-902-540-3927	Sequence 3927, Ap	1378	44.2	4.5	21758	4	US-09-902-540-1238	Sequence 1238, Ap
c1306	44.2	4.5	720	4	US-09-902-540-4895	Sequence 4895, Ap	c1379	44.2	4.5	28493	4	US-09-902-540-1241	Sequence 1241, A
c1307	44.2	4.5	765	4	US-09-252-991A-3922	Sequence 3922, Ap	1380	44.2	4.5	31713	4	US-09-949-016-16960	Sequence 16960, A
c1308	44.2	4.5	798	4	US-09-252-991A-9181	Sequence 9181, Ap	1381	44.2	4.5	34552	4	US-09-902-540-1262	Sequence 1262, Ap
1309	44.2	4.5	810	4	US-09-902-540-8741	Sequence 8741, Ap	c1382	44.2	4.5	36778	3	US-09-105-537-5	Sequence 5, Appli
1310	44.2	4.5	837	4	US-09-252-991A-3647	Sequence 3647, Ap	c1383	44.2	4.5	38506	3	US-09-320-878-19	Sequence 19, Appl
1311	44.2	4.5	879	4	US-09-252-991A-3602	Sequence 3602, Ap	c1384	44.2	4.5	38506	4	US-09-141-908-1	Sequence 1, Appli
c1312	44.2	4.5	888	4	US-09-902-540-8741	Sequence 8741, Ap	c1385	44.2	4.5	38506	4	US-09-657-440-19	Sequence 19, Appl
1313	44.2	4.5	903	4	US-09-252-991A-8894	Sequence 8894, Ap	c1386	44.2	4.4	426	4	US-09-252-991A-16285	Sequence 16285, A
1314	44.2	4.5	930	4	US-09-902-540-8794	Sequence 8794, Ap	c1387	44.2	4.4	426	4	US-09-252-991A-2270	Sequence 2270, Ap
1315	44.2	4.5	942	4	US-09-902-540-8794	Sequence 8794, Ap	c1388	44.2	4.4	492	4	US-09-252-991A-4051	Sequence 4051, Ap
1316	44.2	4.5	975	4	US-09-252-991A-12244	Sequence 12244, A	1389	44.2	4.4	537	4	US-09-902-540-3308	Sequence 3308, Ap
c1317	44.2	4.5	999	4	US-09-252-991A-14326	Sequence 14326, A	1390	44.2	4.4	765	4	US-09-902-540-8591	Sequence 8591, Ap
1318	44.2	4.5	1005	4	US-09-902-540-6685	Sequence 6685, Ap	1391	44.2	4.4	897	3	US-09-434-288-6	Sequence 6, Appli
1319	44.2	4.5	1018	1	US-08-444-083-6	Sequence 6, Appli	1392	44.2	4.4	948	4	US-09-252-991A-2569	Sequence 2569, Ap
1320	44.2	4.5	1018	1	US-08-286-304-6	Sequence 6, Appli	c1393	44.2	4.4	957	4	US-09-252-991A-5476	Sequence 5476, Ap
1321	44.2	4.5	1018	1	US-08-442-745-6	Sequence 6, Appli	1394	44.2	4.4	981	4	US-09-252-991A-5453	Sequence 5453, Ap
1322	44.2	4.5	1018	1	US-08-443-129-6	Sequence 6, Appli	c1395	44.2	4.4	1026	4	US-09-252-991A-2349	Sequence 2349, Ap
1323	44.2	4.5	1018	1	US-08-443-952-6	Sequence 6, Appli	1396	44.2	4.4	1062	4	US-09-252-991A-16067	Sequence 16067, A
1324	44.2	4.5	1018	1	US-08-443-130-6	Sequence 6, Appli	c1397	44.2	4.4	1110	4	US-09-252-991A-1858	Sequence 1858, Ap
1325	44.2	4.5	1018	3	US-08-898-911-6	Sequence 6, Appli	c1398	44.2	4.4	1110	4	US-09-252-991A-8823	Sequence 8823, Ap
1326	44.2	4.5	1018	5	PCT-US95-04667-6	Sequence 6, Appli	1399	44.2	4.4	1116	4	US-09-252-991A-2104	Sequence 2104, Ap
1327	44.2	4.5	1080	4	US-09-902-540-9563	Sequence 9563, Ap	c1400	44.2	4.4	1126	3	US-08-949-155-5	Sequence 5, Appli
c1328	44.2	4.5	1116	4	US-09-252-991A-13384	Sequence 13384, A	c1401	44.2	4.4	1126	3	US-09-819-964-5	Sequence 5, Appli
c1329	44.2	4.5	1194	4	US-09-252-991A-4021	Sequence 4021, Ap	c1402	44.2	4.4	1152	4	US-09-252-991A-1791	Sequence 1791, Ap
1330	44.2	4.5	1233	4	US-09-252-991A-15366	Sequence 15366, A	1403	44.2	4.4	1281	4	US-09-902-540-2838	Sequence 2838, Ap
c1331	44.2	4.5	1257	4	US-09-252-991A-15464	Sequence 15464, A	1404	44.2	4.4	1332	4	US-09-902-540-8694	Sequence 8694, Ap
1332	44.2	4.5	1290	4	US-09-902-540-5641	Sequence 5641, Ap	1405	44.2	4.4	1333	3	US-09-372-422A-9	Sequence 9, Appli
c1333	44.2	4.5	1292	4	US-09-902-540-137	Sequence 127, App	1406	44.2	4.4	1338	4	US-09-902-540-7158	Sequence 7158, Ap
1334	44.2	4.5	1377	4	US-09-252-991A-13964	Sequence 13964, A	1407	44.2	4.4	1611	4	US-09-902-540-5936	Sequence 5836, Ap
1335	44.2	4.5	1392	4	US-09-902-540-6975	Sequence 6975, Ap	1408	44.2	4.4	1612	4	US-09-902-540-128	Sequence 128, App
1336	44.2	4.5	1518	4	US-09-252-991A-12104	Sequence 12104, A	1409	44.2	4.4	1683	4	US-09-252-991A-11226	Sequence 11226, A
c1337	44.2	4.5	1530	4	US-09-902-540-8329	Sequence 8329, Ap	1410	44.2	4.4	1716	4	US-09-902-540-9034	Sequence 9034, Ap
c1338	44.2	4.5	1539	4	US-09-648-183-1	Sequence 1, Appli	1411	44.2	4.4	1734	4	US-09-252-991A-9061	Sequence 9061, Ap
c1339	44.2	4.5	1539	4	US-09-648-183-2	Sequence 2, Appli	1412	44.2	4.4	1755	4	US-09-949-016-2716	Sequence 2716, Ap
1340	44.2	4.5	1593	4	US-09-252-991A-14376	Sequence 14376, A	1413	44.2	4.4	1902	4	US-09-902-540-2344	Sequence 2344, Ap
1341	44.2	4.5	1614	4	US-09-252-991A-10453	Sequence 10453, A	c1414	44.2	4.4	1908	4	US-09-252-991A-16529	Sequence 16529, A



Db 628 TACCCGGAATACCTGGAGGCGCGCTGGGCTGGTGGCGACGCTGGGCTGGTCTTTTC 687  
Qy 714 CTCAGAGTCTGTGGCGCGGGAAGTGTGCAACCTCCGAAGGGAGACGTGGCGCGGAG 773  
Db 688 GACAACTGCTGTGGAGCGCGCGGGTGTCTCGAAGCGCAGCCGAAGAGTCCGATACCCGC 747  
Qy 774 TGTGTCCGAAACCTAAACGACATCCCGCGGGAGTCAAGGCTCTACATCAGCCTCCGTG 833  
Db 748 GGCATCCAGAGCTCAACTTGGCGCTGAAGACGACGCGGGTGAATCTCGCTGTCTG 807  
Qy 834 CCCCTGGCGGATGACTCACTTTGGCCCTTCAAGATCT 870  
Db 808 CCGATCGCGGCGGGCTGAGCGTCTCTCGCAAGCGCT 844

## RESULT 2

US-09-452-239-45

; Sequence 45, Application US/09452239

; Patent No. 6465229

; GENERAL INFORMATION:

; APPLICANT: Rafaleki, Antoni J.

; APPLICANT: Fader, Gary M.

; APPLICANT: Cahoon, Rebecca E.

; TITLE OF INVENTION: Plant Caffeoyl-CoA O-Methyltransferase

; FILE REFERENCE: BB1284 US NA

; CURRENT APPLICATION NUMBER: US/09/452,239

; CURRENT FILING DATE: 1999-12-01

; EARLIER APPLICATION NUMBER: 60/110,594

; EARLIER FILING DATE: 1998-December-02

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 45

; LENGTH: 953

; TYPE: DNA

; ORGANISM: Triticum aestivum

US-09-452-239-45

Query Match 16.4%; Score 161.8; DB 3; Length 953;  
Best Local Similarity 55.1%; Pred. No. 1.2e-22;  
Matches 338; Conservative 0; Mismatches 272; Indels 3; Gaps 1;

Qy 273 CGGGAGCACCCGCGCTCGGAAGCCCTGAGGCTGTGACCTCGAGCAGCGCCGAGGGGAT 332  
Db 186 CGGGAGCACAGTGTGATGCGGACCTGCGCTCATCACGACAGCCATGGGGTTAC 245

Qy 333 TCTATGATGACCTGAGCAGGCGCCAGCTCTTGGCCAACTTGGCGGGCTCATCCAGGCC 392  
Db 246 ATGCAGTCTCTCGGACGAGCGCAGCTGCTGGGGATGCTGATCAAGATGGCGGCGCC 305

Qy 393 AAGAGGCGCTGGACCTGGGCACTTACGGGCTACTCCGCTTGGCCCTGGCCCTGGCG 452  
Db 306 AAGAAGACATGAGGTGGGCGCTGTTCACGGGGTACTCGCTGTGGCCACCGCGTGGCG 365

Qy 453 CTGCCCGGACGCGGCGCTGTGTGACTCTGAGGTGGAGCGCAGCGCCCGAGCTGGGA 512  
Db 366 CTCGCCGAGAGCGGAGTGTGTGGCCATCGACCGAGTGTCTACAGGTGGGT 425

Qy 513 CGGCCCCCTGTGGAGGCGAGCCGAGCGGAGCACAAGATCGACTCTCGGCTGAAGCCCGCC 572  
Db 426 CGCCCCCTTCATCGAAGGCGCGCATGGCGCACAGGTGGACTTCGCGAGGGCACCGGC 485

Qy 573 TTGGAGACCTTGAAGTGTCTGGCGGCGGCGGA---GGCCGGACCTTCACGTGGCC 629  
Db 486 CTGGCGCGCTGGACGAGTCTCTGCTCGAGGACGACGCGCGCGCGAGCTACGACTTCGG 545

Qy 630 GTGGTGGATGCGGACAAAGAGAACTGTCTCCGCTACTACGAGCGCTGCTGAGCTGTCTG 689  
Db 546 TTCGTGGACCGCGACAGGCCAACTACGTGGCGCTACCAAGAGCTGTGAAGTGGTC 605

Qy 690 CGACCGGAGGATCTCTCGCCCTCTCAGATCTCTGTGGCGCGGGAAGGTCTGCAACT 749  
Db 606 CGCGTGGCGGCGCATCTATCTACGACAAACGCTCTGGGGCGGACGCTGGCGGTGGCG 665

Qy 750 CCGAAGGGGAGCCTGGCGCGCGAGTGTGTGCGAAACCTAAACGCAACGCAATCCGGCGGAC 809  
Db 666 GGGGCAACCCCATGTCCGACCTCGACACCCCGCTTCTCCGCGCCCTCAGGACCTCAAC 725  
Qy 810 GTCAGGGTCTACATCAGGCTCTTGGCCCTTGGCGGATGGACTCACCTTGGCCCTTCAAGATC 869  
Db 726 GCGAAGCTCGCGCGCGACCCGCGCATCGAGGTCTGCAGCTCGCCATCGCCGACGAGTC 785  
Qy 870 TAGGGCTGGCCCC 882  
Db 786 ACCATCTGCCGCC 798

## RESULT 3

US-09-452-239-43

; Sequence 43, Application US/09452239

; Patent No. 6465229

; GENERAL INFORMATION:

; APPLICANT: Rafaleki, Antoni J.

; APPLICANT: Fader, Gary M.

; APPLICANT: Cahoon, Rebecca E.

; TITLE OF INVENTION: Plant Caffeoyl-CoA O-Methyltransferase

; FILE REFERENCE: BB1284 US NA

; CURRENT APPLICATION NUMBER: US/09/452,239

; CURRENT FILING DATE: 1999-12-01

; EARLIER APPLICATION NUMBER: 60/110,594

; EARLIER FILING DATE: 1998-December-02

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 43

; LENGTH: 1049

; TYPE: DNA

; ORGANISM: Triticum aestivum

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (352)

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (948)

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (992)

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (994)

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (999)

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1003)

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1038)

US-09-452-239-43

Query Match 16.1%; Score 159.2; DB 3; Length 1049;  
Best Local Similarity 54.8%; Pred. No. 4e-22;  
Matches 336; Conservative 0; Mismatches 274; Indels 3; Gaps 1;

Qy 273 CGGGAGCACCCGCGCTCGGAAGCCCTGAGGCTGTGACCTCGAGCAGCGCCGAGGGGAT 332  
Db 186 CGCGAGCAGAGTGTATGCGGACCTGCGCTCATCACGACAGCACCCATGGGGTTAC 245

Qy 333 TCTATGATGACCTGCGAGCAGGCCAGCTCTTGGCCAACTTGGCGGGCTCATCCAGGCC 392  
Db 246 ATGCAGTCTCTCGGACGAGGCGCAGCTGCTGGGGATGCTGATCAAGATGGCGGCGCC 305

Qy 393 AAGAGGCGCTGGACCTTGGGACCTTACGGGCTACTCGCCCTGCGCCCTGGCCCTGGCG 452  
Db 306 AAGAAGAAGATCGAGGTGGGGGTGTTTTCAGCGGGCTACTCGCTGCTGNCACCGCGCTGGCG 365

QY 453 CTGCCCGCGGACCGGCGCTGTGACCTGGAGGTGGAACGCGAGCCCGCGAGCTGGGA 512  
DB 366 CTCCCGAGGACCGCAAGGTGTGGGATCGACACCGACCGAGTGTCTACGAGTGGGT 425  
QY 513 CGGCCCTGTGAGGAGCGGAGCGGAGGAGCAAGATCGACCTCCGGCTGAAGCCCGGC 572  
DB 426 CGCCCTTTCATTGAGAAAGCGGCATGGCGCAACAGGTGATCTCCGAGGGCACCGGC 485  
QY 573 TTGGAGACCTGGACGAGCTGTGGCGGCGGGCGA---GGCCGGCACCTTTCGAGTGGCC 629  
DB 486 CTGGCGCGCTGGACGAGCTCTCTCGTGGAGGACGACGCGCGCGGAGCTACGACTTCGCG 545  
QY 630 GTGGTGGATCGGACAGGAGAACTGCTCGGCTACTACAGAGCGCTGCTGAGCTGCTG 689  
DB 546 TTCTGTGGACGCGGACAAAGCCCACTACGTGCGTACACAGAGAGCTGTGAGCTGGTC 605  
QY 690 CGACCCGAGGAGATCTCGCCGCTCTCAGAGTCTGTGGCGGCGGAGGTGCTGCAACT 749  
DB 606 CGGCTCGGCGGCACTATCTACGACACACGCTCTGGGCGGCGACGGTGGCGCTGCGG 665  
QY 750 CGGAAAGGGGACGTGGCGGCGGAGTGTGCGAAACCTTAAACGACGATCTCGGCGGGAC 809  
DB 666 GCGGGACCCCATGTCGACCTCGACACCCGCTTCTCGCGCGCTCAGGGACCTCAAC 725  
QY 810 GTGAGGCTTACATGAGCTCTCGCCCTCGGCGGAGTGGATCACTTGGCTTTCAAGATC 869  
DB 726 GCGAAGCTCGCGCGGACCGCGCATCGAGTCTGCGAGTCTGCCATCGCCATCGCGACGCGTC 785  
QY 870 TAGGCTGGCCCC 882  
DB 786 ACATCTGCGGCC 798

## RESULT 4

US-09-452-239-13

; Sequence 13, Application US/09452239

; Patent No. 6465229

; GENERAL INFORMATION:

; APPLICANT: Rafaleki, Antoni J.

; APPLICANT: Fader, Gary M.

; APPLICANT: Cahoon, Rebecca E.

; TITLE OF INVENTION: Plant Caffeoyle-CoA O-Methyltransferase

; FILE REFERENCE: BB1284 US NA

; CURRENT APPLICATION NUMBER: US/09/452,239

; EARLIER FILING DATE: 1999-12-01

; EARLIER APPLICATION NUMBER: 60/110,594

; EARLIER FILING DATE: 1998-December-02

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 13

; LENGTH: 997

; TYPE: DNA

; ORGANISM: Oryza sativa

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (483)

US-09-452-239-13

Query Match 16.0%; Score 158.6; DB 3; Length 997;

Best Local Similarity 54.2%; Pred. No. 5.1e-22;

Matches 373; Conservative 0; Mismatches 300; Indels 15; Gaps 2;

QY 273 CGGAGCACCGCGGCTGCGAAGCCTGAGGCTGCTGACCTCGAGAGAGCGCGAGGGGAT 332  
DB 187 CGGAGCGCGAGTGCATGCGGATCTGCGCTCATCCGGAACGACCAAGCAGATGGGGGTTT 246  
QY 333 TCTATGATGACCTGCGAGAGCGGCCAGCTCTTGGCCCAACCTGCGCGGCTCATCCAGGCC 392  
DB 247 ATGCACTGCTGCGCGGATGAGGCGAGCTGCTGGGATGCTGTAAGATGGCGGAGCG 306  
QY 393 AGAAGGCGCTGAGCTTGGGACCTTTCAGGGGTACTCGCCCTTGGCCCTGGCCCTGGCG 452  
DB 307 AAGAGGACAAATCGAGGTGGGTGTCTTTCACCGGCTACTCGCTGCTGCGAGCGGCGCTGGCG 366

QY 453 CTGCCCGCGGACCGGCGCTGTGACCTGGAGGTGGAACGCGAGCCCGCGAGCTGGGA 512  
DB 366 CTCCCGAGGACCGCAAGGTGTGGGATCGACACCGACCGAGTGTCTACGAGTGGGT 425  
QY 513 CGGCCCTGTGAGGAGCGGAGCGGAGGAGCAAGATCGACCTCCGGCTGAAGCCCGGC 572  
DB 426 CGCCCTTTCATTGAGAAAGCGGCATGGCGCAACAGGTGATCTCCGAGGGCACCGGC 485  
QY 573 TTGGAGACCTGGACGAGCTGTGGCGGCGGGCGA---GGCCGGCACCTTTCGAGTGGCC 629  
DB 486 CTGGAGAACTGGACGAGCTGTCTCGCCGAGGAGGCGGCGCGGCGCGGAGTTC 546  
QY 621 GACGTGGCGGTGTGATCGGACAAAGGAGAACTGTCTCGCCTACTACGAGAGCTGCTG 680  
DB 547 GACTTCGCTTCTGTGACGCGGACAAAGCCCACTACGTCAAGTACCAACGAGCAGCTG 606  
QY 681 GACGTGCTCGGACCGGAGGATCTCTCGCGCTCTCAGAGTCTGTGGCGGCGGAGAGT 740  
DB 607 GACGTGCTCGGCTCGGCGGCGCATCTGTGTACGAAACACGCTGTGGCGCGGACGGT 666  
QY 741 CTGCAACCTCCGAAAGGGGACGTGGCGGCGGAGTGTGCGAAACCTTAAACGACGATC 800  
DB 667 GCGCTCGCGCGGACACGCGCTGTCTCGGACCTTGGACCGGAGGTCTCTCGCTCGCATCAG 726  
QY 801 CGGCGGAGCTCAGGCTTACATCAGCTCTCTGCCCTCGGCGGAGTGGATCACTTGGCC 860  
DB 727 GACCTCAACTCTCAGGCTCGCGCGGACCGCGCATCGAGCTGTCTGCAACTCGCCATCGCC 786  
QY 861 TTCAGAT---CTAGGGCTGGCCCTAGTGTGAGTGGGCTCGAGGAGGGTGTCTTGGGAC 917  
DB 787 GACGGGATCACCATCTGCGCGCGGCTCTGTGTGAGGTGAGACCGAGACCTTACCGGCCGA 846  
QY 918 CCAGGAATTGACCTGAGTGTAAATT 945  
DB 847 TCATTCATCGCTCTCGCGTGAATAATT 874

## RESULT 5

US-09-452-239-41

; Sequence 41, Application US/09452239

; Patent No. 6465229

; GENERAL INFORMATION:

; APPLICANT: Rafaleki, Antoni J.

; APPLICANT: Fader, Gary M.

; APPLICANT: Cahoon, Rebecca E.

; TITLE OF INVENTION: Plant Caffeoyle-CoA O-Methyltransferase

; FILE REFERENCE: BB1284 US NA

; CURRENT APPLICATION NUMBER: US/09/452,239

; CURRENT FILING DATE: 1999-12-01

; EARLIER APPLICATION NUMBER: 60/110,594

; EARLIER FILING DATE: 1998-December-02

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 41

; LENGTH: 1078

; TYPE: DNA

; ORGANISM: Triticum aestivum

US-09-452-239-41

Query Match 15.9%; Score 157.2; DB 3; Length 1078;

Best Local Similarity 57.1%; Pred. No. 9.7e-22;

Matches 307; Conservative 0; Mismatches 228; Indels 3; Gaps 1;

QY 214 AGTGCTGCTTCCCGGAGGACGCGGCTGTGGAGTATCTTCTGAGCGGCTCCATGC 273  
DB 200 AGAGCCTGTCTCAGAGCGACGCTCTACCACTATCTTGAGAGAGCGGTGTACCCGC 259  
QY 274 GCGAGCACCGCGGCTGCGAAGCTTGAGGCTGTGTGACCTCTGAGAGCGCGAGGGGATT 333  
DB 260 GCGAGCACGAGTGCATGAAGGAGCTCCGCGAGATCACCGGCAACCACTGAACTGA 319  
QY 334 CTATGATGACCTGCGAGAGGCGCCAGCTCTTGGCCAACTTGGCGCGGCTCATCCAGGCCA 393



```
Db 320 TGACGACGTCGGGGACGAGGGCCAGTTCTCTCAACATGCTGTCTCAAGCTCATCGGGGCCA 379
Qy 394 AGAAGCGCTGACCTGGGACACTTACCGGGCTACTCCGGCCCTGGGCCCTGGCCCTGGCGC 453
Db 380 AGAAGACCATGGAGATCGGGCTTACACCGGCTACTCCCTCTCGCCACCGCGCTCGCCA 439
Qy 454 TGCCCGGACGAGCGCGCTGTGTCACCTGCGAGGTGGACGGCGCAGCCCCCGGAGCTGGGAC 513
Db 440 TCCCCGACGACGCGCACATCTTGGCCATGGAATCAACCGCGAAGACTAGAGCTGGGGC 499
Qy 514 GGCCTCTGTGGAGCGAGCGGCGAGCGAGCACAAAGATCGACCTTCCGGCTGAAGCCCGCCT 573
Db 500 TGCCGTGTCATCGAAGAGCGCGGCTGGCGCACAAAGATCGACTTCCCGAGGGGCCCGGCGC 559
Qy 574 TGGAGACCTTGGACGAGCTGCTGGCGC---GGCGAGGCGCGCACCTTCGAGCTGGCGC 630
Db 560 TGCCGTGTGGACGCGCTGCTGGAGGACGAGGCGCAACACCGCACCTTTCGACTTCGTCT 619
Qy 631 TGTGTGATCGGACAAAGGAGAACTGCTCGCCCTACTACGAGCGCTGCTGCGAGCTGCTGC 690
Db 620 TGTGTGACGCGGACAGGACAACTACTCAACTACCGAGCGCTCATGAAGCTGCTCA 679
Qy 691 GACCCGGAGGCAATCTCGCGCTCTCAGAGTCTGTGGCGCGGAAAGGTGCTGCAACC 748
Db 680 AGCTCGGCGCTCTCTCGGCTACGACAAACAGCGCTCTGGAACGGCTCCGTCGTGCTCCC 737

RESULT 6
US-09-452-239-35
; Sequence 35, Application US/09452239
; Patent No. 6465229
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni J.
; APPLICANT: Fader, Gary M.
; APPLICANT: Cahoon, Rebecca E.
; TITLE OF INVENTION: Plant Caffeoyle-CoA O-Methyltransferase
; FILE REFERENCE: BB1284 US NA
; CURRENT APPLICATION NUMBER: US/09/452,239
; CURRENT FILING DATE: 1999-12-01
; EARLIER FILING DATE: 1998-December-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 35
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (817)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (826)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (874)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (891)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (924)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (934)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (961)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (970)..(971)
; FEATURE:
```

```
; NAME/KEY: unsure
; LOCATION: (1012)
US-09-452-239-35
Query Match 15.7%; Score 155.6; DB 3; Length 1018;
Best Local Similarity 56.6%; Pred. No. 2e-21;
Matches 309; Conservative 0; Mismatches 234; Indels 3; Gaps 1;

Qy 214 AGTGTCTGCTTCCCCCGGAGGACAGCCGCTGTGGCAGTATCTTCTGAGCGCGCTCCATGC 273
Db 177 AGAGCCTGTCTAAGAGCGACGACCTGTGACAGTACATCTCTGGACACAGAGCGTGTACCCGC 236
Qy 274 GGGAGCACCCGCGCTGCGAAGCCTGAGGCTGTGACCTCTGGAGCAGCGCAGGGGGATT 333
Db 237 GGGAGCGGAGAGCATGAGGAGCTGCGGAGATCACCGCCAAAGCACCCATGGAACCTGA 296
Qy 334 CTATGATGACCTTGGAGAGGCGGACGCTTGTGGCCAACTTGGGGGGGCTCATTCAGGCCA 393
Db 297 TGACCACCTTCCGCCGACGAGGGCCAGTTCTCTCAACATGCTCATCAAGCTCATCGGGGCCA 356
Qy 394 AGAAGCGCTGACCTTGGGCACCTTTCACGGGCTACTTCGCCCTTGGCCCTGGCCCTGGCGC 453
Db 357 AGAAGACCATGAGATCGCGCTTACACCGGCTACTTCTCTGCTCGCCACCGCGCTCGCCA 416
Qy 454 TGCCCGCGGACGCGCGCTGTGTGACCTGCGAGGTGGACGCGCAGCCCCCGGAGCTGGGAC 513
Db 417 TCCCCGACGACGCGCACCATCTTTGGCCATGGACATCAACCGCGAGAACTACGAGCTGGGC 476
Qy 514 GGGCCCTGTGGAGGAGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 573
Db 477 TGCCGTGTCATCGAAGAGCGCGCGCTGGCGCACAAAGATCGACTTCCGCGAGGGCCCGCGC 536
Qy 574 TGGAGACCTTGGACGAGCTGTGGCGGC---GGCGAGGCGCGCACCTTTCGAGCTGGCGC 630
Db 537 TGCCGTCTTGGAGCGCTGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 596
Qy 631 TGTGTGATCGGACAAAGGAGAACTGCTCGCCCTACTACGAGCGCTGCTGCGAGCTGCTGC 690
Db 597 TCGTGGACGCGGACAAAGGAGAACTACTCAACTACCGAGCGCTCATGAAGCTGCTCA 656
Qy 691 GACCCGGAGGCAATCTCGCGCTCTCAGAGTCTGTGGCGCGGAAAGGTGCTGCAACCTC 750
Db 657 AGTGTGGCGGCTCTCGGCTACGACAAACACCTCTGGAACGGCTCCGTCGTGCTCCCCC 716
Qy 751 CGAAG 756
Db 717 CGGAG 722

RESULT 7
US-09-452-239-1
; Sequence 1, Application US/09452239
; Patent No. 6465229
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni J.
; APPLICANT: Fader, Gary M.
; APPLICANT: Cahoon, Rebecca E.
; TITLE OF INVENTION: Plant Caffeoyle-CoA O-Methyltransferase
; FILE REFERENCE: BB1284 US NA
; CURRENT APPLICATION NUMBER: US/09/452,239
; CURRENT FILING DATE: 1999-12-01
; EARLIER FILING DATE: 1998-December-02
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 891
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (806)
; FEATURE:
```



NAME/KEY: unsure  
LOCATION: (810)  
US-09-452-239-1

Query Match 15.6%; Score 154; DB 3; Length 891;  
Best Local Similarity 56.7%; Pred. No. 4e-21;  
Matches 305; Conservative 0; Mismatches 230; Indels 3; Gaps 1;

QY 214 ATGTCCTGTTCCCGGAGGACAGCCGCTGTGGCAGTATCTTCTGAGCCGCTCCATGC 273  
DB 181 AGAGCCTGTCTAAGAGCGAGCAGCTCTACAGTACATCTCTGGACACGAGCGTGTACCCGC 240  
QY 274 GGGAGACCCGCGCTGCGAAGCCTCAGCTGTGACCTCTGGAGCAGCCGAGGGGATT 333  
DB 241 GGGAGCCGAGAGCATGAAGAGCTCCGAGATCACCCGCAAGCACCCTGAACCTGA 300  
QY 334 CTATGATGACCTGCGAGCAGGCCAGCTCTTGGCCAACTTGGCGCGCTCATCCAGGCCA 393  
DB 301 TGACGACCTCCGCCGAGGAGGCGAGTTCTTGNACATGTCTCATCAAGCTCATCGGCGCCA 360  
QY 394 AGAAGCGCTGAGACCTGGGACCTTCAACGGGCTACTCCGCGCTTGGCCCTTGGCCCTGGGCG 453  
DB 361 AGAAGACCATGAGATCGCGCTCTACACCGGCTACTCGCTCTCTCGCCACCGCGCTCGCAC 420  
QY 454 TGGCCGCGAGCGCGCTGTGACCTCGAGGTGGAACGCGAGCCCCCGAGCTGGGAC 513  
DB 421 TCCCGAGAGCGGACGACATCTTGGCCATGGACATCAACCGCGAGAACTACGAGCTAGGCC 480  
QY 514 GGGCCCTGTGGAGGAGCGGAGCGGAGCAGCAAGATCGACCTCCGGCTGAGCGCCGCT 573  
DB 481 TTCCCTGCAATCAAGAGCGCGGCTGGGCCAAGATGCACTTCCGAGGCGCCCGCGC 540  
QY 574 TGGAGACCTTGGAGCTGCTGGCGC---GGGCGAGCCGCGACCTTTCGAGCTGGCCG 630  
DB 541 TCCCGCTCTGGAGCAGCTCGTGGCGGACAGGAGCAGCAGCGTGTTCGACTTGGCCT 600  
QY 631 TGGTGAATCGGACAGAGAACTGTCTCGCCTACTACAGCGCTGCTGAGCTGCTGCTGC 690  
DB 601 TGTGAGCCGACAGAGCAACTACTCTCAGCTTACCACGAGCGGCTCTTGAAGCTGGTGA 660  
QY 691 GACCGGAGCATCTCCGCGCTCAGAGTCTGTGGCGCGGAGGTGCTGCAACC 748  
DB 661 GGGCCGCGGCTCATCGGCTACGACACACGCTGTGGAAAGCGCTCCGCTGCTGCC 718

## RESULT 8

US-09-410-551B-1  
Sequence 1, Application US/09410551B  
Patent No. 6503737  
GENERAL INFORMATION:  
APPLICANT: KOSAN BIOSCIENCES, Inc.  
APPLICANT: REEVES, CHRISTOPHER  
APPLICANT: CHU, DANIEL  
APPLICANT: KHOSLA, CHAITAN  
APPLICANT: SANTI, DANIEL  
APPLICANT: WU, KAI  
TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA  
FILE REFERENCE: 30062-20026.00  
CURRENT APPLICATION NUMBER: US/09/410,551B  
CURRENT FILING DATE: 1999-10-01  
PRIOR APPLICATION NUMBER: US 60/139,650  
PRIOR FILING DATE: 1999-06-17  
PRIOR APPLICATION NUMBER: US 60/123,810  
PRIOR FILING DATE: 1999-03-11  
PRIOR APPLICATION NUMBER: US 60/102,748  
PRIOR FILING DATE: 1998-10-02  
NUMBER OF SEQ ID NOS: 72  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 77536  
TYPE: DNA  
ORGANISM: Streptomyces hygroscopicus

FEATURE:  
NAME/KEY: CDS  
LOCATION: (52275) ... (71465)  
US-09-410-551B-1

Query Match 15.5%; Score 153; DB 4; Length 77536;  
Best Local Similarity 55.4%; Pred. No. 1.1e-20;  
Matches 341; Conservative 0; Mismatches 265; Indels 9; Gaps 2;

QY 252 TATCTTCTGAGCGCTCCATGCGGGAGCACCCGGGCTCGGAAGCCTGAGGCTGTGACG 311  
DB 8195 TAGTACGGAAGGTGTCCCTGCGCGATGACGAGTGTCTGAGCCGCTGCGCGCAGACG 8254  
QY 312 CTGGAGCAGCCGAGGGGATTTCTAT---GATGACCTGCGAGCAGCCGAGCTCTTGGCC 368  
DB 8255 GCCGAGCTCCCGGCGGTGCGCTACTGCGCGTGCAGGCCGAGGAGGACAGTTCTCGAG 8314  
QY 369 AACCTGGGCGGCTCATCCAGGCCAAGAGGCGCTGGACCTCGGACCTTACGGGCTAC 428  
DB 8315 TTCTTGTGCGTTTACCGGCGCGGTGAGTGTGAGATCGGAGCTGACACCGGCTAC 8374  
QY 429 TCCGCCCTGGCCCTGCGCTGCGCGCGGACGCGCGCTGTGAGCTTCGAGGTG 488  
DB 8375 AGCAGCTCTGCTGGCCCGGATTTGGCGCCGCGGCGGTGTGTGACGTGCGATGTC 8434  
QY 489 GAGGCGCAGCCCGGAGCTGGGACGCGCCCTGTGAGGCGAGCCGCGGAGCAGCAAG 548  
DB 8435 ATGCCGAAGTGGCCGAGGTGGCGGAGCGGTACTTGGGAGGAGCGGGGTTCGCGACCG 8494  
QY 549 ATCGACCTCCGCTGAAGCCCGCTTGGAGACCTTGGAGAGCTGTGAGAGCTGCT 602  
DB 8495 ATCGACCTCCGATCGGAGCAGCCCGGACCGCTCTACCGGCTGTCTGACGAGGCGGCG 8554  
QY 603 GCGGAGCGCGCACCTTTCGACCTGGCGCGTGTGGATGCGGACAAAGAGAACTGCTCCGCG 662  
DB 8555 GCGGCGCGGAGTGTTCGACATGTGTTCATCGAGCGGACAGGCGCGCTTACCCGCGC 8614  
QY 663 TACTACGAGCGTGTGCTGAGCTGTGAGCAGCCGAGGAGTCTCGCCGCTCTCAGAGTC 722  
DB 8615 TACTACGAGCGCGCTGCGCTGTGTAAGCGCGCGGCTGATGCTCTGCGACACAG 8674  
QY 723 CTGTGGCGGGAAGGTGCTGCAACTCCGAAGGGGAGCTGGCGCGAGTGTGCGCA 782  
DB 8675 CTGTCTTTCGCGCGGTGGCCGACGAGCGGTGCGAGGCCCGGACACGCGTTCGCGTAC 8734  
QY 783 AACCTAAACGAACGATCCGCGCGGACGTCAGGCTCTACATCAGCTCTGCGCCCTGGGC 842  
DB 8735 GAACCTAACCGCGACTGCGCGACGACGACCGGTTGGACCTGGCGATGCTGACGAGCGC 8794  
QY 843 GATGACTCACCTTG 857  
DB 8795 GACGGCGTCACTG 8809

RESULT 9  
US-09-940-316B-1  
Sequence 1, Application US/09940316B  
Patent No. 6759536  
GENERAL INFORMATION:  
APPLICANT: KOSAN BIOSCIENCES, Inc.  
APPLICANT: REEVES, CHRISTOPHER  
APPLICANT: CHU, DANIEL  
APPLICANT: KHOSLA, CHAITAN  
APPLICANT: SANTI, DANIEL  
APPLICANT: WU, KAI  
TITLE OF INVENTION: POLYKETIDES ENCODING THE fkbA GENE OF THE PK-520 POLYKETIDE SYNTHASE  
FILE REFERENCE: 30062-20026.11  
CURRENT APPLICATION NUMBER: US/09/940,316B  
CURRENT FILING DATE: 2001-08-27  
PRIOR APPLICATION NUMBER: 09/410,551  
PRIOR FILING DATE: 1999-10-01  
PRIOR APPLICATION NUMBER: US 60/139,650



; APPLICANT: Fader, Gary M.  
; APPLICANT: Cahoon, Rebecca E.  
; TITLE OF INVENTION: Plant Caffeoyle-CoA O-Methyltransferase  
; FILE REFERENCE: BB1284 US NA  
; CURRENT APPLICATION NUMBER: US/09/452,239  
; CURRENT FILING DATE: 1999-12-01  
; EARLIER APPLICATION NUMBER: 60/110,594  
; EARLIER FILING DATE: 1998-December-02  
; SOFTWARE: Microsoft Office 97  
; NUMBER OF SEQ ID NOS: 50  
; SEQ ID NO 3  
; LENGTH: 1146  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-09-452-239-3

Query Match 15.0%; Score 148; DB 3; Length 1146;  
Best Local Similarity 53.7%; Pred. No. 6e-20;  
Matches 366; Conservative 0; Mismatches 295; Indels 21; Gaps 2;  
QY 214 AGTGCCTGCTTCCCGCCGAGGACAGCGCGCTGTGGCAGTATCTTCTGAGCCGCTCCATGC 273  
DB 189 AGAGCTGTCTCAAGAGCGAGCACTCTACAGTACATCTTGGACAGCGGTGTACCCGC 248  
QY 274 GGGAGACCCCGCGCTGCGAAGCCTGAGGCTGTGACCTCTGGAGAGCGCGAGGGGAT 333  
DB 249 GGGAGCGGAGAGCATGAAGGAGCTCCGGAGATCACCGCAAGCACCCATGGAACCTGA 308  
QY 334 CTATGATGACCTGCGAGAGGCGCCAGCTCTTGSCCAACCTGGCGCGCTCATCCAGGCCA 393  
DB 309 TGACGACCTTCCCGCGAGAGGGGAGTCTCTGAACATGCTCATCAAGCTCATCGGGCCA 368  
QY 394 AGAAGCGCTGAGCTGGGCACCTTCAACGGGCTACTCCGCGCTTGGCCCTGGCCCTGGCGC 453  
DB 369 AGAAGACCATGAGATCGCGCTCTACACGGCTACTCCCTCTCGCCACGGCGCTCGCC 428  
QY 454 TGCCCGGAGAGCGGCGCGTGTGACTGTGAGGTGGAGCGGAGCGCCCGAGCTGGGAC 513  
DB 429 TCCCGGAGAGCGGACGATCTTGGCCATGACATCAACCGCGAGAACTACGAGCTGGGC 488  
QY 514 GCGCCCTGTGGAGGAGCGGAGCGGAGGAGCACAAGATCGACCTCCGCGCTGAAGCCGCGCT 573  
DB 489 TGGCTGTGATCGAAGAGGCGCGGTGCGCCACAAGATCGACTTCCGGAGGGTCCCGCGC 548  
QY 574 TGAGACCTTGGACGAGCTGCTGGCGCGGCGAG---GCGCGACCTTTCAGCTGGCGC 630  
DB 549 TCCCGCTCTCGACGACTCATCGCGAGGAGAGAACCAACCGGTGTTTCGACTTGTCT 608  
QY 631 TGGTGAATGCGGACAAAGGAACTGTTCGCCCTACTACGAGCGCTGCTGAGCTGTGC 690  
DB 609 TCGTGACGCGACAAGGACAACTACTCACTTACCACGAGCGGCTGCTGAAGCTGGTGA 668  
QY 691 GACCGGAGCATCTTCCCGCTCTCAGAGTCTGTGGCGGAGAGGTGCTGCAACCTC 750  
DB 669 AGCTGGCGCGCTCATCGGCTACGACAACACGCTGTGGAAACGCTCCGCTGCTCCCG 728  
QY 751 CGAAAGGAGAGCTGGCGGC-----CGAGTGTGTCGAAACCTAAACG 792  
DB 729 ACGACGCGCCATGCGCAAGTACATCGGCTTCTACCGGACTCTGCTCGTCTCAACA 788  
QY 793 AAGCATTCGCGGAGAGCTGAGGGTCTACATAGCTCTTCCCGCTGGGCGATGAGACTCA 852  
DB 789 AGCGCTCGCGCGGAGAGCGGCTCGAGATCTGCCAGCTTCCCGCTCGGCGAGGGGTCA 848  
QY 853 CTTGGCTTCAAGATCTAGG 874  
DB 849 CCCTGCTCGCGCGCTCAAGT 870

RESULT 12  
US-09-452-239-5  
; Sequence 5, Application US/09452239  
; Patent No. 6465229

; GENERAL INFORMATION:  
; APPLICANT: Rafalski, Antoni J.  
; APPLICANT: Fader, Gary M.  
; APPLICANT: Cahoon, Rebecca E.  
; TITLE OF INVENTION: Plant Caffeoyle-CoA O-Methyltransferase  
; FILE REFERENCE: BB1284 US NA  
; CURRENT APPLICATION NUMBER: US/09/452,239  
; CURRENT FILING DATE: 1999-12-01  
; EARLIER APPLICATION NUMBER: 60/110,594  
; EARLIER FILING DATE: 1998-December-02  
; SOFTWARE: Microsoft Office 97  
; NUMBER OF SEQ ID NOS: 50  
; SEQ ID NO 5  
; LENGTH: 1057  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-09-452-239-5

Query Match 14.6%; Score 144.4; DB 3; Length 1057;  
Best Local Similarity 57.3%; Pred. No. 3e-19;  
Matches 281; Conservative 0; Mismatches 206; Indels 3; Gaps 1;  
QY 272 GCGGAGACACCCGCGCTCGAAGCTGTGAGGCTGTGACCTTGAGCAGCGCCGAGGGGA 331  
DB 192 GCAGAGCGGAGAGCATGCTGAGCTGCGGTGTGTGACCGACAAGCAGAGTGGGGTT 251  
QY 332 TTCTATGATGACTGCGAGCAGGCCAGCTCTTGGCCAACTTGGCGCGGCTCATTCAGGC 391  
DB 252 CATGCAGTCTCCCGGAGAGGCGTCTGTGCGGATGCTGATCAAGCTGAGCGCGC 311  
QY 392 CAAGAAGGCGCTGGACCTGGGACCTTACGGGCTACTCGGCCCTGGCCCTGGCCCTGGC 451  
DB 312 GCGCGCACCTTGGAGGTGGGCTGTTCACGGGCTACTCGCTGCTGGCGACGCGCTTGGC 371  
QY 452 GCTGCCCGGAGCGGCGGTGTGTGACCTTGCAGGTGGAGCGCGCACGCCCGGAGCTGGG 511  
DB 372 GCTGCCCGGAGCGGCAAGGTCTATCGCATTCGACGTGAGCGCGGAGTACTACGACATCG 431  
QY 512 ACGGCCCTTGTGGAGCAGCGGAGCGGAGCACAAGATCGACCTCCGCTGAAGCCCGC 571  
DB 432 CCGCCCTTTCATCGAGCGCGCGGGGTGGCGGAAGGTGGACTTCCGGAGGGCCCGC 491  
QY 572 CTTGGAGACCTTGGAGCAGCTGCTGGCG---CGGCGAGGGCGGACCTTTCAGCTGGC 628  
DB 492 GCTGGAGCAGCTGGAGCAGCTCTTCCCGACCCCGCAACACCGCGCGCTTTCAGCTTGC 551  
QY 629 CTTGTGTGATGCGGACAAGAGAACTGCTCCGCTACTACGAGCGCTGCTGAGCTGTCT 688  
DB 552 CTTGTGTGAGCGGAGACGCTAACTACGCTCGGTACGAGCAGCTGCTCGCCCTGGT 611  
QY 689 GCGACCCGAGGAGCATCTTCCCGCTCTCAGAGTCTTGTGGCGGGGAAGGTGCTGCAACC 748  
DB 612 GCGCGTGGGGGTACCGTCTGTGACACAACGCTGTGGCGGCTACTGTGGCGCTTCC 671  
QY 749 TCCGAAGGG 758  
DB 672 CCGCGAGCG 681

RESULT 13  
US-09-452-239-11  
; Sequence 11, Application US/09452239  
; Patent No. 6465229  
; GENERAL INFORMATION:  
; APPLICANT: Rafalski, Antoni J.  
; APPLICANT: Fader, Gary M.  
; APPLICANT: Cahoon, Rebecca E.  
; TITLE OF INVENTION: Plant Caffeoyle-CoA O-Methyltransferase  
; FILE REFERENCE: BB1284 US NA  
; CURRENT APPLICATION NUMBER: US/09/452,239  
; CURRENT FILING DATE: 1999-12-01  
; EARLIER APPLICATION NUMBER: 60/110,594  
; EARLIER FILING DATE: 1998-December-02

; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 11  
; LENGTH: 1058  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
US-09-452-239-11

Query Match 14.2%; Score 140.6; DB 3; Length 1058;  
Best Local Similarity 50.6%; Pred. No. 1.6e-18;  
Matches 409; Conservative 0; Mismatches 379; Indels 21; Gaps 2;  
QY 87 ACCACCGGTGCGCGGCTCTCCGTGCGCGCGCGCTGCGCCCTGGCTCAGCGCAGCTG 146  
DB 53 AGCAAGCTCTACAGAGATCTACGACATGCGCGAGCGCGCTGCGCGGCGCGCGGCG 112  
QY 147 GCGCGCGCTTCCGCACTTCTTCTTCTGGGAGGCGGTGCGCCCATGGGAGGCCGG 206  
DB 113 ACACGAGGAGCGGAATGGGAGCAGCGCGCGGAGAGAGAGAGAGAGAGAGAGAG 172  
QY 207 CGAGAGCAGTCTGCTTCCCCCGAGGACAGCGCGCTTGGCAGTATCTTCTGAGCGC 266  
DB 173 GGCCACAGAGCTCTCAAGAGCGAGCATCTTACAGTACATCTGGAGAGAGCGGTG 232  
QY 267 TCCATGCGGAGCACCCGCGCTGCGAAGCTGAGGCTGTGACCTGAGCAGCGCGAG 326  
DB 233 TACCGCGCGAGCAGAGTGATGAAGAGCTCCGCGAGGTCAACGCCAACCCATCG 292  
QY 327 GGGGATTTATGATGACTGTGAGAGAGGCGGAGCTTGGCCAACTGCGCGGCTCATC 386  
DB 293 AACCTGATGACGACGTGCGCGGAGGAGGCGAATTCCTGAACCTGTGCTGAAGCTCATC 352  
QY 387 CAGGCCAAGAGCGGTGACCTGCGGACCTTACCGGCTACTCCGCCCTGGCCCTGGCC 446  
DB 353 GCGCGCAAGAGACCATCAAGAGTCCGCGTCTACACCGGCTACTCCCTCTCCGCAACCGCC 412  
QY 447 CTGGCGCTCCCGCGAGCGCGGCGGTGTGACCTGCGAGGTGAGCGCGAGCGCCCGAG 506  
DB 413 CTCGCATCTCCGACGAGCGGCGAGCTTTGGCGATGGAATCAACCGGAGAACTACGAG 472  
QY 507 CTGGAGCGGCTCTGTGGAGGAGGCGGAGGAGGAGCAAGATCGACTTCCGGGTGAAG 566  
DB 473 CTGGGCTCCCGTCGATCGAGAAGGCGGAGTGGCGCAAGATCGACTTCCGGAGGGA 532  
QY 567 CCGCGCTTGAGACCTCGACGAGCTGTGCGGCGC---GGGAGGCGCGGACCTTCGAC 623  
DB 533 CCGCGCTCCCGGTGTGAGACGAGCTGTGTGGAGGAGGAGGCAACCATGCGGTCTGTGAC 592  
QY 624 GTGGCGGTGATGCGGACAGGAGAACTGTCCGCTACTACGAGCGCTGCTGCGAG 683  
DB 593 TTCGTGTTCTGACGCGCGAAGAGGAACTACTCACTCACTCACTCACTCACTCACTCA 652  
QY 684 CTGCTGCGACCGGAGGCACTCTCGCGCTCTCTCAGAGTCTCTGTGGCGGGAAGGTG 743  
DB 653 CTGGTCAAGGTGCGGCGCTCTGTGGCTACGACAAACGCTCTGGAAACGGCTCGTCTG 712  
QY 744 CAACCTCCGAAGAGGAGCGTG-----GGGCGGAGTGTGTGGAAC 785  
DB 713 CTCCCGCGCGAGCGCCCCCTATGCGCAAGTACATCCGCTACTACCGGACTTCTGTCTGAG 772  
QY 786 CTAAACGAACGATCCGCGGAGGAGTCAAGGTCTACATCAGCTCTCTGCGCCCTGGGCGGAT 845  
DB 773 CTCACAGGCGCTTCCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 832  
QY 846 GGACTCACCTTGGCTTCAAGATCTAGGG 874  
DB 833 GGATCACCTTCTGCGCGCGGTCAAGTG 861

RESULT 14  
US-09-452-239-7  
; Sequence 7, Application US/09452239  
; Patent No. 6465229

; GENERAL INFORMATION:  
; APPLICANT: Rafaleki, Antoni J.  
; APPLICANT: Fader, Gary M.  
; APPLICANT: Cahoon, Rebecca E.  
; TITLE OF INVENTION: Plant Caffeyol-CoA O-Methyltransferase  
; FILE REFERENCE: BB1284 US NA  
; CURRENT APPLICATION NUMBER: US/09/452,239  
; CURRENT FILING DATE: 1999-12-01  
; EARLIER APPLICATION NUMBER: 60/110,594  
; EARLIER FILING DATE: 1998-December-02  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 7  
; LENGTH: 923  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (887)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (895)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (914)  
US-09-452-239-7

Query Match 12.7%; Score 126; DB 3; Length 923;

Best Local Similarity 56.6%; Pred. No. 1.1e-15;  
Matches 275; Conservative 0; Mismatches 205; Indels 6; Gaps 2;

QY 261 AGCCGCTCCATCGCGGAGCACCCGCGCTGCGAAGCTGAGGCTGTGACCTGAGAGCAG 320  
DB 138 ACCGTCTTCCACGAGCGGAGCTGCGCGGAGCTCGGCTGCGCACCGCCACCCAC 197  
QY 321 CCGCAGGGGGATTTATGATGACTGTGCGAGCAGGCGGAGCTTGGCCAACTGGCGCG 380  
DB 198 CCATGCGGCGCATGGCTGCGTCCGCGGAGAGGTGCGAGCTGCTGAGCTCTGATCGAG 257  
QY 381 CTCATCCAGGCCAAGAGCGCTGACCTGGGACCTTACCGGCTACTTCCGCCCTGGCC 440  
DB 258 ATTCTTGGCGCCAAAGACGCCATCGAGGTGGCGTCTTCCCGGCTACTCTGCTCGCC 317  
QY 441 CTGGCCCTTGGCGCTGCCCGCGAGCGGCGCTGTGTGACCTGCGAGGTGAGCGCGAGCCC 500  
DB 318 ACGCCCTTCCGCTCCCGACGCGGCAAGATTGTGGCCATCGACTTACCGCGAGAGC 377  
QY 501 CCGGAGCTGGGACGCGCCCTCTGTGGA---GGCAGGCGGAGGAGGAGCAAGATCGACCTC 557  
DB 378 TACGACCAAGATAGGTTCGCGGTGATCGAAGAGCGCGCTGCGCAAGATCGACTTC 437  
QY 558 CGGCTGAAGCCCGCTTGGAGACCTTGGACGAGCTGTGCGC---GGCGGCGAGGCGCGC 614  
DB 438 CCGCTCGGCTCGCGCTCGCGTGTGGACCAAGATGGTGGCGGAGGAGGAGGAGGAGG 497  
QY 615 ACCTTTCGAGCTGCGCGTGTGTGATCGGACAAAGGAGAACTGTCTCGCCCTACTACGAGCG 674  
DB 498 AGTTTCGACTTTCGCTTGTGGAACGCGGAGAGGTGAATCTTCTCACTACCGAGCGG 557  
QY 675 TGCCTGCACTGCTGCGACCGCGAGGAGTCTCTGCGCGCTCTCAGAGTCTGTGGCGCGG 734  
DB 558 CTGCTGCACTGCTCAGGCTCGGCGGCTCATCGCTACGACAAACGCTGTGTGGGCGCGC 617  
QY 735 AAGGTG 740  
DB 618 TCCGTG 623

RESULT 15  
US-07-708-866A-1  
; Sequence 1, Application US/07708866A  
; Patent No. 5322937  
; GENERAL INFORMATION:

APPLICANT: Akira ARISAWA et al.  
TITLE OF INVENTION: Genes Encoding A 3-Acylation  
TITLE OF INVENTION: Enzyme For Macrolide Antibodies  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: DisplayWrite  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/708,866A  
FILING DATE: 19910531  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX: 202-371-8856  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1810 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Streptomyces thermotolerans  
STRAIN: ATCC 11416  
FEATURE:  
NAME/KEY: -35 signal  
LOCATION: 120..125  
IDENTIFICATION METHOD: S  
FEATURE:  
NAME/KEY: -10 signal  
LOCATION: 143..148  
IDENTIFICATION METHOD: S  
FEATURE:  
NAME/KEY: RBS  
LOCATION: 194..198 AND 201..205  
IDENTIFICATION METHOD: S  
US-07-708-866A-1

Query Match 12.4%; Score 122.8; DB 1; Length 1810;  
Best Local Similarity 58.5%; Pred. No. Se-15;  
Matches 233; Conservative 0; Mismatches 162; Indels 3; Gaps 1;  
QY 243 CTGTGGCAGTATCTTCTGAGCGCTCCATGCGGGAGCACCGCGCGCTGCGAAGCCCTGAGG 302  
DB 1412 CTGCTGGATACGCCAGGAGCGTCTGCTGCGGACGACGCCGTGCTGCGGAGCTGCGG 1471  
QY 303 CTGCTGACCTGGAGCAGCGCAGGGGGATTCTAT---GATGACCTGCGAGCAGGCCCCAG 359  
DB 1472 GAGTTGACGGCGGCCCTGCGGGCGGACGCGCCATGCGATGCGGAGGAGGCCCCAG 1531  
QY 360 CTCCTGGCCAACTGGCGGGCTCATCCAGGCCAAGACGCGTGGACCTGGGACCTTC 419  
DB 1532 CTCCTCGCGCTGCTCATCCGGGCTCACGGGCGCGCCCGCCAGGTCTTGAGATCGGACGTTTC 1591  
QY 420 ACGGGCTACTTCGCGCCCTGGCCCTGGCGCTGCGCGGACCGGCGCGTGGTGACC 479  
DB 1592 ACCGGGTACAGCAGCTGTGATGGCCCGGGGACACTGCCGCGCGCGCGGATCGTCACC 1651

QY 480 TCGGAGGTGGACGCGCAGCCCCCGGAGCTGGGACGGCCCTCTGGAGGCGAGCCCGAGGCG 539  
DB 1652 TCGGACATCACGAGCGGTGGCCCGCGCTCGGCGGCCCGTTCTGGCGGCGAGGCGGGGTC 1711  
QY 540 GAGCACAAAGATCGACCTCCGGGCTGAAGCCCGCTTGGAGACCTTGACGAGCTGCTGGCG 599  
DB 1712 GCGGACCGCATCGACCTTCGCATCGGCGACGCGCGCCGACCCCTGTCCGAGCTGCGTGCA 1771  
QY 600 GCGGGCGAGGCGCGCACCTTCGACGCTGGCCGTGGTGA 637  
DB 1772 CACGAAGGCGACGGCATCTTCGACCTGGTGTTCGTGA 1809

Search completed: April 19, 2005, 20:55:24  
Job time : 255 secs

**THIS PAGE BLANK (USPTO)**

```
Run on: April 19, 2005, 17:29:29 ; Search time 1403 Seconds
        (without alignments)
        4172.932 Million cell updates/sec

Title: US-10-017-407A-305
Perfect score: 989
Sequence: 1 GCGGCCCGCGAGTCGAGA.....caaaaaaaaaaaaaaaaaa 989
Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0
               4390206 seqs, 2959870667 residues
               Total number of hits satisfying chosen parameters: 8780412
               Minimum DB seq length: 0
               Maximum DB seq length: 2000000000
               Post-processing: Minimum Match 0%
                           Maximum Match 10%

Database : N_Geneseq_16Dec04.*
Listing first 1500 summaries
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

No.  Score  Match Length DB ID  Description
RESULT 1
ID AAA37107 standard; cDNA; 989 BP.
DE Human PRO1558 (UNQ766) cDNA sequence SEQ ID NO:305.
PN WO200012708-A2.
PD 09-MAR-2000.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 3; Length 989;
Best Local Similarity 100.0%; Pred. No. 5.1e-156;
RESULT 2
ID AAF34419 standard; DNA; 989 BP.
DE DNA encoding protein of the invention #84.
PN WO200078961-A1.
PD 28-DEC-2000.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 3; Length 989;
Best Local Similarity 100.0%; Pred. No. 5.1e-156;
RESULT 3
ID ABK40264 standard; cDNA; 989 BP.
DE cDNA encoding human PRO1558 polypeptide.
PN WO200153486-A1.
PD 26-JUL-2001.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 4; Length 989;
Best Local Similarity 100.0%; Pred. No. 5.1e-156;
RESULT 4
ID ACD58458 standard; cDNA; 989 BP.
DE Novel human secreted and transmembrane protein PRO1558 cDNA.
PN US2003073130-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 9; Length 989;
Best Local Similarity 100.0%; Pred. No. 5.1e-156;
RESULT 5
ID ACH04560 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003044841-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 5.1e-156;
RESULT 6
ID ACD68104 standard; cDNA; 989 BP.
DE Novel human secreted and transmembrane protein PRO1558 cDNA.
PN US2003073129-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 9; Length 989;
Best Local Similarity 100.0%; Pred. No. 5.1e-156;
RESULT 7
ID ADC18174 standard; cDNA; 989 BP.
DE Human PRO polynucleotide #86.
PN US2003064925-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 5.1e-156;
RESULT 8
ID ADD70820 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003099625-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 5.1e-156;
RESULT 9
ID ADD39897 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003083462-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 5.1e-156;
RESULT 10
ID ADD70343 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003054406-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 5.1e-156;
RESULT 11
ID ADD38464 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003096955-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 5.1e-156;
RESULT 12
ID ADD39420 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003096954-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 5.1e-156;
RESULT 13
ID ADD38943 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003092061-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 5.1e-156;
RESULT 14
ID ADD40374 standard; cDNA; 989 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1558.
PN US2003082627-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 989; DB 10; Length 989;
Best Local Similarity 100.0%; Pred. No. 5.1e-156;
```



Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 15  
ID ADE50595 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003069179-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 10; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 16  
ID ADE20207 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003092883-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 10; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 17  
ID ADE50118 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003082626-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 10; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 18  
ID ADE21676 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003082628-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 10; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 19  
ID ADF30101 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003204053-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 10; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 20  
ID ADF55994 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003204054-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 10; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 21  
ID ADH99498 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003065142-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 10; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 22  
ID ADJ37302 standard; cDNA; 989 BP.  
DE Human tumour therapy associated PRO1558 cDNA.  
PN US2003211096-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 10; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 23  
ID ADE96678 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003195347-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 12; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 24  
ID ADF25989 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003199675-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 12; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 25  
ID ADF24888 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003198993-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 12; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 26  
ID ADF29624 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003203401-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 12; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 27  
ID ADE97155 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003195334-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 12; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 28  
ID ADH03193 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003216562-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 12; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 29  
ID ADH04147 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003220471-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 12; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 30  
ID ADH03670 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003224478-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 12; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 31  
ID ADG68226 standard; cDNA; 989 BP.  
DE Human PRO polypeptide cDNA #11.  
PN US2003170228-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 12; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 32  
ID ADH04624 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2004005626-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 12; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
RESULT 33  
ID ADH03193 standard; cDNA; 989 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
PN US2003216562-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 989; DB 12; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.1e-156;

ID ADH61625 standard; cDNA; 989 BP.  
 DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
 PN US2004014130-A1.  
 PD 22-JAN-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 989; DB 12; Length 989;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
 RESULT 34  
 ID ADL94824 standard; cDNA; 989 BP.  
 DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
 PN US2004073015-A1.  
 PD 15-APR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 989; DB 12; Length 989;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
 RESULT 35  
 ID ADO42276 standard; cDNA; 989 BP.  
 DE Human NOVX polynucleotide #63.  
 PN US2004058338-A1.  
 PD 25-MAR-2004.  
 PA (AGEE/) AGEE M L.  
 PA (ALSO/) ALSOBROOK J P.  
 PA (ANDE/) ANDERSON D W.  
 PA (BERG/) BERGHS C.  
 PA (BOLD/) BOLDOG F L.  
 PA (BURG/) BURGESS C E.  
 PA (CATT/) CATTERTON E.  
 PA (DIPI/) DIPIPO V A.  
 PA (EDIN/) EDINGER S R.  
 PA (EISE/) EISEN A.  
 PA (ELLE/) ELLERMAN K.  
 PA (GANG/) GANGOLLI E A.  
 PA (GERL/) GERLACH V.  
 PA (GORM/) GORMAN L.  
 PA (ROTH/) ROTHBERG B G.  
 PA (GUOX/) GUO X S.  
 PA (HERR/) HERRMANN J L.  
 PA (HALV/) HALVORSEN Y.  
 PA (JIWV/) JI W.  
 PA (KEKU/) KEKUDA R.  
 PA (KHRA/) KHRAMTSOV N V.  
 PA (LARO/) LAROCHELLE W J.  
 PA (LEPL/) LEPLEY D M.  
 PA (LILL/) LI L.  
 PA (MACD/) MACDOUGALL J R.  
 PA (MILL/) MILLER C E.  
 PA (ORTT/) ORT T.  
 PA (PADI/) PADIGARU M.  
 PA (PATT/) PATTURAJAN M.  
 PA (PENA/) PENA C E A.  
 PA (PEYM/) PEYMAN J A.  
 PA (RIEG/) RIEGER D K.  
 PA (ROTH/) ROTHENBERG M E.  
 PA (SHEN/) SHENOY S G.  
 PA (SMIT/) SMITHSON G.  
 PA (SPAD/) SPADERNA S K.  
 PA (SPYT/) SPYTEK K A.  
 PA (STON/) STONE D J.  
 PA (TAUP/) TAUPIER R J.  
 PA (VERN/) VERNET C A M.  
 PA (VOSS/) VOSS E Z.  
 PA (ZHON/) ZHONG M.  
 Query Match 100.0%; Score 989; DB 12; Length 989;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-156;  
 RESULT 36  
 ID ABA05419 standard; cDNA; 1037 BP.  
 DE Human O-methyltransferase family member 25692 encoding cDNA.  
 PN WO200183719-A2.  
 PD 08-NOV-2001.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 99.7%; Score 985.8; DB 6; Length 1037;  
 Best Local Similarity 99.8%; Pred. No. 1.7e-155;  
 RESULT 37

ID AAZ98166 standard; cDNA; 985 BP.  
 DE Human signal peptide containing protein HSPP-58 cDNA SEQ ID NO:192.  
 PN WO20000610-A2.  
 PD 06-JAN-2000.  
 PA (INCY-) INCYTE PHARM INC.  
 Query Match 99.3%; Score 981.8; DB 3; Length 985;  
 Best Local Similarity 99.8%; Pred. No. 8.1e-155;  
 RESULT 38  
 ID ABQ61039 standard; cDNA; 1100 BP.  
 DE Human PRO1558 protein encoding sequence.  
 PN WO200231111-A2.  
 PD 18-APR-2002.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 99.3%; Score 981.8; DB 6; Length 1100;  
 Best Local Similarity 99.8%; Pred. No. 8e-155;  
 RESULT 39  
 ID ADO42272 standard; cDNA; 988 BP.  
 DE Human NOVX polynucleotide #61.  
 PN US2004058338-A1.  
 PD 25-MAR-2004.  
 PA (AGEE/) AGEE M L.  
 PA (ALSO/) ALSOBROOK J P.  
 PA (ANDE/) ANDERSON D W.  
 PA (BERG/) BERGHS C.  
 PA (BOLD/) BOLDOG F L.  
 PA (BURG/) BURGESS C E.  
 PA (CATT/) CATTERTON E.  
 PA (DIPI/) DIPIPO V A.  
 PA (EDIN/) EDINGER S R.  
 PA (EISE/) EISEN A.  
 PA (ELLE/) ELLERMAN K.  
 PA (GANG/) GANGOLLI E A.  
 PA (GERL/) GERLACH V.  
 PA (GORM/) GORMAN L.  
 PA (ROTH/) ROTHBERG B G.  
 PA (GUOX/) GUO X S.  
 PA (HERR/) HERRMANN J L.  
 PA (HALV/) HALVORSEN Y.  
 PA (JIWV/) JI W.  
 PA (KEKU/) KEKUDA R.  
 PA (KHRA/) KHRAMTSOV N V.  
 PA (LARO/) LAROCHELLE W J.  
 PA (LEPL/) LEPLEY D M.  
 PA (LILL/) LI L.  
 PA (MACD/) MACDOUGALL J R.  
 PA (MILL/) MILLER C E.  
 PA (ORTT/) ORT T.  
 PA (PADI/) PADIGARU M.  
 PA (PATT/) PATTURAJAN M.  
 PA (PENA/) PENA C E A.  
 PA (PEYM/) PEYMAN J A.  
 PA (RIEG/) RIEGER D K.  
 PA (ROTH/) ROTHENBERG M E.  
 PA (SHEN/) SHENOY S G.  
 PA (SMIT/) SMITHSON G.  
 PA (SPAD/) SPADERNA S K.  
 PA (SPYT/) SPYTEK K A.  
 PA (STON/) STONE D J.  
 PA (TAUP/) TAUPIER R J.  
 PA (VERN/) VERNET C A M.  
 PA (VOSS/) VOSS E Z.  
 PA (ZHON/) ZHONG M.  
 Query Match 98.8%; Score 977; DB 12; Length 988;  
 Best Local Similarity 99.9%; Pred. No. 5.1e-154;  
 RESULT 40  
 ID AAH33455 standard; cDNA; 967 BP.  
 DE Human colon cancer antigen encoding cDNA SEQ ID NO:511.  
 PN WO200122920-A2.  
 PD 05-APR-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 94.9%; Score 938.2; DB 4; Length 967;  
 Best Local Similarity 99.4%; Pred. No. 1.5e-147;  
 RESULT 41

ID ADQ87466 standard; cDNA; 927 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #4343.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH) GENENTECH INC.  
PA (WUTD) WU T D.  
PA (ZHOU) ZHOU Y.  
Query Match 93.5%; Score 925; DB 13; Length 927;  
Best Local Similarity 100.0%; Pred. No. 2.4e-145;  
RESULT 42  
ID AAC76634 standard; cDNA; 812 BP.  
DE Human ORFX ORF2189 polynucleotide sequence SEQ ID NO:4377.  
PN WO200508473-A2.  
PD 05-OCT-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match 80.9%; Score 799.8; DB 3; Length 812;  
Best Local Similarity 99.1%; Pred. No. 1.8e-124;  
RESULT 43  
ID ABA05420 standard; cDNA; 789 BP.  
DE Human O-methyltransferase family member 25692 coding sequence.  
PN WO2001083719-A2.  
PD 08-NOV-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 79.8%; Score 789; DB 6; Length 789;  
Best Local Similarity 100.0%; Pred. No. 1.1e-122;  
RESULT 44  
ID AAD56372 standard; DNA; 876 BP.  
DE Human secreted protein-encoding gene 11 cDNA clone HTAQO19, SEQ ID NO:32.  
PN WO2003038038-A2.  
PD 08-MAY-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 71.0%; Score 701.8; DB 9; Length 876;  
Best Local Similarity 86.5%; Pred. No. 3.9e-108;  
RESULT 45  
ID AAD56361 standard; DNA; 885 BP.  
DE Human secreted protein-encoding gene 11 cDNA clone HTAQO18, SEQ ID NO:21.  
PN WO2003038038-A2.  
PD 08-MAY-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 70.9%; Score 701; DB 9; Length 885;  
Best Local Similarity 86.2%; Pred. No. 5.3e-108;  
RESULT 46  
ID ADO42274 standard; cDNA; 787 BP.  
DE Human NOVX polynucleotide #62.  
PN US2004058338-A1.  
PD 25-MAR-2004.  
PA (AGEE) AGEE M L.  
PA (ALSO) ALSOBOOK J P.  
PA (ANDE) ANDERSON D W.  
PA (BERG) BERGHS C.  
PA (BOLD) BOLDOG F L.  
PA (BURG) BURGESS C E.  
PA (CATT) CATTERTON E.  
PA (DIP) DIPIPPO V A.  
PA (EDIN) EDINGER S R.  
PA (EISE) EISEN A.  
PA (ELLE) ELLERMAN K.  
PA (GANG) GANGOLLI E A.  
PA (GERL) GERLACH V.  
PA (GORM) GORMAN L.  
PA (ROTH) ROTHBERG B G.  
PA (GUOX) GUO X S.  
PA (HERR) HERRMANN J L.  
PA (HALV) HALVORSEN Y.  
PA (JIWW) JI W.  
PA (KEKU) KEKUDA R.  
PA (KHRA) KHRAMTSOV N V.  
PA (LARO) LAROCHELLE W J.  
PA (LEPL) LEFLEY D M.  
PA (LILL) LI L.  
PA (MACD) MACDOUGALL J R.  
PA (MILL) MILLER C E.  
PA (ORTT) ORT T.

PA (PADI) PADIGARU M.  
PA (PATT) PATTURAJAN M.  
PA (PENA) PENA C E A.  
PA (PEYN) PEYMAN J A.  
PA (RIEG) RIEGER D K.  
PA (ROTH) ROTHENBERG M E.  
PA (SHEN) SHENOY S G.  
PA (SMIT) SMITHSON G K.  
PA (SPAD) SPADERNA S K.  
PA (SPYT) SPYTEK K A.  
PA (STON) STONE D J.  
PA (TAUP) TAUPIER R J.  
PA (VERN) VERNET C A M.  
PA (VOSS) VOSS E Z.  
PA (ZHON) ZHONG M.  
Query Match 59.0%; Score 583.6; DB 12; Length 787;  
Best Local Similarity 90.1%; Pred. No. 2e-88;  
RESULT 47  
ID ACH35195 standard; cDNA; 474 BP.  
DE Human endothelial cell cDNA #3328.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA) DRMANAC R T.  
PA (LABA) LABAT I.  
PA (STAC) STACHE-CRAIN B.  
PA (DICK) DICKSON M C.  
PA (JONE) JONES L W.  
Query Match 42.7%; Score 422; DB 9; Length 474;  
Best Local Similarity 100.0%; Pred. No. 1.8e-61;  
RESULT 48  
ID ACH35890 standard; cDNA; 458 BP.  
DE Human endothelial cell cDNA #4023.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA) DRMANAC R T.  
PA (LABA) LABAT I.  
PA (STAC) STACHE-CRAIN B.  
PA (DICK) DICKSON M C.  
PA (JONE) JONES L W.  
Query Match 41.8%; Score 413; DB 9; Length 458;  
Best Local Similarity 100.0%; Pred. No. 5.6e-60;  
RESULT 49  
ID ADD34178 standard; DNA; 770 BP.  
DE Mouse mitochondrial DNA sequence SEQ ID NO:1956.  
PN WO2003020220-A2.  
PD 13-MAR-2003.  
PA (UYEM) UNIV EMORY.  
Query Match 40.9%; Score 404.4; DB 10; Length 770;  
Best Local Similarity 80.4%; Pred. No. 1.5e-58;  
RESULT 50  
ID ABN94134 standard; DNA; 326 BP.  
DE Gene #632 used to diagnose liver cancer.  
PN WO200229103-A2.  
PD 11-APR-2002.  
PA (GENE) GENE LOGIC INC.  
Query Match 31.5%; Score 312; DB 6; Length 326;  
Best Local Similarity 99.7%; Pred. No. 3.9e-43;  
RESULT 51  
ID ADS72763 standard; cDNA; 257 BP.  
DE Human kidney tumour specific cDNA, SEQ ID 1360.  
PN US2003109434-A1.  
PD 12-JUN-2003.  
PA (CORI) CORIXA CORP.  
Query Match 26.0%; Score 257; DB 7; Length 257;  
Best Local Similarity 100.0%; Pred. No. 5.8e-34;  
RESULT 52  
ID ADS72855 standard; cDNA; 257 BP.  
DE Human kidney tumour specific cDNA, SEQ ID 1452.  
PN US2003109434-A1.  
PD 12-JUN-2003.  
PA (CORI) CORIXA CORP.  
Query Match 25.7%; Score 254.4; DB 7; Length 257;  
Best Local Similarity 99.2%; Pred. No. 1.6e-33;

RESULT 53  
ID ADM80035 standard; DNA; 11171 BP.  
DE Spiramycin biosynthesis related DNA, SEQ ID 2.  
PN FR2845394-A1.  
PD 09-APR-2004.  
PA (AVET ) AVENTIS PHARMA SA.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 19.7%; Score 194.8; DB 12; Length 11171;  
Best Local Similarity 55.1%; Pred. No. 1.2e-23;  
RESULT 54  
ID ADN97551 standard; DNA; 11171 BP.  
DE S ambofaciens spiramycin biosynthetic enzyme genomic region #2.  
PN WO2004033689-A2.  
PD 22-APR-2004.  
PA (AVET ) AVENTIS PHARMA SA.  
PA (CNRS ) CNRS.  
Query Match 19.7%; Score 194.8; DB 12; Length 11171;  
Best Local Similarity 55.1%; Pred. No. 1.2e-23;  
RESULT 55  
ID ADM80044 standard; DNA; 675 BP.  
DE Spiramycin biosynthesis orfs\*, SEQ ID 11.  
PN FR2845394-A1.  
PD 09-APR-2004.  
PA (AVET ) AVENTIS PHARMA SA.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 19.6%; Score 193.8; DB 12; Length 675;  
Best Local Similarity 58.1%; Pred. No. 1.9e-23;  
RESULT 56  
ID ADN97560 standard; DNA; 675 BP.  
DE S ambofaciens spiramycin biosynthetic gene ORF5\*.  
PN WO2004033689-A2.  
PD 22-APR-2004.  
PA (AVET ) AVENTIS PHARMA SA.  
PA (CNRS ) CNRS.  
Query Match 19.6%; Score 193.8; DB 12; Length 675;  
Best Local Similarity 58.1%; Pred. No. 1.9e-23;  
RESULT 57  
ID ABD04592 standard; DNA; 846 BP.  
DE Pseudomonas aeruginosa polynucleotide #3196.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 19.1%; Score 189; DB 11; Length 846;  
Best Local Similarity 56.0%; Pred. No. 1.2e-22;  
RESULT 58  
ID AAQ44449 standard; DNA; 2381 BP.  
DE 3-acylating enzyme coding sequence.  
PN JP6038750-A.  
PD 15-FEB-1994.  
PA (MEIJ ) MEIJI SEIKA KAISHA.  
Query Match 18.8%; Score 185.8; DB 2; Length 2381;  
Best Local Similarity 57.3%; Pred. No. 4e-22;  
RESULT 59  
ID ADM45913 standard; DNA; 84428 BP.  
DE Streptomyces mycarofaciens midecamycin polyketide synthetase DNA.  
PN JP2004049100-A.  
PD 19-FEB-2004.  
PA (MEIJ ) MEIJI SEIKA KAISHA LTD.  
Query Match 18.8%; Score 185.8; DB 12; Length 84428;  
Best Local Similarity 57.3%; Pred. No. 3.6e-22;  
RESULT 60  
ID ADI39159 standard; DNA; 85692 BP.  
DE Streptomyces hygroscopicus geldanamycin gene cluster, SEQ ID NO:1.  
PN WO2003106653-A2.  
PD 24-DEC-2003.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
PA (REID/) REID R C.  
Query Match 18.4%; Score 182.4; DB 12; Length 85692;  
Best Local Similarity 57.4%; Pred. No. 1.3e-21;  
RESULT 61  
ID ADI39160 standard; DNA; 86941 BP.  
DE Streptomyces hygroscopicus herbimycin gene cluster, SEQ ID NO:2.  
PN WO2003106653-A2.

PD 24-DEC-2003.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
PA (REID/) REID R C.  
Query Match 18.1%; Score 179.2; DB 12; Length 86941;  
Best Local Similarity 57.9%; Pred. No. 4.6e-21;  
RESULT 62  
ID AAC89765 standard; cDNA; 178 BP.  
DE Human gastrointestinal inflammation-related cDNA, SEQ ID NO: 34.  
PN WO200073324-A2.  
PD 07-DEC-2000.  
PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.  
Query Match 17.7%; Score 174.8; DB 4; Length 178;  
Best Local Similarity 98.9%; Pred. No. 2.9e-20;  
RESULT 63  
ID ABS63429 standard; cDNA; 953 BP.  
DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAFALSKI J A.  
Query Match 16.4%; Score 161.8; DB 6; Length 953;  
Best Local Similarity 55.1%; Pred. No. 4.1e-18;  
RESULT 64  
ID ABS63428 standard; cDNA; 1049 BP.  
DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAFALSKI J A.  
Query Match 16.1%; Score 159.2; DB 6; Length 1049;  
Best Local Similarity 54.8%; Pred. No. 1.1e-17;  
RESULT 65  
ID ABS63413 standard; cDNA; 997 BP.  
DE DNA encoding rice caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAFALSKI J A.  
Query Match 16.0%; Score 158.6; DB 6; Length 997;  
Best Local Similarity 54.2%; Pred. No. 1.4e-17;  
RESULT 66  
ID ADA71076 standard; DNA; 1338 BP.  
DE Rice gene, SEQ ID 4399.  
PN WO2003000898-A1.  
PD 03-JAN-2003.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
Query Match 16.0%; Score 158.6; DB 8; Length 1338;  
Best Local Similarity 55.2%; Pred. No. 1.4e-17;  
RESULT 67  
ID ABS63427 standard; cDNA; 1078 BP.  
DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAFALSKI J A.  
Query Match 15.9%; Score 157.2; DB 6; Length 1078;  
Best Local Similarity 57.1%; Pred. No. 2.4e-17;  
RESULT 68  
ID ABS63424 standard; cDNA; 1018 BP.  
DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAFALSKI J A.  
Query Match 15.7%; Score 155.6; DB 6; Length 1018;  
Best Local Similarity 56.6%; Pred. No. 4.5e-17;  
RESULT 69  
ID ABS63407 standard; cDNA; 891 BP.

DE DNA encoding corn caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Query Match 15.6%; Score 154; DB 6; Length 891;  
 Best Local Similarity 56.7%; Pred. No. 8.3e-17;  
 RESULT 70  
 ID AAA14651 standard; DNA; 77536 BP.  
 DE Nucleotide sequence of the FK-520 biosynthetic gene cluster.  
 Query Match 15.5%; Score 153; DB 3; Length 77536;  
 Best Local Similarity 55.4%; Pred. No. 1.1e-16;  
 RESULT 71  
 ID ADA49019 standard; DNA; 1112 BP.  
 DE Wheat gene conferring disease resistance in plants.  
 PN WO2003000906-A2.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Query Match 15.4%; Score 152.8; DB 9; Length 1112;  
 Best Local Similarity 58.3%; Pred. No. 1.3e-16;  
 RESULT 72  
 ID AAX25215 standard; cDNA; 1218 BP.  
 DE Maize caffeoyl-CoA 3-O-methyltransferase cDNA.  
 PN WO9910498-A2.  
 PD 04-MAR-1999.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Query Match 15.4%; Score 152.4; DB 2; Length 1218;  
 Best Local Similarity 56.5%; Pred. No. 1.5e-16;  
 RESULT 73  
 ID AAD05742 standard; cDNA; 1218 BP.  
 DE Maize caffeoyl-CoA 3-O-methyltransferase (CCOA-OMT) cDNA.  
 PN WO200134817-A2.  
 PD 17-MAY-2001.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Query Match 15.4%; Score 152.4; DB 5; Length 1218;  
 Best Local Similarity 56.5%; Pred. No. 1.5e-16;  
 RESULT 74  
 ID AAL61224 standard; DNA; 82746 BP.  
 DE Actinosynnema pretiosum ansamitocin biosynthetic gene cluster I.  
 PN WO2003045312-A2.  
 PD 05-JUN-2003.  
 PA (UNIW) UNIV WASHINGTON.  
 Query Match 15.3%; Score 151.4; DB 8; Length 82746;  
 Best Local Similarity 57.3%; Pred. No. 2e-16;  
 RESULT 75  
 ID ABZ40101 standard; DNA; 666 BP.  
 DE N. gonorrhoeae nucleotide sequence SEQ ID 4791.  
 PN WO200279243-A2.  
 PD 10-OCT-2002.  
 PA (CHIR-) CHIRON SPA.  
 Query Match 15.1%; Score 149.2; DB 10; Length 666;  
 Best Local Similarity 53.5%; Pred. No. 5.3e-16;  
 RESULT 76  
 ID AAX25210 standard; cDNA; 1003 BP.  
 DE Maize caffeoyl-CoA 3-O-methyltransferase cDNA.  
 PN WO9910498-A2.  
 PD 04-MAR-1999.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Query Match 15.1%; Score 149.2; DB 2; Length 1003;  
 Best Local Similarity 58.0%; Pred. No. 5.2e-16;  
 RESULT 77  
 ID ADA49212 standard; DNA; 798 BP.  
 DE Maize gene conferring disease resistance in plants.  
 PN WO2003000906-A2.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Query Match 15.0%; Score 148; DB 9; Length 798;  
 Best Local Similarity 53.7%; Pred. No. 8.3e-16;  
 RESULT 78  
 ID ABS63425 standard; cDNA; 1118 BP.  
 DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.

PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Query Match 15.0%; Score 148; DB 6; Length 1118;  
 Best Local Similarity 53.7%; Pred. No. 8.2e-16;  
 RESULT 79  
 ID ABS63408 standard; cDNA; 1146 BP.  
 DE DNA encoding corn caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Query Match 15.0%; Score 148; DB 6; Length 1146;  
 Best Local Similarity 53.7%; Pred. No. 8.2e-16;  
 RESULT 80  
 ID ADR73686 standard; DNA; 1252 BP.  
 DE Rice promoter putative caffeoyl CoA3O methyltransferase CDS.  
 PN WO2004070039-A2.  
 PD 19-AUG-2004.  
 PA (CROP-) CROPDESIGN NV.  
 Query Match 14.9%; Score 147.6; DB 13; Length 1252;  
 Best Local Similarity 54.2%; Pred. No. 9.5e-16;  
 RESULT 81  
 ID ADD34177 standard; DNA; 407 BP.  
 DE Mouse mitochondrial DNA sequence SEQ ID NO:1955.  
 PN WO2003020220-A2.  
 PD 13-MAR-2003.  
 PA (UYEM-) UNIV EMORY.  
 Query Match 14.9%; Score 147.4; DB 10; Length 407;  
 Best Local Similarity 73.3%; Pred. No. 1.1e-15;  
 RESULT 82  
 ID AAA81501 standard; DNA; 48275 BP.  
 DE N. meningitidis partial DNA sequence gnm\_48 SEQ ID NO:48.  
 PN WO200022430-A2.  
 PD 20-APR-2000.  
 PA (CHIR) CHIRON CORP.  
 Query Match 14.8%; Score 146.8; DB 3; Length 48275;  
 Best Local Similarity 53.1%; Pred. No. 1.2e-15;  
 RESULT 83  
 ID AAA81489 standard; DNA; 837096 BP.  
 DE N. meningitidis partial DNA sequence gnm\_37 SEQ ID NO:37.  
 PN WO200022430-A2.  
 PD 20-APR-2000.  
 PA (CHIR) CHIRON CORP.  
 Query Match 14.8%; Score 146.8; DB 3; Length 110000;  
 Best Local Similarity 53.1%; Pred. No. 1.1e-15;  
 RESULT 84  
 ID AAF21610 standard; DNA; 349980 BP.  
 DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:111.  
 PN WO200066791-A1.  
 PD 09-NOV-2000.  
 PA (CHIR) CHIRON CORP.  
 Query Match 14.8%; Score 146.8; DB 3; Length 349980;  
 Best Local Similarity 53.1%; Pred. No. 1.1e-15;  
 RESULT 85  
 ID AAL61190 standard; DNA; 504 BP.  
 DE Actinosynnema pretiosum O-methyltransferase gene.  
 PN WO2003045312-A2.  
 PD 05-JUN-2003.  
 PA (UNIW) UNIV WASHINGTON.  
 Query Match 14.8%; Score 146.6; DB 8; Length 504;  
 Best Local Similarity 57.7%; Pred. No. 1.4e-15;  
 RESULT 86  
 ID AAX25208 standard; cDNA; 1160 BP.  
 DE Maize caffeoyl-CoA 3-O-methyltransferase cDNA.  
 PN WO9910498-A2.  
 PD 04-MAR-1999.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Query Match 14.8%; Score 146.4; DB 2; Length 1160;  
 Best Local Similarity 53.5%; Pred. No. 1.5e-15;

RESULT 87  
 ID ABS63409 standard; cDNA; 1057 BP.  
 DE DNA encoding corn caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Query Match 14.6%; Score 144.4; DB 6; Length 1057;  
 Best Local Similarity 57.3%; Pred. No. 3.3e-15;  
 RESULT 88  
 ID ADA71075 standard; DNA; 783 BP.  
 DE Rice gene, SEQ ID 4398.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Query Match 14.3%; Score 141.8; DB 8; Length 783;  
 Best Local Similarity 57.4%; Pred. No. 9e-15;  
 RESULT 89  
 ID ACL23248 standard; DNA; 509 BP.  
 DE DNA clone originating in barley containing SNP encoding sequence #13239.  
 PN WO2003057877-A1.  
 PD 17-JUL-2003.  
 PA (UYNI-) UNIV JAPAN OKAYAMA.  
 Query Match 14.2%; Score 140.8; DB 9; Length 509;  
 Best Local Similarity 60.3%; Pred. No. 1.3e-14;  
 RESULT 90  
 ID ABS63412 standard; cDNA; 1058 BP.  
 DE DNA encoding rice caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Query Match 14.2%; Score 140.6; DB 6; Length 1058;  
 Best Local Similarity 50.6%; Pred. No. 1.4e-14;  
 RESULT 91  
 ID ADA70823 standard; DNA; 783 BP.  
 DE Rice gene, SEQ ID 4146.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Query Match 14.2%; Score 140; DB 8; Length 783;  
 Best Local Similarity 52.9%; Pred. No. 1.8e-14;  
 RESULT 92  
 ID ABN87118 standard; cDNA; 1103 BP.  
 DE Lolium perenne LpCCoMTb nucleotide sequence SEQ ID NO:12.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Query Match 13.7%; Score 135.6; DB 6; Length 1103;  
 Best Local Similarity 57.0%; Pred. No. 9.6e-14;  
 RESULT 93  
 ID ABN87121 standard; cDNA; 773 BP.  
 DE Lolium perenne LpCCoMTb partial nucleotide sequence SEQ ID NO:16.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Query Match 13.7%; Score 135; DB 6; Length 773;  
 Best Local Similarity 56.9%; Pred. No. 1.2e-13;  
 RESULT 94  
 ID ABN87122 standard; cDNA; 789 BP.  
 DE Lolium perenne LpCCoMTb partial nucleotide sequence SEQ ID NO:17.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Query Match 13.7%; Score 135; DB 6; Length 789;  
 Best Local Similarity 56.9%; Pred. No. 1.2e-13;  
 RESULT 95  
 ID ABN87120 standard; cDNA; 693 BP.  
 DE Lolium perenne LpCCoMTb partial nucleotide sequence SEQ ID NO:15.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Query Match 13.3%; Score 131.6; DB 6; Length 693;  
 Best Local Similarity 56.9%; Pred. No. 4.5e-13;  
 RESULT 96  
 ID AAS08693 standard; DNA; 109519 BP.  
 DE Micromonospora DNA encoding biosynthetic enzymes for Everninomycin.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Query Match 12.9%; Score 127.4; DB 5; Length 109519;  
 Best Local Similarity 55.8%; Pred. No. 2e-12;  
 RESULT 97  
 ID ABN87126 standard; cDNA; 689 BP.  
 DE Lolium perenne LpCCoMTb nucleotide sequence SEQ ID NO:21.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Query Match 12.8%; Score 126.8; DB 6; Length 689;  
 Best Local Similarity 57.1%; Pred. No. 2.8e-12;  
 RESULT 98  
 ID ABS63410 standard; cDNA; 923 BP.  
 DE DNA encoding corn caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Query Match 12.7%; Score 126; DB 6; Length 923;  
 Best Local Similarity 56.6%; Pred. No. 3.8e-12;  
 RESULT 99  
 ID AAX25209 standard; cDNA; 944 BP.  
 DE Maize caffeoyl-CoA 3-O-methyltransferase cDNA.  
 PN WO9910498-A2.  
 PD 04-MAR-1999.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Query Match 12.7%; Score 126; DB 2; Length 944;  
 Best Local Similarity 56.6%; Pred. No. 3.8e-12;  
 RESULT 100  
 ID ADA48371 standard; DNA; 835 BP.  
 DE Rice gene conferring disease resistance in plants.  
 PN WO2003000906-A2.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Query Match 12.7%; Score 125.4; DB 9; Length 835;  
 Best Local Similarity 55.0%; Pred. No. 4.9e-12;  
 RESULT 101  
 ID ADC68436 standard; cDNA; 1051 BP.  
 DE Lolium perenne lignin biosynthesis protein cDNA SEQ ID NO:146.  
 PN WO2003040306-A2.  
 PD 15-MAY-2003.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (WRIG-) WRIGHTSON SEEDS LTD.  
 Query Match 12.6%; Score 125; DB 10; Length 1051;  
 Best Local Similarity 54.0%; Pred. No. 5.6e-12;  
 RESULT 102  
 ID ADC68544 standard; cDNA; 1059 BP.  
 DE Lolium perenne lignin biosynthesis protein cDNA SEQ ID NO:36.  
 PN WO2003040306-A2.  
 PD 15-MAY-2003.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (WRIG-) WRIGHTSON SEEDS LTD.  
 Query Match 12.5%; Score 123.4; DB 10; Length 1059;  
 Best Local Similarity 53.9%; Pred. No. 1e-11;  
 RESULT 103  
 ID ADC68545 standard; cDNA; 1063 BP.  
 DE S. arundinaceus lignin biosynthesis protein cDNA SEQ ID NO:37.  
 PN WO2003040306-A2.  
 PD 15-MAY-2003.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (WRIG-) WRIGHTSON SEEDS LTD.  
 Query Match 12.4%; Score 122.6; DB 10; Length 1063;

Best Local Similarity 54.2%; Pred. No. 1.4e-11;  
RESULT 104  
ID ABN87112 standard; cDNA; 765 BP.  
DE Lolium perenne LpCCoAMTA partial nucleotide sequence SEQ ID NO:6.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Query Match 12.0%; Score 118.4; DB 6; Length 765;  
Best Local Similarity 53.7%; Pred. No. 7.1e-11;  
RESULT 105  
ID AAQ14978 standard; DNA; 1810 BP.  
DE Acya gene.  
PN EP459525-A.  
PD 04-DEC-1991.  
PA (SAOC) MERCIAN CORP.  
Query Match 11.9%; Score 118; DB 2; Length 1810;  
Best Local Similarity 57.8%; Pred. No. 8.1e-11;  
RESULT 106  
ID ABN87245 standard; cDNA; 1161 BP.  
DE Lolium perenne CCoAMT1 cDNA sequence SEQ ID NO:168.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Query Match 11.9%; Score 117.8; DB 6; Length 1161;  
Best Local Similarity 53.7%; Pred. No. 8.9e-11;  
RESULT 107  
ID ABN87110 standard; cDNA; 758 BP.  
DE Lolium perenne LpCCoAMTA partial nucleotide sequence SEQ ID NO:4.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Query Match 11.7%; Score 115.6; DB 6; Length 758;  
Best Local Similarity 52.8%; Pred. No. 2.1e-10;  
RESULT 108  
ID ABN87115 standard; cDNA; 793 BP.  
DE Lolium perenne LpCCoAMTA partial nucleotide sequence SEQ ID NO:9.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Query Match 11.7%; Score 115.6; DB 6; Length 793;  
Best Local Similarity 52.8%; Pred. No. 2.1e-10;  
RESULT 109  
ID ABN87108 standard; cDNA; 1113 BP.  
DE Lolium perenne LpCCoAMTA nucleotide sequence SEQ ID NO:1.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Query Match 11.6%; Score 115; DB 6; Length 1113;  
Best Local Similarity 52.8%; Pred. No. 2.6e-10;  
RESULT 110  
ID ABN87246 standard; cDNA; 1199 BP.  
DE Lolium perenne CCoAMT2 cDNA sequence SEQ ID NO:170.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Query Match 11.6%; Score 115; DB 6; Length 1199;  
Best Local Similarity 52.8%; Pred. No. 2.6e-10;  
RESULT 111  
ID ABN87111 standard; cDNA; 774 BP.  
DE Lolium perenne LpCCoAMTA partial nucleotide sequence SEQ ID NO:5.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Query Match 11.5%; Score 113.8; DB 6; Length 774;  
Best Local Similarity 53.0%; Pred. No. 4.2e-10;  
RESULT 112

ID ABN87113 standard; cDNA; 777 BP.  
DE Lolium perenne LpCCoAMTA partial nucleotide sequence SEQ ID NO:7.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Query Match 11.4%; Score 113.2; DB 6; Length 777;  
Best Local Similarity 52.2%; Pred. No. 5.3e-10;  
RESULT 113  
ID ABN87114 standard; cDNA; 792 BP.  
DE Lolium perenne LpCCoAMTA partial nucleotide sequence SEQ ID NO:8.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Query Match 11.1%; Score 110; DB 6; Length 792;  
Best Local Similarity 51.9%; Pred. No. 1.8e-09;  
RESULT 114  
ID AAT24153 standard; cDNA to mRNA; 111 BP.  
DE Human gene signature HUMGS06156.  
PN WO9514772-A1.  
PD 01-JUN-1995.  
PA (MATS) MATSUBARA K.  
PA (OKUB) OKUBO K.  
Query Match 10.8%; Score 106.8; DB 2; Length 111;  
Best Local Similarity 97.3%; Pred. No. 6.5e-09;  
RESULT 115  
ID ABK2368 standard; cDNA; 343 BP.  
DE Rat sequence differentially expressed in response to a hepatotoxin #275.  
PN WO200210453-A2.  
PD 07-FEB-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 10.5%; Score 103.6; DB 6; Length 343;  
Best Local Similarity 68.7%; Pred. No. 2.1e-08;  
RESULT 116  
ID ADB5562 standard; DNA; 343 BP.  
DE Toxicity-related gene, SEQ ID 688.  
PN WO2003064624-A2.  
PD 07-AUG-2003.  
PA (GENE-) GENE LOGIC INC.  
Query Match 10.5%; Score 103.6; DB 10; Length 343;  
Best Local Similarity 68.7%; Pred. No. 2.1e-08;  
RESULT 117  
ID ABT40596 standard; DNA; 343 BP.  
DE Toxicity modelling related rat gene SEQ ID No 298.  
PN WO200295000-A2.  
PD 28-NOV-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 10.5%; Score 103.6; DB 10; Length 343;  
Best Local Similarity 68.7%; Pred. No. 2.1e-08;  
RESULT 118  
ID AAA68001 standard; DNA; 1012 BP.  
DE Pinus radiata OMT nucleotide sequence SEQ ID NO:94.  
PN WO200022099-A1.  
PD 20-APR-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Query Match 9.8%; Score 96.8; DB 3; Length 1012;  
Best Local Similarity 50.8%; Pred. No. 2.8e-07;  
RESULT 119  
ID ADD41751 standard; DNA; 1012 BP.  
DE O-methyl transferase DNA #9.  
PN US2003131373-A1.  
PD 10-JUL-2003.  
PA (BLOK/) BLOKSBERG L N.  
PA (HAVU/) HAVUKKALA I.  
Query Match 9.8%; Score 96.8; DB 10; Length 1012;  
Best Local Similarity 50.8%; Pred. No. 2.8e-07;  
RESULT 120  
ID AAV23912 standard; DNA; 1026 BP.  
DE Plant OMT enzyme DNA sequence.  
PN WO9811205-A2.  
PD 19-MAR-1998.



PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Query Match 9.8%; Score 96.8; DB 2; Length 1026;  
Best Local Similarity 50.8%; Pred. No. 2.8e-07;  
RESULT 121  
ID AAZ06875 standard; cDNA; 1026 BP.  
DE Pine O-methyl transferase (OMT) partial cDNA 1.  
PN US952486-A.  
PD 14-SEP-1999.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Query Match 9.8%; Score 96.8; DB 2; Length 1026;  
Best Local Similarity 50.8%; Pred. No. 2.8e-07;  
RESULT 122  
ID AAA67913 standard; DNA; 1026 BP.  
DE Pinus radiata OMT nucleotide sequence SEQ ID NO:6.  
PN WO200022099-A1.  
PD 20-APR-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Query Match 9.8%; Score 96.8; DB 3; Length 1026;  
Best Local Similarity 50.8%; Pred. No. 2.8e-07;  
RESULT 123  
ID ADD41663 standard; DNA; 1026 BP.  
DE O-methyl transferase DNA #1.  
PN US2003131373-A1.  
PD 10-JUL-2003.  
PA (BLOK/) BLOKSBERG L N.  
PA (HAVU/) HAVUKKALA I.  
Query Match 9.8%; Score 96.8; DB 10; Length 1026;  
Best Local Similarity 50.8%; Pred. No. 2.8e-07;  
RESULT 124  
ID ABN87119 standard; cDNA; 628 BP.  
DE Lollium perenne LpCCOAMTB partial nucleotide sequence SEQ ID NO:14.  
PN WO200226994-A1.  
PD 04-APR-2002.  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PA (AGRE-) AGRESEARCH LTD.  
Query Match 9.6%; Score 95.4; DB 6; Length 628;  
Best Local Similarity 53.7%; Pred. No. 4.9e-07;  
RESULT 125  
ID ACL323249 standard; DNA; 542 BP.  
DE DNA clone originating in barley containing SNP encoding sequence #13240.  
PN WO2003057877-A1.  
PD 17-JUL-2003.  
PA (UYNI-) UNIV JAPAN OKAYAMA.  
Query Match 9.6%; Score 95.2; DB 9; Length 542;  
Best Local Similarity 50.9%; Pred. No. 5.3e-07;  
RESULT 126  
ID ADK69906 standard; DNA; 1180 BP.  
DE Maize F4 CCOAOMT2 gene, seq id 3.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Query Match 9.4%; Score 93; DB 10; Length 1181;  
Best Local Similarity 59.7%; Pred. No. 1.2e-06;  
RESULT 127  
ID ADK69926 standard; DNA; 1199 BP.  
DE Maize W64A CCOAOMT2 gene insertion mutant #4.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Query Match 9.4%; Score 93; DB 10; Length 1181;  
Best Local Similarity 59.7%; Pred. No. 1.2e-06;  
RESULT 128  
ID ABD00975 standard; DNA; 675 BP.  
DE Klebsiella pneumoniae polynucleotide seqid 6750.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 9.4%; Score 93.4; DB 11; Length 675;  
Best Local Similarity 52.3%; Pred. No. 1.1e-06;  
RESULT 129  
ID ADK69918 standard; DNA; 1172 BP.  
DE Maize W64A CCOAOMT2 gene deletion mutant #1.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Query Match 9.4%; Score 93; DB 10; Length 1172;  
Best Local Similarity 59.7%; Pred. No. 1.2e-06;  
RESULT 130  
ID ADK69927 standard; DNA; 1178 BP.  
DE Maize W64A CCOAOMT2 gene deletion mutant #2.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Query Match 9.4%; Score 93; DB 10; Length 1178;  
Best Local Similarity 59.7%; Pred. No. 1.2e-06;  
RESULT 131  
ID ADK69919 standard; DNA; 1181 BP.  
DE Maize W64A CCOAOMT2 gene substitution mutant #1.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Query Match 9.4%; Score 93; DB 10; Length 1181;  
Best Local Similarity 59.7%; Pred. No. 1.2e-06;  
RESULT 132  
ID ADK69920 standard; DNA; 1181 BP.  
DE Maize W64A CCOAOMT2 gene substitution mutant #2.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Query Match 9.4%; Score 93; DB 10; Length 1181;  
Best Local Similarity 59.7%; Pred. No. 1.2e-06;  
RESULT 133  
ID ADK69928 standard; DNA; 1181 BP.  
DE Maize W64A CCOAOMT2 gene substitution mutant #7.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Query Match 9.4%; Score 93; DB 10; Length 1181;  
Best Local Similarity 59.7%; Pred. No. 1.2e-06;  
RESULT 134  
ID ADK69923 standard; DNA; 1181 BP.  
DE Maize W64A CCOAOMT2 gene substitution mutant #5.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Query Match 9.4%; Score 93; DB 10; Length 1181;  
Best Local Similarity 59.7%; Pred. No. 1.2e-06;  
RESULT 135  
ID ADK69904 standard; DNA; 1181 BP.  
DE Maize W64A CCOAOMT2 gene, seq id 1.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Query Match 9.4%; Score 93; DB 10; Length 1181;  
Best Local Similarity 59.7%; Pred. No. 1.2e-06;  
RESULT 136  
ID ADK69922 standard; DNA; 1181 BP.  
DE Maize W64A CCOAOMT2 gene substitution mutant #4.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Query Match 9.4%; Score 93; DB 10; Length 1181;  
Best Local Similarity 59.7%; Pred. No. 1.2e-06;  
RESULT 137  
ID ADK69924 standard; DNA; 1181 BP.  
DE Maize W64A CCOAOMT2 gene substitution mutant #6.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Query Match 9.4%; Score 93; DB 10; Length 1181;  
Best Local Similarity 59.7%; Pred. No. 1.2e-06;  
RESULT 138  
ID ADK69929 standard; DNA; 1181 BP.

DE Maize W64A CCOAOMT2 gene substitution mutant #8.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Query Match 9.4%; Score 93; DB 10; Length 1181;  
Best Local Similarity 59.7%; Pred. No. 1.2e-06;  
RESULT 139  
ID ADK69931 standard; DNA; 1181 BP.  
DE Maize W64A CCOAOMT2 gene substitution mutant #10.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Query Match 9.4%; Score 93; DB 10; Length 1181;  
Best Local Similarity 59.7%; Pred. No. 1.2e-06;  
RESULT 140  
ID ADK69921 standard; DNA; 1181 BP.  
DE Maize W64A CCOAOMT2 gene substitution mutant #3.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Query Match 9.4%; Score 93; DB 10; Length 1181;  
Best Local Similarity 59.7%; Pred. No. 1.2e-06;  
RESULT 141  
ID ADK69930 standard; DNA; 1181 BP.  
DE Maize W64A CCOAOMT2 gene substitution mutant #9.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Query Match 9.4%; Score 93; DB 10; Length 1181;  
Best Local Similarity 59.7%; Pred. No. 1.2e-06;  
RESULT 142  
ID ADK69917 standard; DNA; 1186 BP.  
DE Maize W64A CCOAOMT2 gene insertion mutant #1.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Query Match 9.4%; Score 93; DB 10; Length 1186;  
Best Local Similarity 59.7%; Pred. No. 1.2e-06;  
RESULT 143  
ID ADK69925 standard; DNA; 1196 BP.  
DE Maize W64A CCOAOMT2 gene insertion mutant #3.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Query Match 9.4%; Score 93; DB 10; Length 1196;  
Best Local Similarity 59.7%; Pred. No. 1.2e-06;  
RESULT 144  
ID ADK69932 standard; DNA; 1199 BP.  
DE Maize W64A CCOAOMT2 gene insertion mutant #5.  
PN FR2833615-A1.  
PD 20-JUN-2003.  
PA (GENO-) GENOPLANTE-VALOR SAS.  
Query Match 9.4%; Score 93; DB 10; Length 1199;  
Best Local Similarity 59.7%; Pred. No. 1.2e-06;  
RESULT 145  
ID ABS63415 standard; cDNA; 931 BP.  
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAFALSKI J A.  
Query Match 8.9%; Score 88; DB 6; Length 931;  
Best Local Similarity 50.7%; Pred. No. 8.3e-06;  
RESULT 146  
ID ABS63430 standard; cDNA; 534 BP.  
DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAFALSKI J A.  
Query Match 8.9%; Score 87.8; DB 6; Length 534;  
Best Local Similarity 50.7%; Pred. No. 8.3e-06;

Best Local Similarity 54.1%; Pred. No. 9.1e-06;  
RESULT 147  
ID ADR62522 standard; cDNA; 995 BP.  
DE Cotton cDNA sequence, SEQ ID 3303.  
PN US2004181830-A1.  
PD 16-SEP-2004.  
PA (KOVA/) KOVALIC D K.  
PA (ZHOU/) ZHOU Y.  
PA (CAOY/) CAO Y.  
Query Match 8.8%; Score 86.8; DB 13; Length 995;  
Best Local Similarity 50.6%; Pred. No. 1.3e-05;  
RESULT 148  
ID ACN60610 standard; cDNA; 617 BP.  
DE Cotton gynoecium tissue EST Clone ID: LIB3829-025-Q6-K6-F5, SEQ:15391.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 8.7%; Score 85.6; DB 13; Length 617;  
Best Local Similarity 47.9%; Pred. No. 2.1e-05;  
RESULT 149  
ID ABS63418 standard; cDNA; 962 BP.  
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAFALSKI J A.  
Query Match 8.7%; Score 85.6; DB 6; Length 962;  
Best Local Similarity 52.2%; Pred. No. 2.1e-05;  
RESULT 150  
ID ABS63419 standard; cDNA; 1023 BP.  
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAFALSKI J A.  
Query Match 8.7%; Score 85.6; DB 6; Length 1023;  
Best Local Similarity 52.2%; Pred. No. 2.1e-05;  
RESULT 151  
ID AAQ32259 standard; cDNA; 1258 BP.  
DE Caffeoyl-CoA-3-O-methyltransferase gene (pL2-4).  
PN DE4117747-A.  
PD 03-DEC-1992.  
PA (FARB ) BAYER AG.  
Query Match 8.5%; Score 84.4; DB 2; Length 1258;  
Best Local Similarity 49.8%; Pred. No. 3.3e-05;  
RESULT 152  
ID ADN74200 standard; cDNA; 780 BP.  
DE Thale cress cDNA repressed in E2Fa/Dpa expressing plants SeqID 2095.  
PN WO2004035798-A2.  
PD 29-APR-2004.  
PA (CROP-) CROPDESIGN NV.  
Query Match 8.5%; Score 84; DB 12; Length 780;  
Best Local Similarity 51.9%; Pred. No. 3.9e-05;  
RESULT 153  
ID ADN73162 standard; cDNA; 780 BP.  
DE Thale cress cDNA upregulated in E2Fa/Dpa expressing plants SeqID 1057.  
PN WO2004035798-A2.  
PD 29-APR-2004.  
PA (CROP-) CROPDESIGN NV.  
Query Match 8.5%; Score 84; DB 12; Length 780;  
Best Local Similarity 51.9%; Pred. No. 3.9e-05;  
RESULT 154  
ID AAC4547 standard; DNA; 1032 BP.  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 46896.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 8.5%; Score 84; DB 3; Length 1032;  
Best Local Similarity 51.9%; Pred. No. 3.8e-05;

RESULT 155  
ID AAC2559 standard; DNA; 1033 BP.  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 36009.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 8.5%; Score 84; DB 3; Length 1033;  
Best Local Similarity 51.9%; Pred. No. 3.8e-05;  
RESULT 156  
ID ABN98364 standard; DNA; 1072 BP.  
DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 132.  
PN US2002023281-A1.  
PD 21-FEB-2002.  
PA (GORL/) GORLACH J.  
PA (ANYI/) AN Y.  
PA (HAMI/) HAMILTON C M.  
PA (PRIC/) PRICE J L.  
PA (RAIN/) RAINES T M.  
PA (YUYV/) YU Y.  
PA (RAME/) RAMEAKA J G.  
PA (PAGE/) PAGE A.  
PA (MATH/) MATHAW A V.  
PA (LEDF/) LEDFORD B L.  
PA (WOES/) WOESSNER J P.  
PA (HAAS/) HAAS W D.  
PA (GARC/) GARCIA C A.  
PA (KRIC/) KRICKER M.  
PA (SLAT/) SLATER T.  
PA (DAVI/) DAVIS K R.  
PA (ALLE/) ALLEN K.  
PA (HOFF/) HOFFMAN N.  
PA (HURE/) HUREAN P.  
Query Match 8.5%; Score 84; DB 6; Length 1072;  
Best Local Similarity 51.9%; Pred. No. 3.8e-05;  
RESULT 157  
ID AAC44172 standard; DNA; 1180 BP.  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 41890.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 8.5%; Score 84; DB 3; Length 1180;  
Best Local Similarity 51.9%; Pred. No. 3.8e-05;  
RESULT 158  
ID ADR5554 standard; cDNA; 1233 BP.  
DE Cotton cDNA sequence, SEQ ID 6335.  
PN US2004181830-A1.  
PD 16-SEP-2004.  
PA (KOVA/) KOVALIC D K.  
PA (ZHOU/) ZHOU Y.  
PA (CAOY/) CAO Y.  
Query Match 8.0%; Score 79.6; DB 13; Length 1233;  
Best Local Similarity 49.2%; Pred. No. 0.00021;  
RESULT 159  
ID ABS63417 standard; cDNA; 980 BP.  
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAFALSKI J A.  
Query Match 8.0%; Score 79.2; DB 6; Length 980;  
Best Local Similarity 51.2%; Pred. No. 0.00024;  
RESULT 160  
ID AAV23845 standard; DNA; 760 BP.  
DE Plant OMT enzyme DNA sequence.  
PN WO9811205-A2.  
PD 19-MAR-1998.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Query Match 7.7%; Score 76.2; DB 2; Length 760;  
Best Local Similarity 56.6%; Pred. No. 0.00078;  
RESULT 161  
ID AAZ06846 standard; cDNA; 760 BP.  
DE Eucalyptus O-methyl transferase (OMT) partial cDNA 4.  
PN US5952486-A.

PD 14-SEP-1999.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Query Match 7.7%; Score 76.2; DB 2; Length 760;  
Best Local Similarity 56.6%; Pred. No. 0.00078;  
RESULT 162  
ID AAA9584 standard; cDNA; 760 BP.  
DE Eucalyptus grandis cinnamoyl-CoA reductase cDNA SEQ ID NO:58.  
PN WO200036081-A2.  
PD 22-JUN-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Query Match 7.7%; Score 76.2; DB 3; Length 760;  
Best Local Similarity 56.6%; Pred. No. 0.00078;  
RESULT 163  
ID AAA67932 standard; DNA; 760 BP.  
DE Eucalyptus grandis OMT nucleotide sequence SEQ ID NO:25.  
PN WO200022099-A1.  
PD 20-APR-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Query Match 7.7%; Score 76.2; DB 3; Length 760;  
Best Local Similarity 56.6%; Pred. No. 0.00078;  
RESULT 164  
ID ADD41682 standard; DNA; 760 BP.  
DE O-methyl transferase DNA #5.  
PN US200313173-A1.  
PD 10-JUL-2003.  
PA (BLOK/) BLOKSBERG L N.  
PA (HAVU/) HAVUKKALA I.  
Query Match 7.7%; Score 76.2; DB 10; Length 760;  
Best Local Similarity 56.6%; Pred. No. 0.00078;  
RESULT 165  
ID ABS63416 standard; cDNA; 929 BP.  
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAFALSKI J A.  
Query Match 7.5%; Score 74.4; DB 6; Length 929;  
Best Local Similarity 50.5%; Pred. No. 0.0015;  
RESULT 166  
ID ABS54112 standard; DNA; 870 BP.  
DE Tobacco caffeoyl CoA O-methyltransferase-1 (CCOAMT-1) cDNA.  
PN US6441272-B1.  
PD 27-AUG-2002.  
PA (UYGE-) UNIV GEORGIA RES FOUND INC.  
Query Match 7.4%; Score 73.2; DB 6; Length 870;  
Best Local Similarity 48.4%; Pred. No. 0.0024;  
RESULT 167  
ID ACN55288 standard; cDNA; 546 BP.  
DE Cotton androecium tissue EST Clone ID: LTB3828-032-Q6-K6-D4, SEQ:10069.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 7.4%; Score 72.8; DB 13; Length 546;  
Best Local Similarity 50.2%; Pred. No. 0.0029;  
RESULT 168  
ID ACN40884 standard; cDNA; 1067 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA326926, SEQ ID NO:5958.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH-) GENENTECH INC.  
Query Match 7.2%; Score 71; DB 13; Length 1067;  
Best Local Similarity 50.7%; Pred. No. 0.0057;  
RESULT 169  
ID AAQ13306 standard; DNA; 1107 BP.  
DE Human catechol-O-methyltransferase gene.  
PN WO9111513-A.

PD 08-AUG-1991.  
 PA (ORIN ) ORION YHTYMAE OY.  
 Query Match 7.2%; Score 71; DB 2; Length 1107;  
 Best Local Similarity 50.7%; Pred. No. 0.0056;  
 RESULT 170  
 ID ACN40883 standard; cDNA; 1289 BP.  
 DE Tumour-associated antigenic target (TAT) cDNA DNA226561, SEQ ID NO:5956.  
 PN WO2004030615-A2.  
 PD 15-APR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.2%; Score 71; DB 13; Length 1289;  
 Best Local Similarity 50.7%; Pred. No. 0.0056;  
 RESULT 171  
 ID AAC77872 standard; cDNA; 1350 BP.  
 DE Human cancer associated gene sequence SEQ ID NO:266.  
 PN WO200055350-A1.  
 PD 21-SEP-2000.  
 PA (HUNA-) HUMAN GENOME SCI INC.  
 Query Match 7.1%; Score 70.6; DB 3; Length 1350;  
 Best Local Similarity 50.4%; Pred. No. 0.0065;  
 RESULT 172  
 ID ABS54113 standard; DNA; 811 BP.  
 DE Tobacco caffeoyl CoA O-methyltransferase-2 (CCoAOMT-2) cDNA.  
 PN US6441272-B1.  
 PD 27-AUG-2002.  
 PA (UYGE-) UNIV GEORGIA RES FOUND INC.  
 Query Match 7.1%; Score 70; DB 6; Length 811;  
 Best Local Similarity 47.9%; Pred. No. 0.0084;  
 RESULT 173  
 ID ADH02845 standard; cDNA; 888 BP.  
 DE Petunia E2O cDNA #SEQ ID 4.  
 PN WO2003062428-A1.  
 PD 31-JUL-2003.  
 PA (ITFL-) INT FLOWER DEV PTY LTD.  
 Query Match 7.0%; Score 69.6; DB 10; Length 888;  
 Best Local Similarity 50.3%; Pred. No. 0.0097;  
 RESULT 174  
 ID ADH02842 standard; cDNA; 969 BP.  
 DE Petunia dife cDNA #SEQ ID 1.  
 PN WO2003062428-A1.  
 PD 31-JUL-2003.  
 PA (ITFL-) INT FLOWER DEV PTY LTD.  
 Query Match 7.0%; Score 69.6; DB 10; Length 969;  
 Best Local Similarity 50.3%; Pred. No. 0.0097;  
 RESULT 175  
 ID ABZ83278 standard; cDNA; 1024 BP.  
 DE Toxicologically relevant human nucleotide sequence #437.  
 PN WO2003016500-A2.  
 PD 27-FEB-2003.  
 PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.  
 Query Match 7.0%; Score 69.4; DB 10; Length 1024;  
 Best Local Similarity 50.4%; Pred. No. 0.01;  
 RESULT 176  
 ID ADE84973 standard; DNA; 1206 BP.  
 DE Farnesyl transferase inhibitor modulated leukemia associated gene #192.  
 PN WO2003038129-A2.  
 PD 08-MAY-2003.  
 PA (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.  
 Query Match 7.0%; Score 69.4; DB 10; Length 1206;  
 Best Local Similarity 50.4%; Pred. No. 0.01;  
 RESULT 177  
 ID ADQ85986 standard; cDNA; 1291 BP.  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #2858.  
 PN WO2004060270-A2.  
 PD 22-JUL-2004.  
 PA (GETH ) GENENTECH INC.  
 PA (WUTD/) WU T D.  
 PA (ZHOU/) ZHOU Y.  
 Query Match 7.0%; Score 69.4; DB 12; Length 1291;  
 Best Local Similarity 50.4%; Pred. No. 0.01;  
 RESULT 178  
 ID ACN44731 standard; cDNA; 1311 BP.  
 DE Human mRNA sequence hCT1955643.

PN WO2003073826-A2.  
 PD 12-SEP-2003.  
 PA (SAGR-) SAGRES DISCOVERY.  
 Query Match 7.0%; Score 69.4; DB 11; Length 1311;  
 Best Local Similarity 50.4%; Pred. No. 0.01;  
 RESULT 179  
 ID ABX63642 standard; cDNA; 1327 BP.  
 DE Human cDNA #642 differentially expressed in activated vascular tissue.  
 PN US2002137081-A1.  
 PD 26-SEP-2002.  
 PA (BAND/) BANDMAN O.  
 Query Match 7.0%; Score 69.4; DB 8; Length 1327;  
 Best Local Similarity 50.4%; Pred. No. 0.01;  
 RESULT 180  
 ID ADH02882 standard; cDNA; 841 BP.  
 DE Fuchsia FMT (3282) cDNA #SEQ ID 41.  
 PN WO2003062428-A1.  
 PD 31-JUL-2003.  
 PA (ITFL-) INT FLOWER DEV PTY LTD.  
 Query Match 7.0%; Score 69.2; DB 10; Length 841;  
 Best Local Similarity 49.5%; Pred. No. 0.011;  
 RESULT 181  
 ID ADH02884 standard; cDNA; 943 BP.  
 DE Fuchsia FMT full (3289) cDNA #SEQ ID 43.  
 PN WO2003062428-A1.  
 PD 31-JUL-2003.  
 PA (ITFL-) INT FLOWER DEV PTY LTD.  
 Query Match 7.0%; Score 69.2; DB 10; Length 943;  
 Best Local Similarity 49.5%; Pred. No. 0.011;  
 RESULT 182  
 ID AAC42096 standard; DNA; 1186 BP.  
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 34272.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Query Match 6.9%; Score 68.6; DB 3; Length 1186;  
 Best Local Similarity 46.7%; Pred. No. 0.014;  
 RESULT 183  
 ID ADR65555 standard; cDNA; 749 BP.  
 DE Cotton cDNA sequence, SEQ ID 6336.  
 PN US2004181830-A1.  
 PD 16-SEP-2004.  
 PA (KOVA/) KOVALIC D K.  
 PA (ZHOU/) ZHOU Y.  
 PA (CAOY/) CAO Y.  
 Query Match 6.9%; Score 68; DB 13; Length 749;  
 Best Local Similarity 49.5%; Pred. No. 0.018;  
 RESULT 184  
 ID ADH02852 standard; cDNA; 1006 BP.  
 DE Torenia TMT5.nt cDNA #SEQ ID 11.  
 PN WO2003062428-A1.  
 PD 31-JUL-2003.  
 PA (ITFL-) INT FLOWER DEV PTY LTD.  
 Query Match 6.8%; Score 67.4; DB 10; Length 1006;  
 Best Local Similarity 50.1%; Pred. No. 0.023;  
 RESULT 185  
 ID ABA90338 standard; cDNA; 1149 BP.  
 DE Human polynucleotide #13.  
 PN WO200181363-A1.  
 PD 01-NOV-2001.  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 Query Match 6.8%; Score 67; DB 6; Length 1149;  
 Best Local Similarity 51.5%; Pred. No. 0.026;  
 RESULT 186  
 ID AAV23874 standard; DNA; 1074 BP.  
 DE Plant OMT enzyme DNA sequence.  
 PN WO9811205-A2.  
 PD 19-MAR-1998.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Query Match 6.8%; Score 66.8; DB 2; Length 1074;  
 Best Local Similarity 49.3%; Pred. No. 0.028;  
 RESULT 187

ID AAZ06877 standard; cDNA; 1074 BP.  
 DE Fine O-methyl transferase (OMT) partial cDNA 3.  
 PN US952486-A.  
 PD 14-SEP-1999.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Query Match 6.8%; Score 66.8; DB 2; Length 1074;  
 Best Local Similarity 49.3%; Pred. No. 0.028;  
 RESULT 188  
 ID AAA67961 standard; DNA; 1074 BP.  
 DE Pinus radiata OMT nucleotide sequence SEQ ID NO:54.  
 PN WO200022099-A1.  
 PD 20-APR-2000.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Query Match 6.8%; Score 66.8; DB 3; Length 1074;  
 Best Local Similarity 49.3%; Pred. No. 0.028;  
 RESULT 189  
 ID ADD41711 standard; DNA; 1074 BP.  
 DE O-methyl transferase DNA #7.  
 PN US2003131373-A1.  
 PD 10-JUL-2003.  
 PA (BLOK/) BLOKSBERG L N.  
 PA (HAVU/) HAVUKKALA I.  
 Query Match 6.8%; Score 66.8; DB 10; Length 1074;  
 Best Local Similarity 49.3%; Pred. No. 0.028;  
 RESULT 190  
 ID AAV23875 standard; DNA; 1075 BP.  
 DE Plant OMT enzyme DNA sequence.  
 PN WO9811205-A2.  
 PD 19-MAR-1998.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Query Match 6.8%; Score 66.8; DB 2; Length 1075;  
 Best Local Similarity 49.3%; Pred. No. 0.028;  
 RESULT 191  
 ID AAZ06878 standard; cDNA; 1075 BP.  
 DE Fine O-methyl transferase (OMT) partial cDNA 4.  
 PN US952486-A.  
 PD 14-SEP-1999.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Query Match 6.8%; Score 66.8; DB 2; Length 1075;  
 Best Local Similarity 49.3%; Pred. No. 0.028;  
 RESULT 192  
 ID AAA67962 standard; DNA; 1075 BP.  
 DE Pinus radiata OMT nucleotide sequence SEQ ID NO:55.  
 PN WO200022099-A1.  
 PD 20-APR-2000.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 Query Match 6.8%; Score 66.8; DB 3; Length 1075;  
 Best Local Similarity 49.3%; Pred. No. 0.028;  
 RESULT 193  
 ID ADD41712 standard; DNA; 1075 BP.  
 DE O-methyl transferase DNA #8.  
 PN US2003131373-A1.  
 PD 10-JUL-2003.  
 PA (BLOK/) BLOKSBERG L N.  
 PA (HAVU/) HAVUKKALA I.  
 Query Match 6.8%; Score 66.8; DB 10; Length 1075;  
 Best Local Similarity 49.3%; Pred. No. 0.028;  
 RESULT 194  
 ID AAX53491 standard; DNA; 114955 BP.  
 DE Human adenosine A1 receptor antisense oligonucleotide fragment.  
 PN WO9913886-A1.  
 PD 25-MAR-1999.  
 PA (UYEC-) UNIV EAST CAROLINA.  
 Query Match 6.7%; Score 66.6; DB 2; Length 114955;  
 Best Local Similarity 33.8%; Pred. No. 0.027;  
 RESULT 195  
 ID AAD19545 standard; cDNA; 744 BP.  
 DE Medicago sativa caffeic acid 3-O-methyltransferase (COMT) cDNA.

PN WO200173090-A2.  
 PD 04-OCT-2001.  
 PA (ROBE-) ROBERTS NOBLE FOUND INC SAMMUEL.  
 Query Match 6.7%; Score 66.4; DB 4; Length 744;  
 Best Local Similarity 49.3%; Pred. No. 0.033;  
 RESULT 196  
 ID ADI30327 standard; cDNA; 744 BP.  
 DE Alfalfa harvest inducible cDNA sequence H12.  
 PN WO2004002216-A2.  
 PD 08-JAN-2004.  
 PA (UYGU-) UNIV GUELPH.  
 Query Match 6.7%; Score 66.4; DB 12; Length 744;  
 Best Local Similarity 49.3%; Pred. No. 0.033;  
 RESULT 197  
 ID ADI30333 standard; DNA; 1906 BP.  
 DE Alfalfa harvest inducible H12 gene genomic DNA sequence.  
 PN WO2004002216-A2.  
 PD 08-JAN-2004.  
 PA (UYGU-) UNIV GUELPH.  
 Query Match 6.7%; Score 66.4; DB 12; Length 1906;  
 Best Local Similarity 49.3%; Pred. No. 0.033;  
 RESULT 198  
 ID ABS63420 standard; cDNA; 912 BP.  
 DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Query Match 6.7%; Score 66.2; DB 6; Length 912;  
 Best Local Similarity 47.9%; Pred. No. 0.036;  
 RESULT 199  
 ID ABS54115 standard; DNA; 967 BP.  
 DE Tobacco caffeoyl CoA O-methyltransferase-9 (CCOAMT-9) cDNA.  
 PN US6441272-B1.  
 PD 27-AUG-2002.  
 PA (UYGE-) UNIV GEORGIA RES FOUND INC.  
 Query Match 6.6%; Score 64.8; DB 6; Length 967;  
 Best Local Similarity 49.0%; Pred. No. 0.061;  
 RESULT 200  
 ID ABO55289 standard; cDNA; 553 BP.  
 DE Human ovarian antigen HCOQX38 cDNA, SEQ ID NO:1169.  
 PN WO200200677-A1.  
 PD 03-JAN-2002.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 6.5%; Score 64.6; DB 6; Length 553;  
 Best Local Similarity 49.5%; Pred. No. 0.067;  
 RESULT 201  
 ID AAC11287 standard; cDNA; 143 BP.  
 DE Human secreted protein 5' EST, SEQ ID NO: 15362.  
 PN EP1033401-A2.  
 PD 06-SEP-2000.  
 PA (GEST ) GENSET.  
 Query Match 6.5%; Score 64.4; DB 3; Length 143;  
 Best Local Similarity 98.5%; Pred. No. 0.075;  
 RESULT 202  
 ID ABS63426 standard; cDNA; 600 BP.  
 DE DNA encoding wheat caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.  
 Query Match 6.5%; Score 64.2; DB 6; Length 600;  
 Best Local Similarity 53.4%; Pred. No. 0.078;  
 RESULT 203  
 ID ABS63411 standard; cDNA; 510 BP.  
 DE DNA encoding rice caffeoyl-CoA O-methyltransferase (CCOMT).  
 PN US2002081693-A1.  
 PD 27-JUN-2002.  
 PA (CAHO/) CAHOON R E.  
 PA (FADE/) FADER G M.  
 PA (RAFA/) RAFALSKI J A.

Query Match 6.4%; Score 63.6; DB 6; Length 510;  
Best Local Similarity 45.9%; Pred. No. 0.099;  
RESULT 204  
ID ADQ19501 standard; DNA; 135005 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2320.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 6.4%; Score 63; DB 12; Length 135005;  
Best Local Similarity 47.8%; Pred. No. 0.11;  
RESULT 205  
ID ABX09141 standard; DNA; 75216 BP.  
DE Mycobacterium tuberculosis H37Rv BAC clone BAC-Rv230.  
PN WO200274903-A2.  
PD 26-SEP-2002.  
PA (INSP) INST PASTEUR.  
Query Match 6.3%; Score 62.8; DB 6; Length 75216;  
Best Local Similarity 46.4%; Pred. No. 0.12;  
RESULT 206  
Query Match 6.3%; Score 62.8; DB 4; Length 110000;  
Best Local Similarity 46.4%; Pred. No. 0.12;  
RESULT 207  
Query Match 6.3%; Score 62.8; DB 4; Length 110000;  
Best Local Similarity 46.4%; Pred. No. 0.12;  
RESULT 208  
Query Match 6.3%; Score 62.4; DB 4; Length 110000;  
Best Local Similarity 49.7%; Pred. No. 0.13;  
RESULT 209  
Query Match 6.3%; Score 62.4; DB 4; Length 110000;  
Best Local Similarity 49.7%; Pred. No. 0.13;  
RESULT 210  
ID ABS54114 standard; DNA; 845 BP.  
DE Tobacco caffeoyl CoA O-methyltransferase-3 (CCOAMT-3) cDNA.  
PN US641272-B1.  
PD 27-AUG-2002.  
PA (UYGE-) UNIV GEORGIA RES FOUND INC.  
Query Match 6.2%; Score 61.6; DB 6; Length 845;  
Best Local Similarity 48.5%; Pred. No. 0.21;  
RESULT 211  
ID AAX53491 standard; DNA; 114955 BP.  
DE Human adenosine A1 receptor antisense oligonucleotide fragment.  
PN WO9913886-A1.  
PD 25-MAR-1999.  
PA (UYEC-) UNIV EAST CAROLINA.  
Query Match 6.2%; Score 61.2; DB 2; Length 114955;  
Best Local Similarity 31.2%; Pred. No. 0.21;  
RESULT 212  
ID AAQ61817 standard; DNA; 1578 BP.  
DE Open reading frame of pseudorabies virus.  
PN WO9408000-A1.  
PD 14-APR-1994.  
PA (ALKU) AKZO NV.  
Query Match 6.1%; Score 60.8; DB 2; Length 1578;  
Best Local Similarity 45.3%; Pred. No. 0.28;  
RESULT 213  
ID ABQ61846 standard; DNA; 349980 BP.  
DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1102.  
PN EP1227152-A1.  
PD 31-JUL-2002.  
PA (NEST) SOC PROD NESTLE SA.  
Query Match 6.1%; Score 60.4; DB 6; Length 349980;  
Best Local Similarity 49.0%; Pred. No. 0.28;  
RESULT 214  
ID ABZ14595 standard; DNA; 729 BP.  
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2400.  
PN WO200216655-A2.  
PD 28-FEB-2002.  
PA (SCRI) SCRIPPS RES INST.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 6.1%; Score 60; DB 6; Length 729;  
Best Local Similarity 48.5%; Pred. No. 0.39;  
RESULT 215  
ID AAC45004 standard; DNA; 917 BP.

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 44938.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 6.1%; Score 60; DB 3; Length 917;  
Best Local Similarity 48.5%; Pred. No. 0.39;  
RESULT 216  
ID ABS63422 standard; cDNA; 982 BP.  
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO) CAHOON R E.  
PA (FADE) FADER G M.  
PA (RAFA) RAFALSKI J A.  
Query Match 6.1%; Score 60; DB 6; Length 982;  
Best Local Similarity 48.7%; Pred. No. 0.39;  
RESULT 217  
ID ADH02867 standard; cDNA; 1079 BP.  
DE Petunia E33 (corrected) cDNA #SEQ ID 26.  
PN WO2003062428-A1.  
PD 31-JUL-2003.  
PA (ITFL-) INT FLOWER DEV PTY LTD.  
Query Match 6.1%; Score 60; DB 10; Length 1079;  
Best Local Similarity 48.7%; Pred. No. 0.39;  
RESULT 218  
ID ACA38007 standard; DNA; 1143 BP.  
DE Prokaryotic essential gene #19664.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 6.1%; Score 60; DB 8; Length 1143;  
Best Local Similarity 45.4%; Pred. No. 0.38;  
RESULT 219  
ID AAA68101 standard; DNA; 399 BP.  
DE E. grandis caffeoyl CoA methyl transferase DNA sequence SEQ ID NO:194.  
PN WO200022099-A1.  
PD 20-APR-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Query Match 6.0%; Score 59.6; DB 3; Length 399;  
Best Local Similarity 55.2%; Pred. No. 0.46;  
RESULT 220  
ID ADD41851 standard; DNA; 399 BP.  
DE Caffeoyl CoA methyl transferase DNA #2.  
PN US2003131373-A1.  
PD 10-JUL-2003.  
PA (BLOK) BLOKSBERG L N.  
PA (HAVU) HAVUKKALA I.  
Query Match 6.0%; Score 59.6; DB 10; Length 399;  
Best Local Similarity 55.2%; Pred. No. 0.46;  
RESULT 221  
ID ADI23934 standard; DNA; 7185 BP.  
DE Streptomyces refuineus 024A locus ORF7.  
PN US2003198981-A1.  
PD 23-OCT-2003.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 6.0%; Score 59.6; DB 10; Length 7185;  
Best Local Similarity 46.9%; Pred. No. 0.43;  
RESULT 222  
ID ADI23920 standard; DNA; 61944 BP.  
DE Streptomyces refuineus 024A locus (NRRL 3143).  
PN US2003198981-A1.  
PD 23-OCT-2003.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 6.0%; Score 59.6; DB 10; Length 61944;  
Best Local Similarity 46.9%; Pred. No. 0.4;  
RESULT 223  
ID ADQ22939 standard; DNA; 4667 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5759.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 6.0%; Score 59.2; DB 12; Length 4667;  
Best Local Similarity 44.6%; Pred. No. 0.5;

RESULT 224  
 ID ADQ22939 standard; DNA; 4667 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5759.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Query Match 6.0%; Score 59; DB 12; Length 4667;  
 Best Local Similarity 44.8%; Pred. No. 0.54;  
 RESULT 225  
 ID ABQ93881 standard; DNA; 10800 BP.  
 DE Human laminin alpha-5-like NOVIC DNA, SEQ ID NO:5.  
 PN WO200253742-A2.  
 PD 11-JUL-2002.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 6.0%; Score 59; DB 6; Length 10800;  
 Best Local Similarity 46.8%; Pred. No. 0.53;  
 RESULT 226  
 ID ADO10046 standard; cDNA; 10800 BP.  
 DE Novel human protein Novic cDNA.  
 PN US2004052806-A1.  
 PD 18-MAR-2004.  
 PA (KEKU/) KEKUDA R.  
 PA (ALSO/) ALSOBROOK J P.  
 PA (TCH/) TCHERNEV V T.  
 PA (LIUX/) LIU X.  
 PA (SPYT/) SPYTEK K A.  
 PA (PATT/) PATTURAJAN M.  
 PA (GROS/) GROSSE W M.  
 PA (LEPL/) LEPLY D M.  
 PA (BURG/) BURGESS C E.  
 PA (VERN/) VERNET C A M.  
 PA (LILL/) LI L.  
 PA (GORM/) GORMAN L.  
 PA (EDIN/) EDINGER S R.  
 PA (SCIO/) SCIORE P.  
 PA (ELLE/) ELLERMAN K.  
 PA (MALY/) MALYANKAR U M.  
 PA (STON/) STONE D J.  
 PA (ROTH/) ROTHENBERG M E.  
 PA (BOLD/) BOLDOG F L.  
 PA (GUOX/) GUO X.  
 PA (SHEN/) SHENOY S G.  
 PA (ANDE/) ANDERSON D W.  
 PA (PADI/) PADIGARU M.  
 PA (TAUP/) TAUPIER R J.  
 PA (MILL/) MILLER C E.  
 PA (EISE/) EISEN A.  
 Query Match 6.0%; Score 59; DB 12; Length 10800;  
 Best Local Similarity 46.8%; Pred. No. 0.53;  
 RESULT 227  
 ID ABQ93879 standard; DNA; 10809 BP.  
 DE Human laminin alpha-5-like NOVIA DNA, SEQ ID NO:1.  
 PN WO200253742-A2.  
 PD 11-JUL-2002.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 6.0%; Score 59; DB 6; Length 10809;  
 Best Local Similarity 46.8%; Pred. No. 0.53;  
 RESULT 228  
 ID ADO10042 standard; cDNA; 10809 BP.  
 DE Novel human protein Novia cDNA.  
 PN US2004052806-A1.  
 PD 18-MAR-2004.  
 PA (KEKU/) KEKUDA R.  
 PA (ALSO/) ALSOBROOK J P.  
 PA (TCH/) TCHERNEV V T.  
 PA (LIUX/) LIU X.  
 PA (SPYT/) SPYTEK K A.  
 PA (PATT/) PATTURAJAN M.  
 PA (GROS/) GROSSE W M.  
 PA (LEPL/) LEPLY D M.  
 PA (BURG/) BURGESS C E.  
 PA (VERN/) VERNET C A M.  
 PA (LILL/) LI L.

PA (GORM/) GORMAN L.  
 PA (EDIN/) EDINGER S R.  
 PA (SCIO/) SCIORE P.  
 PA (ELLE/) ELLERMAN K.  
 PA (MALY/) MALYANKAR U M.  
 PA (ROTH/) ROTHENBERG M E.  
 PA (STON/) STONE D J.  
 PA (BOLD/) BOLDOG F L.  
 PA (GUOX/) GUO X.  
 PA (SHEN/) SHENOY S G.  
 PA (ANDE/) ANDERSON D W.  
 PA (PADI/) PADIGARU M.  
 PA (TAUP/) TAUPIER R J.  
 PA (MILL/) MILLER C E.  
 PA (EISE/) EISEN A.  
 Query Match 6.0%; Score 59; DB 12; Length 10809;  
 Best Local Similarity 46.8%; Pred. No. 0.53;  
 RESULT 229  
 ID ADH02847 standard; cDNA; 1077 BP.  
 DE Petunia E33 cDNA #SEQ ID 5.  
 PN WO2003062428-A1.  
 PD 31-JUL-2003.  
 PA (ITEL-) INT FLOWER DEV PTY LTD.  
 Query Match 5.9%; Score 58.8; DB 10; Length 1077;  
 Best Local Similarity 48.5%; Pred. No. 0.61;  
 RESULT 230  
 ID AAF25795 standard; DNA; 3849 BP.  
 DE S. chrysomallus acm-C DNA.  
 PN DE19928313-A1.  
 PD 21-DEC-2000.  
 PA (KELL/) KELLER U.  
 Query Match 5.9%; Score 58.8; DB 4; Length 3849;  
 Best Local Similarity 45.9%; Pred. No. 0.59;  
 RESULT 231  
 ID AAD55726 standard; DNA; 5858 BP.  
 DE Nephila madagascariensis major ampullate spidroin 2 (MaSp2)-like DNA.  
 PN WO2003020916-A2.  
 PD 13-MAR-2003.  
 PA (UYWY-) UNIV WYOMING.  
 Query Match 5.9%; Score 58.8; DB 8; Length 5858;  
 Best Local Similarity 48.3%; Pred. No. 0.58;  
 RESULT 232  
 ID ADA71279 standard; DNA; 897 BP.  
 DE Rice gene, SEQ ID 4602.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Query Match 5.9%; Score 58; DB 8; Length 897;  
 Best Local Similarity 44.9%; Pred. No. 0.84;  
 RESULT 233  
 ID AAL40781 standard; DNA; 88421 BP.  
 DE 88421nt genomic DNA of ramoplanin producing Actinoplanes sp.  
 PN WO200231155-A2.  
 PD 18-APR-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 5.9%; Score 58; DB 6; Length 88421;  
 Best Local Similarity 44.5%; Pred. No. 0.74;  
 RESULT 234  
 ID ABN87109 standard; cDNA; 557 BP.  
 DE Lolium perenne LpCCoAMTA partial nucleotide sequence SEQ ID NO:3.  
 PN WO200226994-A1.  
 PD 04-APR-2002.  
 PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
 PA (AGRE-) AGRESEARCH LTD.  
 Query Match 5.8%; Score 57.8; DB 6; Length 557;  
 Best Local Similarity 49.7%; Pred. No. 0.91;  
 RESULT 235  
 ID ABZ22145 standard; DNA; 1029 BP.  
 DE Thermus thermophilus DNA repair enzyme RecF encoding DNA SEQ ID NO:5.  
 PN JP2002247985-A.  
 PD 03-SEP-2002.  
 PA (RIKA) RIKAGAKU KENKYUSHO.  
 Query Match 5.8%; Score 57.4; DB 8; Length 1029;



Best Local Similarity 48.6%; Pred. No. 1;  
RESULT 236  
ID ADO42841 standard; DNA; 1275 BP.  
DE Pseudomonas aurantiaca S-4380 levansucrase encoding sequence.  
PN KR2003005996-A.  
PD 23-JAN-2003.  
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.  
PA (REAL-) REAL BIOTECH CO LTD.  
Query Match 5.8%; Score 57.4; DB 11; Length 1275;  
Best Local Similarity 45.6%; Pred. No. 1;  
RESULT 237  
ID ADA48866 standard; DNA; 584 BP.  
DE Banana gene conferring disease resistance in plants.  
PN WO200300906-A2.  
PD 03-JAN-2003.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
Query Match 5.8%; Score 57.2; DB 9; Length 584;  
Best Local Similarity 60.1%; Pred. No. 1.1;  
RESULT 238  
ID ADS73531 standard; cDNA; 73882 BP.  
DE tcp gene cluster.  
Query Match 5.8%; Score 57.2; DB 13; Length 73882;  
Best Local Similarity 44.6%; Pred. No. 1;  
RESULT 239  
ID ADR01234 standard; DNA; 1113 BP.  
DE Farnesyl dibenzodiazepinone biosynthetic ORF12 protein SPKG DNA.  
PN WO2004065591-A1.  
PD 05-AUG-2004.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 5.8%; Score 57; DB 13; Length 1113;  
Best Local Similarity 43.2%; Pred. No. 1.2;  
RESULT 240  
ID ADR01210 standard; DNA; 36602 BP.  
DE Farnesyl dibenzodiazepinone biosynthetic locus Contig 1, SEQ ID 1.  
PN WO2004065591-A1.  
PD 05-AUG-2004.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 5.8%; Score 57; DB 13; Length 36602;  
Best Local Similarity 43.2%; Pred. No. 1.1;  
RESULT 241  
ID ADB74275 standard; DNA; 38494 BP.  
DE Mycobacterium leprae DNA #2.  
PN US6583266-B1.  
PD 24-JUN-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.8%; Score 57; DB 10; Length 38494;  
Best Local Similarity 50.9%; Pred. No. 1.1;  
RESULT 242  
ID ADB74386 standard; DNA; 38675 BP.  
DE Mycobacterium leprae DNA #20.  
PN US6583266-B1.  
PD 24-JUN-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.8%; Score 57; DB 10; Length 38675;  
Best Local Similarity 50.9%; Pred. No. 1.1;  
RESULT 243  
ID AAD14507 standard; DNA; 1182 BP.  
DE S. clavuligerus clavulanic acid biosynthesis enzyme DNA #3.  
PN US6232106-B1.  
PD 15-MAY-2001.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 5.7%; Score 56.8; DB 4; Length 1182;  
Best Local Similarity 43.6%; Pred. No. 1.3;  
RESULT 244  
ID ADD26448 standard; DNA; 1182 BP.  
DE Streptomyces clavuligerus ORF6 DNA.  
PN US6589775-B1.  
PD 08-JUL-2003.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 5.7%; Score 56.8; DB 10; Length 1182;  
Best Local Similarity 43.6%; Pred. No. 1.3;  
RESULT 245  
ID ADG47793 standard; DNA; 1182 BP.  
DE Streptomyces clavuligerus 15 kb gene ORF6 DNA.  
PN US2003207411-A1.  
PD 06-NOV-2003.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 5.7%; Score 56.8; DB 10; Length 1182;  
Best Local Similarity 43.6%; Pred. No. 1.3;  
RESULT 246  
ID ACA62930 standard; DNA; 1182 BP.  
DE DNA encoding clavulanic acid synthesis associated protein #6.  
PN US6514735-B1.  
PD 04-FEB-2003.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 5.7%; Score 56.8; DB 10; Length 1182;  
Best Local Similarity 43.6%; Pred. No. 1.3;  
RESULT 247  
ID ADA71938 standard; DNA; 2000 BP.  
DE Rice gene, SEQ ID 5263.  
PN WO200300898-A1.  
PD 03-JAN-2003.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
Query Match 5.7%; Score 56.8; DB 8; Length 2000;  
Best Local Similarity 10.5%; Pred. No. 1.3;  
RESULT 248  
ID AAD14501 standard; DNA; 11604 BP.  
DE Streptomyces clavuligerus genomic DNA fragment.  
PN US6232106-B1.  
PD 15-MAY-2001.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 5.7%; Score 56.8; DB 4; Length 11604;  
Best Local Similarity 43.6%; Pred. No. 1.2;  
RESULT 249  
ID ADD26442 standard; DNA; 11604 BP.  
DE Streptomyces clavuligerus 11.6 kb genomic fragment.  
PN US6589775-B1.  
PD 08-JUL-2003.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 5.7%; Score 56.8; DB 10; Length 11604;  
Best Local Similarity 43.6%; Pred. No. 1.2;  
RESULT 250  
ID ADG47787 standard; DNA; 11604 BP.  
DE Streptomyces clavuligerus 15 kb gene fragment DNA.  
PN US2003207411-A1.  
PD 06-NOV-2003.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 5.7%; Score 56.8; DB 10; Length 11604;  
Best Local Similarity 43.6%; Pred. No. 1.2;  
RESULT 251  
ID ACA62924 standard; DNA; 11604 BP.  
DE Clavulanic acid synthesis associated DNA.  
PN US6514735-B1.  
PD 04-FEB-2003.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 5.7%; Score 56.8; DB 10; Length 11604;  
Best Local Similarity 43.6%; Pred. No. 1.2;  
RESULT 252  
ID AAO91580 standard; DNA; 15079 BP.  
DE S. clavuligerus cla gene region.  
PN CA2108113-A.  
PD 09-APR-1995.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 5.7%; Score 56.8; DB 2; Length 15079;  
Best Local Similarity 43.6%; Pred. No. 1.2;  
RESULT 253  
ID AAD14499 standard; DNA; 15079 BP.  
DE Streptomyces clavuligerus 15 Kb genomic DNA fragment.  
PN US6232106-B1.  
PD 15-MAY-2001.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 5.7%; Score 56.8; DB 4; Length 15079;  
Best Local Similarity 43.6%; Pred. No. 1.2;  
RESULT 254  
ID ACA62922 standard; DNA; 15079 BP.  
DE Streptomyces clavuligerus 15kb genomic DNA sequence.

PN US6514735-B1.  
 PD 04-FEB-2003.  
 PA (UYAL-) UNIV ALBERTA.  
 Query Match 5.7%; Score 56.8; DB 10; Length 15079;  
 Best Local Similarity 43.6%; Pred. No. 1.2;  
 RESULT 255  
 ID ADD26455 standard; DNA; 15120 BP.  
 DE Streptomyces clavuligerus 15 kb genomic fragment.  
 PN US6589775-B1.  
 PD 08-JUL-2003.  
 PA (UYAL-) UNIV ALBERTA.  
 Query Match 5.7%; Score 56.8; DB 10; Length 15120;  
 Best Local Similarity 43.6%; Pred. No. 1.2;  
 RESULT 256  
 ID ADG47775 standard; DNA; 15120 BP.  
 DE Streptomyces clavuligerus 15 kb gene.  
 PN US2003207411-A1.  
 PD 06-NOV-2003.  
 PA (UYAL-) UNIV ALBERTA.  
 Query Match 5.7%; Score 56.8; DB 10; Length 15120;  
 Best Local Similarity 43.6%; Pred. No. 1.2;  
 RESULT 257  
 ID AAX83426 standard; DNA; 22976 BP.  
 DE Genomic region containing human lipolysis stimulated receptor gene.  
 PN WO9907737-A2.  
 PD 18-FEB-1999.  
 PA (GEST) GENSET.  
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.  
 Query Match 5.7%; Score 56.8; DB 2; Length 22976;  
 Best Local Similarity 45.8%; Pred. No. 1.2;  
 RESULT 258  
 ID AAD36874 standard; DNA; 29870 BP.  
 DE Streptomyces clavuligerus clavulanic acid biosynthesis gene cluster.  
 PN WO2003040372-A2.  
 PD 15-MAY-2003.  
 PA (SMIK) SMITHKLINE BEECHAM PLC.  
 PA (UYAL-) UNIV ALBERTA.  
 Query Match 5.7%; Score 56.8; DB 8; Length 29870;  
 Best Local Similarity 43.6%; Pred. No. 1.2;  
 RESULT 259  
 ID ABL67924 standard; DNA; 41936 BP.  
 DE Ovary cancer related gene sequence SEQ ID NO:6261.  
 PN WO200194629-A2.  
 PD 13-DEC-2001.  
 PA (AVAL-) AVALON PHARM.  
 Query Match 5.7%; Score 56.8; DB 6; Length 41936;  
 Best Local Similarity 45.6%; Pred. No. 1.2;  
 RESULT 260  
 ID ADA71360 standard; DNA; 2450 BP.  
 DE Rice gene, SEQ ID 4683.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Query Match 5.7%; Score 56.6; DB 8; Length 2450;  
 Best Local Similarity 43.1%; Pred. No. 1.4;  
 RESULT 261  
 ID ADJ11693 standard; DNA; 3414 BP.  
 DE Rice DNA modulated by post-transcriptional gene silencing SeqID 329.  
 PN US2003135888-A1.  
 PD 17-JUL-2003.  
 PA (ZHUT/) ZHU T.  
 PA (WANG/) WANG X.  
 PA (CHAN/) CHANG H.  
 PA (BRIG/) BRIGGS S P.  
 PA (COOP/) COOPER B.  
 PA (GLAZ/) GLAZEBROOK J.  
 PA (KATA/) KATAGIRI F.  
 PA (KREP/) KREPS J.  
 PA (MOUG/) MOUGHAMER T.  
 PA (PROV/) PROVART N.  
 PA (RICK/) RICKIE D.  
 Query Match 5.7%; Score 56.6; DB 11; Length 3414;

Best Local Similarity 43.1%; Pred. No. 1.4;  
 RESULT 262  
 ID RAD54235 standard; DNA; 25085 BP.  
 DE Streptomyces amphibiosporus lactimidomycin ORF5 DNA.  
 PN WO200286176-A2.  
 PD 07-NOV-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 5.7%; Score 56.6; DB 10; Length 25085;  
 Best Local Similarity 45.1%; Pred. No. 1.3;  
 RESULT 263  
 ID RAD54230 standard; DNA; 50543 BP.  
 DE Streptomyces amphibiosporus lactimidomycin DNA.  
 PN WO200286176-A2.  
 PD 07-NOV-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 5.7%; Score 56.6; DB 10; Length 50543;  
 Best Local Similarity 45.1%; Pred. No. 1.3;  
 RESULT 264  
 ID AAA09696 standard; DNA; 3957 BP.  
 DE HSV-2 immediate early protein ICP4 DNA sequence.  
 PN WO9516779-A1.  
 PD 22-JUN-1995.  
 PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.  
 Query Match 5.7%; Score 56.4; DB 5; Length 3957;  
 Best Local Similarity 49.8%; Pred. No. 1.5;  
 RESULT 265  
 ID ADG75121 standard; DNA; 3957 BP.  
 DE Human herpesvirus 2 ICP4 ORF DNA - SEQ ID 193.  
 PN WO2003086308-A2.  
 PD 23-OCT-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match 5.7%; Score 56.4; DB 10; Length 3957;  
 Best Local Similarity 49.8%; Pred. No. 1.5;  
 RESULT 266  
 ID ADI23932 standard; DNA; 15738 BP.  
 DE Streptomyces refuineus 024A locus ORF6.  
 PN US2003198981-A1.  
 PD 23-OCT-2003.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 5.7%; Score 56.4; DB 10; Length 15738;  
 Best Local Similarity 51.7%; Pred. No. 1.4;  
 RESULT 267  
 ID AAD25519 standard; DNA; 154746 BP.  
 DE Human herpesvirus 2 complete DNA genome.  
 PN WO200176643-A1.  
 PD 18-OCT-2001.  
 PA (BAYU) BAYLOR COLLEGE MEDICINE.  
 Query Match 5.7%; Score 56.4; DB 6; Length 154746;  
 Best Local Similarity 49.8%; Pred. No. 1.3;  
 RESULT 268  
 ID AAD25519 standard; DNA; 154746 BP.  
 DE Human herpesvirus 2 complete DNA genome.  
 PN WO200176643-A1.  
 PD 18-OCT-2001.  
 PA (BAYU) BAYLOR COLLEGE MEDICINE.  
 Query Match 5.7%; Score 56.4; DB 6; Length 154746;  
 Best Local Similarity 49.8%; Pred. No. 1.3;  
 RESULT 269  
 ID ABZ66780 standard; DNA; 1143 BP.  
 DE Orthosomycin biosynthetic polynucleotide SEQ ID NO 222;  
 PN WO200279505-A2.  
 PD 10-OCT-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 5.7%; Score 56.2; DB 10; Length 1143;  
 Best Local Similarity 45.6%; Pred. No. 1.7;  
 RESULT 270  
 ID AAQ98470 standard; cDNA; 2744 BP.  
 DE MiSP1-containing plasmid pMiss1.  
 PN WO9525165-A1.  
 PD 21-SEP-1995.  
 PA (UYWY-) UNIV WYOMING.  
 Query Match 5.7%; Score 56.2; DB 2; Length 2744;  
 Best Local Similarity 48.0%; Pred. No. 1.6;

```
RESULT 271
ID ABL50559 standard; DNA; 14186 BP.
DE Microspora carbonacea everminomicin locus nucleotide contig 5.
PN WO20015180-A2.
PD 02-AUG-2003.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
PA (FARN/) FARNET C.
Query Match
Best Local Similarity 5.7%; Score 56.2; DB 4; Length 14186;
Pred. No. 1.5;
RESULT 272
ID ABZ66811 standard; DNA; 48221 BP.
DE Orthosomycin biosynthetic gene cluster SEQ ID NO 280.
PN WO200279505-A2.
PD 10-OCT-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match
Best Local Similarity 5.7%; Score 56.2; DB 10; Length 48221;
Pred. No. 1.5;
RESULT 273
ID ACH44935 standard; cDNA; 494 BP.
DE Human foetal brain cDNA #5660.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LAGA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match
Best Local Similarity 5.7%; Score 56; DB 9; Length 494;
Pred. No. 1.8;
RESULT 274
ID ABD15803 standard; DNA; 1098 BP.
DE Pseudomonas aeruginosa polynucleotide #14407.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 49.7%; Score 56; DB 11; Length 1098;
Pred. No. 1.8;
RESULT 275
ID ACA42208 standard; DNA; 1473 BP.
DE Prokaryotic essential gene #23865.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 5.7%; Score 56; DB 8; Length 1473;
Pred. No. 1.8;
RESULT 276
ID ABD15660 standard; DNA; 1566 BP.
DE Pseudomonas aeruginosa polynucleotide #14264.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 49.7%; Score 56; DB 11; Length 1566;
Pred. No. 1.8;
RESULT 277
ID ABD15749 standard; DNA; 1908 BP.
DE Pseudomonas aeruginosa polynucleotide #14353.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 49.7%; Score 56; DB 11; Length 1908;
Pred. No. 1.8;
RESULT 278
ID AAZ07194 standard; cDNA; 2109 BP.
DE Human lung tumour protein SAL-50 5' cDNA sequence.
PN WO9338973-A2.
PD 05-AUG-1999.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 5.7%; Score 56; DB 2; Length 2109;
Pred. No. 1.8;
RESULT 279
ID AAC79147 standard; cDNA; 2109 BP.
DE Human lung tumour-specific cDNA #100.
PN WO200060077-A2.
PD 05-FEB-1998.
PD 12-OCT-2000.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 5.7%; Score 56; DB 3; Length 2109;
Pred. No. 1.8;
RESULT 280
ID AAD33222 standard; cDNA; 2109 BP.
DE Human lung tumour-specific protein SAL-50 cDNA.
PN WO200172295-A2.
PD 04-OCT-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 49.3%; Score 56; DB 4; Length 2109;
Pred. No. 1.8;
RESULT 281
ID ADD66461 standard; cDNA; 2109 BP.
DE Human lung tumour-specific related cDNA, SEQ ID NO 153.
PN WO200292001-A2.
PD 21-NOV-2002.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 49.3%; Score 56; DB 10; Length 2109;
Pred. No. 1.8;
RESULT 282
ID ADE87715 standard; cDNA; 2109 BP.
DE Human lung tumour antigen cDNA #100.
PN US2003118599-A1.
PD 26-JUN-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 49.3%; Score 56; DB 10; Length 2109;
Pred. No. 1.8;
RESULT 283
ID AAHI254 standard; cDNA; 2142 BP.
DE Human cDNA sequence SEQ ID NO:13376.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 5.7%; Score 56; DB 4; Length 2142;
Pred. No. 1.8;
RESULT 284
ID AAHI4344 standard; cDNA; 2198 BP.
DE Human cDNA sequence SEQ ID NO:11730.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 5.7%; Score 56; DB 4; Length 2198;
Pred. No. 1.8;
RESULT 285
ID AAX61221 standard; DNA; 2392 BP.
DE Mouse DNA demethylase, dMTase2, coding sequence.
PN WO9324583-A1.
PD 20-MAY-1999.
PA (UYMC-) UNIV MCGILL.
Query Match
Best Local Similarity 5.7%; Score 56; DB 2; Length 2392;
Pred. No. 1.8;
RESULT 286
ID ADD14651 standard; cDNA; 2392 BP.
DE Human src biomarker polynucleotide SEQ ID NO:45.
PN WO2003062395-A2.
PD 31-JUL-2003.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match
Best Local Similarity 5.7%; Score 56; DB 10; Length 2392;
Pred. No. 1.8;
RESULT 287
ID AAV68520 standard; DNA; 4257 BP.
DE The nucleotide sequence of the Herpes simplex virus ICP4.
PN WO9846637-A2.
PD 22-OCT-1998.
PA (ARCH-) ARCH DEV CORP.
Query Match
Best Local Similarity 45.6%; Score 56; DB 2; Length 4257;
Pred. No. 1.7;
RESULT 288
ID AAV10362 standard; cDNA; 4257 BP.
DE Infected cell protein number 4 alpha-4 gene.
PN WO9804709-A2.
PD 05-FEB-1998.
```

PA (ARCH-) ARCH DEV CORP.  
Query Match 5.7%; Score 56; DB 2; Length 4257;  
Best Local Similarity 45.6%; Pred. No. 1.7;  
RESULT 289  
ID ADC59464 standard; DNA; 4943 BP.  
DE DNA sequence encoding novel human tyrosine kinase protein.  
PN JP2003024075-A.  
PD 28-JAN-2003.  
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.  
Query Match 5.7%; Score 56; DB 10; Length 4943;  
Best Local Similarity 49.3%; Pred. No. 1.7;  
RESULT 290  
ID ADO83709 standard; cDNA; 4943 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #523.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Query Match 5.7%; Score 56; DB 12; Length 4943;  
Best Local Similarity 49.3%; Pred. No. 1.7;  
RESULT 291  
ID AAD34321 standard; cDNA; 4988 BP.  
DE Human PKIN-24 cDNA.  
PN WO200218557-A2.  
PD 07-MAR-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 5.7%; Score 56; DB 6; Length 4988;  
Best Local Similarity 49.3%; Pred. No. 1.7;  
RESULT 292  
ID AAG76213 standard; DNA; 12001 BP.  
DE HSV L/ST region.  
PN WO9428156-A1.  
PD 08-DEC-1994.  
PA (DAND) DANA FARBER CANCER INST INC.  
Query Match 5.7%; Score 56; DB 2; Length 12001;  
Best Local Similarity 45.6%; Pred. No. 1.7;  
RESULT 293  
ID AAL02789 standard; DNA; 13862 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 5477.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 5.7%; Score 56; DB 4; Length 13862;  
Best Local Similarity 49.3%; Pred. No. 1.7;  
RESULT 294  
ID AAL07516 standard; DNA; 13862 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 10204.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 5.7%; Score 56; DB 4; Length 13862;  
Best Local Similarity 49.3%; Pred. No. 1.7;  
RESULT 295  
ID ABA08208 standard; DNA; 13862 BP.  
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 1003.  
PN WO200155325-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 5.7%; Score 56; DB 4; Length 13862;  
Best Local Similarity 49.3%; Pred. No. 1.7;  
RESULT 296  
ID ABL64982 standard; DNA; 43058 BP.  
DE Lung cancer related gene sequence SEQ ID NO:3319.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Query Match 5.7%; Score 56; DB 6; Length 43058;  
Best Local Similarity 45.5%; Pred. No. 1.6;  
RESULT 297  
ID ABL65219 standard; DNA; 43058 BP.  
DE Lung cancer related gene sequence SEQ ID NO:3556.  
PN WO200194629-A2.

PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Query Match 5.7%; Score 56; DB 6; Length 43058;  
Best Local Similarity 45.5%; Pred. No. 1.6;  
RESULT 298  
ID ABL97455 standard; DNA; 43058 BP.  
DE Gene #3953 used to diagnose liver cancer.  
PN WO200229103-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 5.7%; Score 56; DB 6; Length 43058;  
Best Local Similarity 45.5%; Pred. No. 1.6;  
RESULT 299  
ID ADH02862 standard; cDNA; 780 BP.  
DE Fuchsia FMT cDNA #SEQ ID 21.  
PN WO2003062428-A1.  
PD 31-JUL-2003.  
PA (ITFL-) INT. FLOWER DEV PTY LTD.  
Query Match 5.6%; Score 55.8; DB 10; Length 780;  
Best Local Similarity 49.1%; Pred. No. 2;  
RESULT 300  
ID ADA70053 standard; DNA; 1152 BP.  
DE Rice gene, SEQ ID 3376.  
PN WO2003000898-A1.  
PD 03-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 5.6%; Score 55.8; DB 8; Length 1152;  
Best Local Similarity 45.5%; Pred. No. 1.9;  
RESULT 301  
ID ADJ11565 standard; DNA; 1152 BP.  
DE Rice DNA modulated by post-transcriptional gene silencing SeqID 201.  
PN US2003135888-A1.  
PD 17-JUL-2003.  
PA (ZHUT/) ZHU T.  
PA (WANG/) WANG X.  
PA (CHAN/) CHANG H.  
PA (BRIG/) BRIGGS S P.  
PA (COOP/) COOPER B.  
PA (GLAZ/) GLAZEBROOK J.  
PA (GOFF/) GOFF S A.  
PA (KATA/) KATAGIRI F.  
PA (KREP/) KREPS J.  
PA (MOUG/) MOUGHAMER T.  
PA (PROV/) PROVART N.  
PA (RICK/) RIQUE D.  
Query Match 5.6%; Score 55.8; DB 11; Length 1152;  
Best Local Similarity 45.5%; Pred. No. 1.9;  
RESULT 302  
ID AAA50254 standard; DNA; 1926 BP.  
DE Epstein Barr virus nuclear antigen 1 protein (EBNA1) DNA.  
PN WO200047778-A1.  
PD 17-AUG-2000.  
PA (PHAR-) PHARMACOPEDIA INC.  
Query Match 5.6%; Score 55.8; DB 3; Length 1926;  
Best Local Similarity 46.7%; Pred. No. 1.9;  
RESULT 303  
ID AAF82902 standard; DNA; 1926 BP.  
DE EBV tethering protein EBNA1 encoding DNA.  
PN WO200125484-A2.  
PD 12-APR-2001.  
PA (UNMI) UNIV MICHIGAN.  
Query Match 5.6%; Score 55.8; DB 4; Length 1926;  
Best Local Similarity 46.7%; Pred. No. 1.9;  
RESULT 304  
ID ADK65580 standard; DNA; 1926 BP.  
DE Human herpesvirus 4 nuclear antigen-1 coding sequence.  
PN DE10207135-A1.  
PD 11-SEP-2003.  
PA (EURO-) EUROIMMUN GMBH.  
Query Match 5.6%; Score 55.8; DB 10; Length 1926;  
Best Local Similarity 46.7%; Pred. No. 1.9;  
RESULT 305  
ID AAA75454 standard; DNA; 2580 BP.

DE Nucleotide sequence of the Epstein Barr nuclear antigen.  
 PN US6114111-A.  
 PD 05-SEP-2000.  
 PA (RIGE-) RIGEL PHARM INC.  
 Query Match 5.6%; Score 55.8; DB 3; Length 2580;  
 Best Local Similarity 46.7%; Pred. No. 1.9;  
 RESULT 306  
 ID AAI64275 standard; DNA; 2580 BP.  
 DE Epstein-Barr virus nuclear antigen coding sequence.  
 PN US6316223-B1.  
 PD 13-NOV-2001.  
 PA (RIGE-) RIGEL PHARM INC.  
 Query Match 5.6%; Score 55.8; DB 6; Length 2580;  
 Best Local Similarity 46.7%; Pred. No. 1.9;  
 RESULT 307  
 ID AAX90923 standard; DNA; 5452 BP.  
 DE Anti-sense strand of pCMVEBNA plasmid.  
 PN WO9947647-A1.  
 PD 23-SEP-1999.  
 PA (PHAR-) PHARMACOEPIA INC.  
 Query Match 5.6%; Score 55.8; DB 2; Length 5452;  
 Best Local Similarity 46.7%; Pred. No. 1.8;  
 RESULT 308  
 ID AAZ33778 standard; DNA; 8705 BP.  
 DE Vector pShuttle DNA.  
 PN WO9950457-A1.  
 PD 07-OCT-1999.  
 PA (UTAH) UNIV UTAH RES FOUND.  
 Query Match 5.6%; Score 55.8; DB 2; Length 8705;  
 Best Local Similarity 46.7%; Pred. No. 1.8;  
 RESULT 309  
 ID ADM10659 standard; DNA; 8705 BP.  
 DE Expression vector pShuttle.  
 PN US2004077082-A1.  
 PD 22-APR-2004.  
 PA (KOEH/) KOEHN R K.  
 PA (RUFF/) RUFFNER D E.  
 PA (PRAK/) PRAKASH R K.  
 Query Match 5.6%; Score 55.8; DB 12; Length 8705;  
 Best Local Similarity 46.7%; Pred. No. 1.8;  
 RESULT 310  
 ID ADP64415 standard; DNA; 9482 BP.  
 DE Vector pCEPpu nucleotide sequence SEQ ID NO:1.  
 PN WO2004053137-A2.  
 PD 24-JUN-2004.  
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 Query Match 5.6%; Score 55.8; DB 12; Length 9482;  
 Best Local Similarity 46.7%; Pred. No. 1.8;  
 RESULT 311  
 ID AAZ22301 standard; cDNA; 9551 BP.  
 DE cDNA encoding a human trichohyalin (TRHY) protein.  
 PN US958752-A.  
 PD 28-SEP-1999.  
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 Query Match 5.6%; Score 55.8; DB 2; Length 9551;  
 Best Local Similarity 49.9%; Pred. No. 1.8;  
 RESULT 312  
 ID AAV21683 standard; DNA; 9600 BP.  
 DE Vector plasmid pCMVKnitr-EPI.  
 PN WO9806437-A2.  
 PD 19-FEB-1998.  
 PA (CHIR) CHIRON CORP.  
 Query Match 5.6%; Score 55.8; DB 2; Length 9600;  
 Best Local Similarity 46.7%; Pred. No. 1.8;  
 RESULT 313  
 ID ABS71027 standard; DNA; 10285 BP.  
 DE pCEP-Xa-Fc construct DNA sequence.  
 PN WO200256905-A2.  
 PD 25-JUL-2002.  
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 Query Match 5.6%; Score 55.8; DB 6; Length 10285;  
 Best Local Similarity 46.7%; Pred. No. 1.8;  
 RESULT 314  
 DE Plasmid pcisEBON for expression of hepatocyte growth factor.  
 ID AAT40348 standard; DNA; 10596 BP.  
 DE Plasmid pcisEBON for expression of hepatocyte growth factor.  
 ID ABS66453 standard; DNA; 10285 BP.  
 DE Plasmid pCEP-Xa-Fc\* expressing human IgG/protease cleavage site.  
 PN WO200256907-A2.  
 PD 25-JUL-2002.  
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 PA (MAUR/) MAURER P.  
 PA (LECH/) LECHNER F.  
 PA (ORTM/) ORTMANN R.  
 PA (LUEO/) LUSOEND R.  
 PA (STAU/) STAUFENBIEL M.  
 PA (FREY/) FREY P.  
 Query Match 5.6%; Score 55.8; DB 6; Length 10285;  
 Best Local Similarity 46.7%; Pred. No. 1.8;  
 RESULT 315  
 ID ADL67154 standard; DNA; 10330 BP.  
 DE Plasmid pCEP-mB7-H6(ECD)-comp-FL-C nucleotide sequence SEQ ID NO:24.  
 PN WO2004022594-A2.  
 PD 18-MAR-2004.  
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 Query Match 5.6%; Score 55.8; DB 12; Length 10330;  
 Best Local Similarity 46.7%; Pred. No. 1.8;  
 RESULT 316  
 ID AAZ22248 standard; DNA; 10380 BP.  
 DE Nucleotide sequence of pCEP4 vector.  
 PN WO9947921-A1.  
 PD 23-SEP-1999.  
 PA (PHAR-) PHARMACOEPIA INC.  
 Query Match 5.6%; Score 55.8; DB 2; Length 10380;  
 Best Local Similarity 46.7%; Pred. No. 1.8;  
 RESULT 317  
 ID ADL67152 standard; DNA; 10477 BP.  
 DE Plasmid pCEP-mB7-H5(ECD)-comp-FL-C nucleotide sequence SEQ ID NO:22.  
 PN WO2004022594-A2.  
 PD 18-MAR-2004.  
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 Query Match 5.6%; Score 55.8; DB 12; Length 10477;  
 Best Local Similarity 46.7%; Pred. No. 1.8;  
 RESULT 318  
 ID ADL67150 standard; DNA; 10516 BP.  
 DE Plasmid pCEP-hsB7-H5(ECD)-comp-FL-C nucleotide sequence SEQ ID NO:20.  
 PN WO2004022594-A2.  
 PD 18-MAR-2004.  
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 Query Match 5.6%; Score 55.8; DB 12; Length 10516;  
 Best Local Similarity 46.7%; Pred. No. 1.8;  
 RESULT 319  
 ID ADL67148 standard; DNA; 10561 BP.  
 DE Plasmid pCEP-hsB7-H4(ECD)-comp-FL-C nucleotide sequence SEQ ID NO:18.  
 PN WO2004022594-A2.  
 PD 18-MAR-2004.  
 PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
 Query Match 5.6%; Score 55.8; DB 12; Length 10561;  
 Best Local Similarity 46.7%; Pred. No. 1.8;  
 RESULT 320  
 ID AAQ51731 standard; DNA; 10596 BP.  
 DE Plasmid pcisEBON for subcloning huHGF variants.  
 PN WO9323541-A1.  
 PD 25-NOV-1993.  
 PA (GETH) GENENTECH INC.  
 Query Match 5.6%; Score 55.8; DB 2; Length 10596;  
 Best Local Similarity 46.7%; Pred. No. 1.8;  
 RESULT 321  
 ID AAX15650 standard; DNA; 10596 BP.  
 DE Nucleotide sequence of plasmid pcis.EBON.  
 PN US5879910-A.  
 PD 09-MAR-1999.  
 PA (GETH) GENENTECH INC.  
 Query Match 5.6%; Score 55.8; DB 2; Length 10596;  
 Best Local Similarity 46.7%; Pred. No. 1.8;  
 RESULT 322  
 ID AAT40348 standard; DNA; 10596 BP.  
 DE Plasmid pcisEBON for expression of hepatocyte growth factor.

PN US5547856-A.  
PD 20-AUG-1996.  
PA (GETH ) GENENTECH INC.  
Query Match 5.6%; Score 55.8; DB 2; Length 10596;  
Best Local Similarity 46.7%; Pred. No. 1.8;  
RESULT 323  
ID ADL67175 standard; DNA; 10615 BP.  
DE Plasmid pCEP-hbB7-H6-COMP-FLAG nucleotide sequence SEQ ID NO:45.  
PN WO2004022594-A2.  
PD 18-MAR-2004.  
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
Query Match 5.6%; Score 55.8; DB 12; Length 10615;  
Best Local Similarity 46.7%; Pred. No. 1.8;  
RESULT 324  
ID ADL67153 standard; DNA; 10774 BP.  
DE Plasmid pCEP-mB7-H6(ECD)-FC nucleotide sequence SEQ ID NO:23.  
PN WO2004022594-A2.  
PD 18-MAR-2004.  
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
Query Match 5.6%; Score 55.8; DB 12; Length 10774;  
Best Local Similarity 46.7%; Pred. No. 1.8;  
RESULT 325  
ID ADL67151 standard; DNA; 10921 BP.  
DE Plasmid pCEP-mB7-H5(ECD)-FC nucleotide sequence SEQ ID NO:21.  
PN WO2004022594-A2.  
PD 18-MAR-2004.  
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
Query Match 5.6%; Score 55.8; DB 12; Length 10921;  
Best Local Similarity 46.7%; Pred. No. 1.8;  
RESULT 326  
ID ADL67149 standard; DNA; 10961 BP.  
DE Plasmid pCEP-hbB7-H5(ECD)-FC nucleotide sequence SEQ ID NO:19.  
PN WO2004022594-A2.  
PD 18-MAR-2004.  
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
Query Match 5.6%; Score 55.8; DB 12; Length 10961;  
Best Local Similarity 46.7%; Pred. No. 1.8;  
RESULT 327  
ID ADL67147 standard; DNA; 11006 BP.  
DE Plasmid pCEP-hbB7-H4(ECD)-FC nucleotide sequence SEQ ID NO:17.  
PN WO2004022594-A2.  
PD 18-MAR-2004.  
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
Query Match 5.6%; Score 55.8; DB 12; Length 11006;  
Best Local Similarity 46.7%; Pred. No. 1.8;  
RESULT 328  
ID ADL67176 standard; DNA; 11059 BP.  
DE Plasmid pCEP-hbB7-H6-Xal-FC\* nucleotide sequence SEQ ID NO:46.  
PN WO2004022594-A2.  
PD 18-MAR-2004.  
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
Query Match 5.6%; Score 55.8; DB 12; Length 11059;  
Best Local Similarity 46.7%; Pred. No. 1.8;  
RESULT 329  
ID ADL2379 standard; DNA; 11693 BP.  
DE Vector pCMR2.  
PN WO2004065561-A2.  
PD 05-AUG-2004.  
PA (PTCT-) PTC THERAPEUTICS INC.  
Query Match 5.8%; Score 55.8; DB 13; Length 11693;  
Best Local Similarity 46.7%; Pred. No. 1.8;  
RESULT 330  
ID ADO07395 standard; DNA; 11924 BP.  
DE Modified human hepsin plasmid pCEP4W/hep36.  
PN WO2004033630-A2.  
PD 22-APR-2004.  
PA (SCHD ) SCHERING AG.  
Query Match 5.6%; Score 55.8; DB 12; Length 11924;  
Best Local Similarity 46.7%; Pred. No. 1.8;  
RESULT 331  
ID ADO07394 standard; DNA; 12242 BP.  
DE Modified human hepsin plasmid pCEP4W/hepEK.  
PN WO2004033630-A2.

PD 22-APR-2004.  
PA (SCHD ) SCHERING AG.  
Query Match 5.6%; Score 55.8; DB 12; Length 12242;  
Best Local Similarity 46.7%; Pred. No. 1.8;  
RESULT 332  
ID AAA59553 standard; DNA; 16080 BP.  
DE DNA clone pCEK Cl.27 encoding a human beta-secretase enzyme.  
PN WO200047618-A2.  
PD 17-AUG-2000.  
PA (ELAN-) ELAN PHARM INC.  
Query Match 5.6%; Score 55.8; DB 3; Length 16080;  
Best Local Similarity 46.7%; Pred. No. 1.8;  
RESULT 333  
ID ADL71910 standard; cDNA; 17753 BP.  
DE Expression vector pCytTs-OPE.  
PN WO2004018506-A2.  
PD 04-MAR-2004.  
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.  
Query Match 5.6%; Score 55.8; DB 12; Length 17753;  
Best Local Similarity 46.7%; Pred. No. 1.8;  
RESULT 334  
ID ADN12161 standard; DNA; 172281 BP.  
DE Epstein-Barr virus genome B95-8.  
PN WO2004027036-A2.  
PD 01-APR-2004.  
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
Query Match 5.6%; Score 55.8; DB 12; Length 172281;  
Best Local Similarity 46.7%; Pred. No. 1.7;  
RESULT 335  
ID AAH03407 standard; cDNA; 726 BP.  
DE Human cDNA clone (5'-primer) SEQ ID NO:242.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 5.6%; Score 55.6; DB 4; Length 726;  
Best Local Similarity 53.5%; Pred. No. 2.1;  
RESULT 336  
ID AAL61200 standard; DNA; 1026 BP.  
DE Actinosynnema pretiosum glucose 1-dehydrogenase gene.  
PN WO2003045312-A2.  
PD 05-JUN-2003.  
PA (UNIW ) UNIV WASHINGTON.  
Query Match 5.6%; Score 55.6; DB 8; Length 1026;  
Best Local Similarity 46.2%; Pred. No. 2.1;  
RESULT 337  
ID ABD11061 standard; DNA; 774 BP.  
DE Pseudomonas aeruginosa polynucleotide #9665.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.6%; Score 55.4; DB 11; Length 774;  
Best Local Similarity 45.2%; Pred. No. 2.3;  
RESULT 338  
ID ABX56066 standard; DNA; 3033 BP.  
DE M. echinospora calicheamicin biosynthesis gene orfVI.  
PN WO200279465-A2.  
PD 10-OCT-2002.  
PA (SLOK ) SLOAN KETTERING INST CANCER RES.  
Query Match 5.6%; Score 55.4; DB 8; Length 3033;  
Best Local Similarity 44.4%; Pred. No. 2.2;  
RESULT 339  
ID AAQ46806 standard; DNA; 29879 BP.  
DE eryA region of S. erythraea chromosome.  
PN WO9313663-A1.  
PD 22-JUL-1993.  
PA (ABBO ) ABBOTT LAB.  
Query Match 5.6%; Score 55.4; DB 2; Length 29879;  
Best Local Similarity 49.3%; Pred. No. 2.1;  
RESULT 340  
ID ADM45913 standard; DNA; 84428 BP.  
DE Streptomyces mycarofaciens midcamycin polyketide synthetase DNA.  
PN JP2004049100-A.  
PD 19-FEB-2004.

PA (MEIJ ) MEIJI SEIKA KAISHA LTD.  
Query Match 5.6%; Score 55.4; DB 12; Length 84428;  
Best Local Similarity 48.3%; Pred. No. 2;  
RESULT 341  
ID ABZ78139 standard; cDNA; 1679 BP.  
DE Human cancer-related coding sequence, 187P3F2.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 5.6%; Score 55.2; DB 8; Length 1679;  
Best Local Similarity 46.9%; Pred. No. 2.4;  
RESULT 342  
ID ACC00700 standard; cDNA; 1885 BP.  
DE Orzva sativa oil trait related cDNA sequence SEQ ID NO:149.  
PN WO2003002751-A2.  
PD 09-JAN-2003.  
PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
PA (PION-) PIONEER HI-BRED INT INC.  
Query Match 5.6%; Score 55.2; DB 8; Length 1885;  
Best Local Similarity 47.8%; Pred. No. 2.4;  
RESULT 343  
ID ACA38134 standard; DNA; 1887 BP.  
DE Prokaryotic essential gene #19791.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.6%; Score 55.2; DB 8; Length 1887;  
Best Local Similarity 45.0%; Pred. No. 2.4;  
RESULT 344  
ID AAA63350 standard; DNA; 21185 BP.  
DE Streptomyces globisporus C-1027 gene cluster ORF 25-42.  
PN WO200040596-A1.  
PD 13-JUL-2000.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 5.6%; Score 55.2; DB 3; Length 21185;  
Best Local Similarity 50.3%; Pred. No. 2.2;  
RESULT 345  
ID AAA63348 standard; DNA; 63164 BP.  
DE Streptomyces globisporus C-1027 gene cluster.  
PN WO200040596-A1.  
PD 13-JUL-2000.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 5.6%; Score 55.2; DB 3; Length 63164;  
Best Local Similarity 50.3%; Pred. No. 2.2;  
RESULT 346  
ID ADK13938 standard; DNA; 2559 BP.  
DE Human methyl-CpG-binding protein DNA #11.  
PN US6709817-B1.  
PD 23-MAR-2004.  
PA (BAVU ) BAYLOR COLLEGE MEDICINE.  
Query Match 5.6%; Score 55; DB 12; Length 2559;  
Best Local Similarity 53.5%; Pred. No. 2.6;  
RESULT 347  
ID ADQ19517 standard; DNA; 2559 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2336.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 5.6%; Score 55; DB 12; Length 2559;  
Best Local Similarity 53.5%; Pred. No. 2.6;  
RESULT 348  
ID ADQ84224 standard; cDNA; 2559 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1038.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH ) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Query Match 5.6%; Score 55; DB 12; Length 2559;  
Best Local Similarity 53.5%; Pred. No. 2.6;  
RESULT 349  
ID ADQ83456 standard; cDNA; 2559 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #270.

PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH ) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Query Match 5.6%; Score 55; DB 12; Length 2559;  
Best Local Similarity 53.5%; Pred. No. 2.6;  
RESULT 350  
ID ADQ86702 standard; cDNA; 2559 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3577.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH ) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Query Match 5.6%; Score 55; DB 12; Length 2559;  
Best Local Similarity 53.5%; Pred. No. 2.6;  
RESULT 351  
ID ADQ84685 standard; cDNA; 2559 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1499.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH ) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Query Match 5.6%; Score 55; DB 13; Length 2559;  
Best Local Similarity 53.5%; Pred. No. 2.6;  
RESULT 352  
ID ADQ85601 standard; cDNA; 2559 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #2415.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH ) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Query Match 5.6%; Score 55; DB 13; Length 2559;  
Best Local Similarity 53.5%; Pred. No. 2.6;  
RESULT 353  
ID ACN40385 standard; cDNA; 2559 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA326502, SEQ ID NO:5131.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 5.6%; Score 55; DB 13; Length 2559;  
Best Local Similarity 53.5%; Pred. No. 2.6;  
RESULT 354  
ID ADM80034 standard; DNA; 30943 BP.  
DE Spiramycin biosynthesis related DNA, SEQ ID 1.  
PN FR2845394-A1.  
PD 09-APR-2004.  
PA (AVET ) AVENTIS PHARMA SA.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 5.6%; Score 55; DB 12; Length 30943;  
Best Local Similarity 44.9%; Pred. No. 2.4;  
RESULT 355  
ID ADN97550 standard; DNA; 30943 BP.  
DE S anobofaciens spiramycin biosynthetic enzyme genomic region.  
PN WO2004033689-A2.  
PD 22-APR-2004.  
PA (AVET ) AVENTIS PHARMA SA.  
PA (CNRS ) CNRS.  
Query Match 5.6%; Score 55; DB 12; Length 30943;  
Best Local Similarity 44.9%; Pred. No. 2.4;  
RESULT 356  
ID AAV21187 standard; DNA; 53789 BP.  
DE Amycolatopsis mediterranei rifamycin synthesis gene cluster fragment.  
PN WO9807868-A1.  
PD 26-FEB-1998.  
PA (NOVS ) NOVARTIS AG.  
Query Match 5.6%; Score 55; DB 2; Length 53789;  
Best Local Similarity 47.9%; Pred. No. 2.4;  
RESULT 357  
ID AAA68012 standard; DNA; 594 BP.



```
DE Eucalyptus grandis OMT nucleotide sequence SEQ ID NO:105.
PN WO200022099-A1.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Query Match 5.5%; Score 54.8; DB 3; Length 594;
Best Local Similarity 57.6%; Pred. No. 2.9;
RESULT 358
ID ADD41762 standard; DNA; 594 BP.
DE O-methyl transferase DNA #11.
PN US2003131373-A1.
PD 10-JUL-2003.
PA (BLOK-) BLOKSBERG L N.
PA (HAVU/) HAVUKKALA I.
Query Match 5.5%; Score 54.8; DB 10; Length 594;
Best Local Similarity 57.6%; Pred. No. 2.9;
RESULT 359
ID AAV23843 standard; DNA; 607 BP.
DE Plant OMT enzyme DNA sequence.
PN WO9811205-A2.
PD 19-MAR-1998.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Query Match 5.5%; Score 54.8; DB 2; Length 607;
Best Local Similarity 57.6%; Pred. No. 2.9;
RESULT 360
ID AAZ06844 standard; cDNA; 607 BP.
DE Eucalyptus O-methyl transferase (OMT) partial cDNA 2.
PN US952486-A.
PD 14-SEP-1999.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Query Match 5.5%; Score 54.8; DB 2; Length 607;
Best Local Similarity 57.6%; Pred. No. 2.9;
RESULT 361
ID AAA69594 standard; cDNA; 607 BP.
DE Eucalyptus grandis O-methyltransferase cDNA SEQ ID NO:68.
PN WO200036081-A2.
PD 22-JUN-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Query Match 5.5%; Score 54.8; DB 3; Length 607;
Best Local Similarity 57.9%; Pred. No. 2.9;
RESULT 362
ID AAA67930 standard; DNA; 607 BP.
DE Eucalyptus grandis OMT nucleotide sequence SEQ ID NO:23.
PN WO200022099-A1.
PD 20-APR-2000.
PA (GENE-) GENESIS RES & DEV CORP LTD.
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
Query Match 5.5%; Score 54.8; DB 3; Length 607;
Best Local Similarity 57.6%; Pred. No. 2.9;
RESULT 363
ID ADD41680 standard; DNA; 607 BP.
DE O-methyl transferase DNA #3.
PN US2003131373-A1.
PD 10-JUL-2003.
PA (BLOK-) BLOKSBERG L N.
PA (HAVU/) HAVUKKALA I.
Query Match 5.5%; Score 54.8; DB 10; Length 607;
Best Local Similarity 57.8%; Pred. No. 2.9;
RESULT 364
ID ABZ77318 standard; cDNA; 2684 BP.
DE Nucleotide sequence of a murine ACDK3 polypeptide.
PN WO2003008557-A2.
PD 30-JAN-2003.
PA (OYFL) UNIV FLORIDA.
Query Match 5.5%; Score 54.8; DB 8; Length 2684;
Best Local Similarity 50.6%; Pred. No. 2.8;
RESULT 365
ID ADA69536 standard; DNA; 980 BP.
DE Rice gene, SEQ ID 2859.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 5.5%; Score 54.6; DB 8; Length 980;
Best Local Similarity 48.5%; Pred. No. 3.1;
RESULT 366
ID ADT43292 standard; cDNA; 1221 BP.
DE Bacterial polynucleotide #18043.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.5%; Score 54.6; DB 13; Length 1221;
Best Local Similarity 49.1%; Pred. No. 3.1;
RESULT 367
ID RAV19115 standard; DNA; 1308 BP.
DE Human secreted apoptosis-related protein hSARP2 DNA.
PN WO9813493-A2.
PD 02-APR-1998.
PA (LXRE-) LXR BIOTECHNOLOGY INC.
Query Match 5.5%; Score 54.6; DB 2; Length 1308;
Best Local Similarity 45.5%; Pred. No. 3;
RESULT 368
ID ADT44641 standard; cDNA; 789 BP.
DE Bacterial polynucleotide #19392.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.5%; Score 54.4; DB 13; Length 789;
Best Local Similarity 50.4%; Pred. No. 3.3;
RESULT 369
ID ADF31997 standard; DNA; 39949 BP.
DE Full length cosmid 2A7.
PN WO2003099993-A2.
PD 04-DEC-2003.
PA (AVET) AVENTIS PHARM INC.
Query Match 5.5%; Score 54.2; DB 12; Length 39949;
Best Local Similarity 45.6%; Pred. No. 3.2;
RESULT 370
ID ADF31998 standard; DNA; 48200 BP.
DE Cosmid 2A7.
PN WO2003099993-A2.
PD 04-DEC-2003.
PA (AVET) AVENTIS PHARM INC.
Query Match 5.5%; Score 54.2; DB 12; Length 48200;
Best Local Similarity 45.6%; Pred. No. 3.2;
RESULT 371
ID AAD17184 standard; DNA; 65140 BP.
DE Streptomyces noursei nysl DNA of nystatin PKS gene cluster.
PN WO200159126-A2.
PD 16-AUG-2001.
PA (UYNO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.
PA (SNTF) SINTEF STIFTELSEN IND TEK FORSK.
PA (ALPH-) ALPHARMA AS.
PA (SINV-) SINVENT AS.
PA (DZIE/) DZIEGLEWSKA H.
PA (ZOTC/) ZOTCHEV S B.
PA (SEKU/) SEKUROVA O N.
PA (FJAE/) FJAERVIK E.
PA (BRAU/) BRAUTASET T.
PA (STRO/) STROM A R.
PA (VALL/) VALLA S.
Query Match 5.5%; Score 54.2; DB 4; Length 65140;
Best Local Similarity 51.9%; Pred. No. 3.2;
RESULT 372
ID AAD17186 standard; DNA; 125401 BP.
DE Streptomyces noursei nystatin PKS gene cluster DNA.
```

PN WO200159126-A2.  
PD 16-AUG-2001.  
PA (UYNO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.  
PA (SNTF) SINTEF STIFTELSEN IND TEK FORSK.  
PA (ALPH-) ALPHARMA AS.  
PA (SINV-) SINVENT AS.  
PA (DZIE/) DZIEGLEWSKA H.  
PA (ZOTC/) ZOTCHEV S B.  
PA (SEKU/) SEKUROVA O N.  
PA (FJAE/) FJAEVRIK E.  
PA (BRAU/) BRAUTASET T.  
PA (STRO/) STROM A R.  
PA (VALL/) VALLA S.  
Query Match 5.5%; Score 54.2; DB 4; Length 125401;  
Best Local Similarity 51.9%; Pred. No. 3.1;  
RESULT 373  
ID ACA23654 standard; DNA; 897 BP.  
DE Prokaryotic essential gene #5311.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.5%; Score 54; DB 8; Length 897;  
Best Local Similarity 44.4%; Pred. No. 3.9;  
RESULT 374  
ID ACC00684 standard; cDNA; 1118 BP.  
DE Oryza sativa oil trait related cDNA sequence SEQ ID NO:117.  
PN WO2003002751-A2.  
PD 09-JAN-2003.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
PA (PION-) PIONEER HI-BRED INT INC.  
Query Match 5.5%; Score 54; DB 8; Length 1118;  
Best Local Similarity 46.2%; Pred. No. 3.9;  
RESULT 375  
ID ADC23596 standard; cDNA; 1118 BP.  
DE cDNA encodes protein used to alter plant oil phenotype (SeqID 101).  
PN WO2003001902-A2.  
PD 09-JAN-2003.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
PA (PION-) PIONEER HI-BRED INT INC.  
Query Match 5.5%; Score 54; DB 10; Length 1118;  
Best Local Similarity 46.2%; Pred. No. 3.9;  
RESULT 376  
ID ABK12029 standard; DNA; 1217 BP.  
DE DNA encoding aminoglycoside multidrug resistance protein.  
PN KE99074514-A.  
PD 05-OCT-1999.  
PA (DONG-) DONGWHA PHARM IND CO LTD.  
PA (SUHJ/) SUH J W.  
Query Match 5.5%; Score 54; DB 3; Length 1217;  
Best Local Similarity 46.3%; Pred. No. 3.8;  
RESULT 377  
ID AAV67187 standard; DNA; 1380 BP.  
DE M. luteus salt-resistant glutaminase encoding DNA.  
PN JP10243787-A.  
PD 14-SEP-1998.  
PA (FUND-) FUNDOKIN SHOYU KK.  
Query Match 5.5%; Score 54; DB 2; Length 1380;  
Best Local Similarity 47.1%; Pred. No. 3.8;  
RESULT 378  
ID AAS85408 standard; cDNA; 4056 BP.  
DE DNA encoding novel human diagnostic protein #21212.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.5%; Score 54; DB 5; Length 4056;  
Best Local Similarity 52.2%; Pred. No. 3.7;  
RESULT 379  
ID ADQ85821 standard; cDNA; 4378 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #2689.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH) GENENTECH INC.  
PA (WUTD/) WU T D.

PA (ZHOU/) ZHOU Y.  
Query Match 5.5%; Score 54; DB 12; Length 4378;  
Best Local Similarity 52.2%; Pred. No. 3.7;  
RESULT 380  
ID ADQ86986 standard; cDNA; 4378 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3861.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Query Match 5.5%; Score 54; DB 12; Length 4378;  
Best Local Similarity 52.2%; Pred. No. 3.7;  
RESULT 381  
ID ADQ83667 standard; cDNA; 4378 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #481.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Query Match 5.5%; Score 54; DB 13; Length 4378;  
Best Local Similarity 52.2%; Pred. No. 3.7;  
RESULT 382  
ID ACN40643 standard; cDNA; 4378 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA326729, SEQ ID NO:5544.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 5.5%; Score 54; DB 13; Length 4378;  
Best Local Similarity 52.2%; Pred. No. 3.7;  
RESULT 383  
ID ABZ11999 standard; cDNA; 4530 BP.  
DE Human polynucleotide SEQ ID NO 881.  
PN WO200270539-A2.  
PD 12-SEP-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.5%; Score 54; DB 6; Length 4530;  
Best Local Similarity 52.2%; Pred. No. 3.7;  
RESULT 384  
ID ADM44517 standard; cDNA; 4530 BP.  
DE Novel human arginine-rich protein cDNA #881.  
PN US2004053250-A1.  
PD 18-MAR-2004.  
PA (TANG/) TANG Y T.  
PA (XUEA/) XUE A.  
PA (DRMA/) DRMANAC R T.  
Query Match 5.5%; Score 54; DB 12; Length 4530;  
Best Local Similarity 52.2%; Pred. No. 3.7;  
RESULT 385  
ID AAA31496 standard; DNA; 451 BP.  
DE Plant microsatellite marker #457.  
PN WO9967421-A1.  
PD 29-DEC-1999.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FOREST LTD.  
Query Match 5.4%; Score 53.8; DB 3; Length 451;  
Best Local Similarity 57.1%; Pred. No. 4.3;  
RESULT 386  
ID ADM80038 standard; DNA; 1272 BP.  
DE Spiramycin biosynthesis orf2\*c, SEQ ID 5.  
PN FR2845394-A1.  
PD 09-APR-2004.  
PA (AVET) AVENTIS PHARMA SA.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
Query Match 5.4%; Score 53.8; DB 12; Length 1272;  
Best Local Similarity 48.0%; Pred. No. 4.1;  
RESULT 387  
ID ADN97554 standard; DNA; 1272 BP.  
DE S ambiofaciens spiramycin biosynthetic gene ORF2\*c.  
PN WO2004033689-A2.  
PD 22-APR-2004.  
PA (AVET) AVENTIS PHARMA SA.

PA (CNRS ) CNRS.  
 Query Match 5.4%; Score 53.8; DB 12; Length 1272;  
 Best Local Similarity 48.0%; Pred. No. 4.1;  
 RESULT 388  
 ID ABA95453 standard; DNA; 2082 BP.  
 DE Thermus thermophilus uvrd coding sequence.  
 PN WO200173052-A2.  
 PD 04-OCT-2001.  
 PA (MCHE/) MCHENRY C S.  
 Query Match 5.4%; Score 53.8; DB 4; Length 2082;  
 Best Local Similarity 48.1%; Pred. No. 4.1;  
 RESULT 389  
 ID ADM80035 standard; DNA; 11171 BP.  
 DE Spiramycin biosynthesis related DNA, SEQ ID 2.  
 PN FR2845394-A1.  
 PD 09-APR-2004.  
 PA (AVET ) AVENTIS PHARMA SA.  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 Query Match 5.4%; Score 53.8; DB 12; Length 11171;  
 Best Local Similarity 48.0%; Pred. No. 3.9;  
 RESULT 390  
 ID ADN97551 standard; DNA; 11171 BP.  
 DE S ambofaciens spiramycin biosynthetic enzyme genomic region #2.  
 PN WO2004033689-A2.  
 PD 22-APR-2004.  
 PA (AVET ) AVENTIS PHARMA SA.  
 PA (CNRS ) CNRS.  
 Query Match 5.4%; Score 53.8; DB 12; Length 11171;  
 Best Local Similarity 48.0%; Pred. No. 3.9;  
 RESULT 391  
 ID AAT80414 standard; DNA; 44377 BP.  
 DE Platenolide synthase gene cluster.  
 PN EP791655-A2.  
 PD 27-AUG-1997.  
 PA (ELIL ) LILLY & CO ELI.  
 Query Match 5.4%; Score 53.8; DB 2; Length 44377;  
 Best Local Similarity 48.0%; Pred. No. 3.8;  
 RESULT 392  
 ID AAT78508 standard; DNA; 44377 BP.  
 DE Platenolide synthase gene cluster.  
 PN EP791656-A2.  
 PD 27-AUG-1997.  
 PA (ELIL ) LILLY & CO ELI.  
 Query Match 5.4%; Score 53.8; DB 2; Length 44377;  
 Best Local Similarity 48.0%; Pred. No. 3.8;  
 RESULT 393  
 ID ADK16023 standard; DNA; 64492 BP..  
 DE Streptomyces halstedii vincenistatin gene cluster seq id 1.  
 PN US2004053274-A1.  
 PD 18-MAR-2004.  
 PA (TOKD ) TOKYO INST TECHNOLOGY.  
 Query Match 5.4%; Score 53.8; DB 12; Length 64492;  
 Best Local Similarity 50.6%; Pred. No. 3.7;  
 RESULT 394  
 ID AAD08215 standard; DNA; 114793 BP.  
 DE Human genome from BAC clone, hbm168.  
 PN WO200142434-A1.  
 PD 14-JUN-2001.  
 PA (MERI ) MERCK & CO INC.  
 Query Match 5.4%; Score 53.8; DB 4; Length 114793;  
 Best Local Similarity 47.2%; Pred. No. 3.7;  
 RESULT 395  
 ID AAZ32020 standard; DNA; 38734 BP.  
 DE Human METH1 related EST AL021529.  
 PN WO9937660-A1.  
 PD 29-JUL-1999.  
 PA (IRUE/) IRUELA-ARISPE L.  
 PA (HAST/) HASTINGS G A.  
 PA (RUBE/) RUBEN S M.  
 Query Match 5.4%; Score 53.6; DB 2; Length 38734;  
 Best Local Similarity 44.9%; Pred. No. 4.1;  
 RESULT 396  
 ID AAC90077 standard; DNA; 38734 BP.

DE AL021529 cDNA clone.  
 PN WO200071577-A1.  
 PD 30-NOV-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.  
 PA (IRUE/) IRUELA-ARISPE L.  
 PA (HAST/) HASTINGS G A.  
 PA (RUBE/) RUBEN S M.  
 PA (JONA/) JONAK Z L.  
 PA (TRUL/) TRULLI S H.  
 PA (FORN/) FORNWALD J A.  
 PA (TERR/) TERRETT J A.  
 Query Match 5.4%; Score 53.6; DB 5; Length 38734;  
 Best Local Similarity 44.9%; Pred. No. 4.1;  
 RESULT 397  
 ID AAL61221 standard; DNA; 1554 BP.  
 DE Actinosynnema pretiosum transcriptional activator gene #2.  
 PN WO2003045312-A2.  
 PD 05-JUN-2003.  
 PA (UNIW ) UNIV WASHINGTON.  
 Query Match 5.4%; Score 53.4; DB 8; Length 1554;  
 Best Local Similarity 48.5%; Pred. No. 4.8;  
 RESULT 398  
 ID AAZ50651 standard; cDNA; 2248 BP.  
 DE Corn starch synthase SSB DNA fragment inserted in pSPB47.  
 PN WO200006755-A2.  
 PD 10-FEB-2000.  
 PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
 Query Match 5.4%; Score 53.4; DB 3; Length 2248;  
 Best Local Similarity 50.2%; Pred. No. 4.8;  
 RESULT 399  
 ID AAQ14183 standard; cDNA; 2338 BP.  
 DE N. clavipes dragline silk protein coding sequence.  
 PN EP452925-A.  
 PD 23-OCT-1991.  
 PA (UYWY-) UNIV OF WYOMING.  
 Query Match 5.4%; Score 53.4; DB 2; Length 2338;  
 Best Local Similarity 45.5%; Pred. No. 4.8;  
 RESULT 400  
 ID AAV23249 standard; cDNA; 2338 BP.  
 DE Nephila clavipes spider silk protein encoding cDNA.  
 PN US5728810-A.  
 PD 17-MAR-1998.  
 PA (UYWY-) UNIV WYOMING.  
 Query Match 5.4%; Score 53.4; DB 2; Length 2338;  
 Best Local Similarity 45.5%; Pred. No. 4.8;  
 RESULT 401  
 ID AAZ36195 standard; cDNA; 2338 BP.  
 DE N. clavipes spider silk protein 1 encoding cDNA.  
 PN US5989894-A.  
 PD 23-NOV-1999.  
 PA (UYWY-) UNIV WYOMING.  
 Query Match 5.4%; Score 53.4; DB 3; Length 2338;  
 Best Local Similarity 45.5%; Pred. No. 4.8;  
 RESULT 402  
 ID AAI57831 standard; cDNA; 4176 BP.  
 DE Human polynucleotide SEQ ID NO 34.  
 PN WO200153312-A1.  
 PD 26-JUL-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 5.4%; Score 53.4; DB 4; Length 4176;  
 Best Local Similarity 48.9%; Pred. No. 4.7;  
 RESULT 403  
 ID AAL61225 standard; DNA; 11905 BP.  
 DE Actinosynnema pretiosum ansamitocin biosynthetic gene cluster II.  
 PN WO2003045312-A2.  
 PD 05-JUN-2003.  
 PA (UNIW ) UNIV WASHINGTON.  
 Query Match 5.4%; Score 53.4; DB 8; Length 11905;  
 Best Local Similarity 48.5%; Pred. No. 4.5;  
 RESULT 404  
 ID ADL15447 standard; DNA; 85915 BP.

DE Streptomyces bikiniensis NRRL 2737 chalcomycin PKS cluster DNA.  
PN WO2004018703-A2.  
PD 04-MAR-2004.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
Query Match 5.4%; Score 53.4; DB 13; Length 85915;  
Best Local Similarity 46.2%; Pred. No. 4.3;  
RESULT 405  
Query Match 5.4%; Score 53.4; DB 11; Length 110000;  
Best Local Similarity 45.7%; Pred. No. 4.3;  
RESULT 406  
ID ACA26842 standard; DNA; 900 BP.  
DE Prokaryotic essential gene #8499.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.4%; Score 53.2; DB 8; Length 900;  
Best Local Similarity 49.6%; Pred. No. 5.3;  
RESULT 407  
ID ABX34289 standard; DNA; 135638 BP.  
DE S. atroolivaceus leinamycin biosynthesis gene cluster.  
PN WO200277179-A2.  
PD 03-OCT-2002.  
PA (REGC) UNIV CALIFORNIA.  
Query Match 5.4%; Score 53.2; DB 10; Length 135638;  
Best Local Similarity 47.9%; Pred. No. 4.6;  
RESULT 408  
ID ADT42272 standard; cDNA; 1695 BP.  
DE Bacterial polynucleotide #17023.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 5.4%; Score 53; DB 13; Length 1695;  
Best Local Similarity 46.2%; Pred. No. 5.6;  
RESULT 409  
ID ADJ27274 standard; cDNA; 1929 BP.  
DE Mouse HSP70.1 coding sequence.  
PN WO2003061684-A2.  
PD 31-JUL-2003.  
PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.  
Query Match 5.4%; Score 53; DB 11; Length 1929;  
Best Local Similarity 44.3%; Pred. No. 5.6;  
RESULT 410  
ID ADT42037 standard; cDNA; 3444 BP.  
DE Bacterial polynucleotide #16788.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 5.4%; Score 53; DB 13; Length 3444;  
Best Local Similarity 48.5%; Pred. No. 5.5;  
RESULT 411  
ID AAT45060 standard; cDNA; 1236 BP.  
DE Maize Tst2 cDNA nucleotide sequence.  
PN WO9505732-A1.  
PD 02-MAR-1995.  
PA (UYIA) UNIV YALE.  
Query Match 5.3%; Score 52.8; DB 2; Length 1236;  
Best Local Similarity 47.3%; Pred. No. 6.1;  
RESULT 412  
ID ACA38386 standard; DNA; 2712 BP.  
DE Prokaryotic essential gene #20043.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.3%; Score 52.8; DB 8; Length 2712;  
Best Local Similarity 46.8%; Pred. No. 6;  
RESULT 413  
ID ACA40526 standard; DNA; 2715 BP.  
DE Prokaryotic essential gene #22183.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.3%; Score 52.8; DB 8; Length 2715;  
Best Local Similarity 46.8%; Pred. No. 6;  
RESULT 414  
ID ADP30617 standard; DNA; 34719 BP.  
DE Micromonospora echinospora gentamycin biosynthesis gene SeqID 1.  
PN JP2004180638-A.  
PD 02-JUL-2004.  
PA (MEIJ) MEIJI SEIKA KAISHA LTD.  
Query Match 5.3%; Score 52.8; DB 12; Length 34719;  
Best Local Similarity 50.4%; Pred. No. 5.6;  
RESULT 415  
Query Match 5.3%; Score 52.8; DB 4; Length 110000;  
Best Local Similarity 46.8%; Pred. No. 5.4;  
RESULT 416  
Query Match 5.3%; Score 52.8; DB 4; Length 110000;  
Best Local Similarity 46.8%; Pred. No. 5.4;  
RESULT 417  
ID ADJ39074 standard; cDNA; 447 BP.  
DE Plant cDNA #74.  
PN US2004016025-A1.  
PD 22-JAN-2004.  
PA (BUDW/) BUDWORTH P.  
PA (MOUG/) MOUGHAMER T.  
PA (BRIG/) BRIGGS S P.  
PA (COOP/) COOPER B.  
PA (GLAZ/) GLAZERBROOK J.  
PA (GOFF/) GOFF S A.  
PA (KATA/) KATAGIRI F.  
PA (KREP/) KREPS J.  
PA (PROV/) PROVART N.  
PA (RICK/) RICKES D.  
PA (ZHUT/) ZHU T.  
Query Match 5.3%; Score 52.6; DB 12; Length 447;  
Best Local Similarity 47.4%; Pred. No. 6.8;  
RESULT 418  
ID ACA03588 standard; DNA; 1275 BP.  
DE Synthetic DNA encoding immunogenic HIV peptide #71.  
PN WO2003004657-A1.  
PD 16-JAN-2003.  
PA (CHIR) CHIRON CORP.  
Query Match 5.3%; Score 52.6; DB 8; Length 1275;  
Best Local Similarity 43.1%; Pred. No. 6.6;  
RESULT 419  
ID ADC13276 standard; DNA; 1275 BP.  
DE DNA of HIV construct TacRevNef-opt-native\_ZA SEQ ID NO 55.  
PN WO2003004620-A2.  
PD 16-JAN-2003.  
PA (CHIR) CHIRON CORP.  
PA (UYST-) UNIV STELLENBOSCH.  
Query Match 5.3%; Score 52.6; DB 10; Length 1275;  
Best Local Similarity 43.1%; Pred. No. 6.6;  
RESULT 420  
ID ACA38006 standard; DNA; 1368 BP.  
DE Prokaryotic essential gene #19663.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.3%; Score 52.6; DB 8; Length 1368;  
Best Local Similarity 43.9%; Pred. No. 6.6;  
RESULT 421  
ID ADG73813 standard; cDNA; 2466 BP.  
DE Human variant subtilase-like serine protease polynucleotide.  
PN WO2003106667-A2.  
PD 24-DEC-2003.  
PA (FARB) BAYER HEALTHCARE AG.  
Query Match 5.3%; Score 52.6; DB 12; Length 2466;

Best Local Similarity 45.8%; Pred. No. 6.5;  
RESULT 422  
ID AAH26500 standard; cDNA; 2561 BP.  
DE Rabbit low density lipoprotein binding protein 2 (LBP-2) cDNA.  
PN WO200164874-A2.  
PD 07-SEP-2001.  
PA (BOST-) BOSTON HEART FOUND INC.  
Query Match 5.3%; Score 52.6; DB 5; Length 2561;  
Best Local Similarity 47.3%; Pred. No. 6.4;  
RESULT 423  
ID ADR07733 standard; cDNA; 2778 BP.  
DE Full length human cDNA useful for treating neurological disease Seq 1239.  
PN EP1447413-A2.  
PD 18-AUG-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 5.3%; Score 52.6; DB 13; Length 2778;  
Best Local Similarity 45.8%; Pred. No. 6.4;  
RESULT 424  
ID ACA03550 standard; DNA; 3624 BP.  
DE Synthetic DNA encoding immunogenic HIV peptide #33.  
PN WO2003004657-A1.  
PD 16-JAN-2003.  
PA (CHIR) CHIRON CORP.  
Query Match 5.3%; Score 52.6; DB 8; Length 3624;  
Best Local Similarity 43.1%; Pred. No. 6.4;  
RESULT 425  
ID ADC13268 standard; DNA; 3624 BP.  
DE DNA of HIV construct p2PolTatRevNef-opt-native\_C SEQ ID NO 47.  
PN WO2003004620-A2.  
PD 16-JAN-2003.  
PA (CHIR) CHIRON CORP.  
PA (OYST-) UNIV STELLENBOSCH.  
Query Match 5.3%; Score 52.6; DB 10; Length 3624;  
Best Local Similarity 43.1%; Pred. No. 6.4;  
RESULT 426  
ID ADG73810 standard; cDNA; 3705 BP.  
DE Human subtilase-like serine protease polynucleotide.  
PN WO2003106667-A2.  
PD 24-DEC-2003.  
PA (FARB) BAYER HEALTHCARE AG.  
Query Match 5.3%; Score 52.6; DB 12; Length 3705;  
Best Local Similarity 45.8%; Pred. No. 6.4;  
RESULT 427  
ID ADO56090 standard; DNA; 4199 BP.  
DE Thermus thermophilus VI ATPase gene operon.  
PN WO2004046350-A1.  
PD 03-JUN-2004.  
PA (NISC-) JAPAN SCI & TECHNOLOGY AGENCY.  
Query Match 5.3%; Score 52.6; DB 12; Length 4199;  
Best Local Similarity 55.1%; Pred. No. 6.4;  
RESULT 428  
Query Match 5.3%; Score 52.6; DB 4; Length 110000;  
Best Local Similarity 52.0%; Pred. No. 5.8;  
RESULT 429  
Query Match 5.3%; Score 52.6; DB 4; Length 110000;  
Best Local Similarity 52.0%; Pred. No. 5.8;  
RESULT 430  
ID ABL61294 standard; DNA; 1227 BP.  
DE N. uniformis p-hydroxymandelate oxidase DNA.  
PN WO200234921-A2.  
PD 02-MAY-2002.  
PA (STAM) DSM NV.  
PA (STAM) DSM BIOTECH GMBH.  
PA (UYJO) UNIV JOHNS HOPKINS.  
Query Match 5.3%; Score 52.4; DB 6; Length 1227;  
Best Local Similarity 45.0%; Pred. No. 7.1;  
RESULT 431  
ID ABL69280 standard; DNA; 1891 BP.  
DE Prostate cancer related gene sequence SEQ ID NO:7617.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Query Match 5.3%; Score 52.4; DB 6; Length 1891;

Best Local Similarity 45.9%; Pred. No. 7;  
RESULT 432  
ID ABV94243 standard; cDNA; 1891 BP.  
DE Breast carcinoma related nucleotide sequence SEQ ID NO:234.  
PN WO200246467-A2.  
PD 13-JUN-2002.  
PA (IPSO-) IPSOGEN.  
Query Match 5.3%; Score 52.4; DB 6; Length 1891;  
Best Local Similarity 45.9%; Pred. No. 7;  
RESULT 433  
ID ABK84580 standard; cDNA; 1891 BP.  
DE Human cDNA differentially expressed in granulocytic cells #1151.  
PN WO200228999-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 5.3%; Score 52.4; DB 6; Length 1891;  
Best Local Similarity 45.9%; Pred. No. 7;  
RESULT 434  
ID ADS88586 standard; cDNA; 1891 BP.  
DE Human housekeeping gene cDNA sequence SEQ ID NO:129.  
PN WO2004035785-A1.  
PD 29-APR-2004.  
PA (NIGA) NGK INSULATORS LTD.  
Query Match 5.3%; Score 52.4; DB 13; Length 1891;  
Best Local Similarity 45.9%; Pred. No. 7;  
RESULT 435  
ID AAS3918 standard; cDNA; 3978 BP.  
DE Adenyl cyclase type I-C1 C1 alpha domain coding sequence.  
PN US6107076-A.  
PD 22-AUG-2000.  
PA (TEXA) UNIV TEXAS SYSTEM.  
Query Match 5.3%; Score 52.4; DB 3; Length 3978;  
Best Local Similarity 47.8%; Pred. No. 6.9;  
RESULT 436  
ID ADL15099 standard; DNA; 5117 BP.  
DE Human male brain KIAA0533 protein DNA for cancer treatment.  
PN WO200308268-A2.  
PD 21-AUG-2003.  
PA (BIOI-) BIOINVENT INT AB.  
Query Match 5.3%; Score 52.4; DB 10; Length 5117;  
Best Local Similarity 50.0%; Pred. No. 6.8;  
RESULT 437  
ID ADN95659 standard; DNA; 5117 BP.  
DE Human BRC/LEC-related gene sequence SeqID583.  
PN WO2003080640-A1.  
PD 02-OCT-2003.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN) LICENTIA LTD.  
Query Match 5.3%; Score 52.4; DB 11; Length 5117;  
Best Local Similarity 50.0%; Pred. No. 6.8;  
RESULT 438  
ID ADR24163 standard; DNA; 5117 BP.  
DE Breast cancer prognosis marker #24.  
PN WO200405545-A2.  
PD 05-AUG-2004.  
PA (ROSE-) ROSETTA INPHARMATICS LLC.  
PA (NECA-) NETHERLANDS CANCER INST.  
Query Match 5.3%; Score 52.4; DB 13; Length 5117;  
Best Local Similarity 50.0%; Pred. No. 6.8;  
RESULT 439  
ID ABQ93882 standard; DNA; 5204 BP.  
DE Human laminin alpha-5-like NOVID DNA, SEQ ID NO:7.  
PN WO200253742-A2.  
PD 11-JUL-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 5.3%; Score 52.4; DB 6; Length 5204;  
Best Local Similarity 50.0%; Pred. No. 6.8;  
RESULT 440  
ID ADM87490 standard; cDNA; 5403 BP.  
DE Human EST derived nucleotide sequence SEQ ID NO:583.  
PN WO2004009834-A2.  
PD 29-JAN-2004.  
PA (NUVE-) NUVELO INC.

Query Match  
Best Local Similarity 5.3%; Score 52.4; DB 12; Length 5403;  
RESULT 441  
ID AAI58165 standard; cDNA; 5640 BP.  
DE Human polynucleotide SEQ ID NO 368.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 5.3%; Score 52.4; DB 4; Length 5640;  
RESULT 442  
ID ADQ98371 standard; cDNA; 5640 BP.  
DE DNA encoding human GPCR-like protein seqid 41.  
PN US6569662-B1.  
PD 27-MAY-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 5.3%; Score 52.4; DB 5; Length 5640;  
RESULT 443  
ID ADB48131 standard; cDNA; 5640 BP.  
DE Novel human cDNA SEQ ID NO 41.  
PN US2003104529-A1.  
PD 05-JUN-2003.  
PA (ZHOU/) ZHOU P.  
PA (TANG/) TANG Y T.  
PA (LIUC/) LIU C.  
PA (ASUN/) ASUNDI V. T.  
PA (DRNA/) DRWANAC R. T.  
Query Match  
Best Local Similarity 5.3%; Score 52.4; DB 9; Length 5640;  
RESULT 444  
ID ABO72930 standard; cDNA; 8296 BP.  
DE Human laminin alpha 5 2743 N-terminal amino acids cDNA SEQ ID NO:35.  
PN WO200250111-A2.  
PD 27-JUN-2002.  
PA (BIOS-) BIOSTRATUM INC.  
Query Match  
Best Local Similarity 5.3%; Score 52.4; DB 6; Length 8296;  
RESULT 445  
ID AAD27805 standard; DNA; 11091 BP.  
DE Human laminin alpha gene, sbg417005LAMININ\_ALPHA #2.  
PN WO200198342-A1.  
PD 27-DEC-2001.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PA (GLAX ) GLAXO GROUP LTD.  
Query Match  
Best Local Similarity 5.3%; Score 52.4; DB 6; Length 11091;  
RESULT 446  
ID AAD27804 standard; DNA; 11118 BP.  
DE Human laminin alpha gene, sbg417005LAMININ\_ALPHA #1.  
PN WO200198342-A1.  
PD 27-DEC-2001.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PA (GLAX ) GLAXO GROUP LTD.  
Query Match  
Best Local Similarity 5.3%; Score 52.4; DB 6; Length 11118;  
RESULT 447  
ID AAD55817 standard; DNA; 11238 BP.  
DE Micromonospora carbonacea polyketide synthase (PKS) type I gene #7.  
PN CA2391131-A1.  
PD 19-NOV-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match  
Best Local Similarity 5.3%; Score 52.4; DB 10; Length 11238;  
RESULT 448  
ID ACN40816 standard; cDNA; 11344 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA326869, SEQ ID NO:5846.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 5.3%; Score 52.4; DB 13; Length 11344;

Best Local Similarity 50.0%; Pred. No. 6.7;  
RESULT 449  
ID ABO72906 standard; cDNA; 11350 BP.  
DE Human laminin alpha 5 encoding cDNA SEQ ID NO:1.  
PN WO200250111-A2.  
PD 27-JUN-2002.  
PA (BIOS-) BIOSTRATUM INC.  
Query Match  
Best Local Similarity 5.3%; Score 52.4; DB 6; Length 11350;  
RESULT 450  
ID ADI28066 standard; cDNA; 11367 BP.  
DE ECMCAD gene clone 6382722CB1.  
PN WO200202634-A2.  
PD 10-JAN-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match  
Best Local Similarity 5.3%; Score 52.4; DB 6; Length 11367;  
RESULT 451  
ID ADN04477 standard; cDNA; 11426 BP.  
DE Antipsoriatic cDNA sequence #440.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 5.3%; Score 52.4; DB 12; Length 11426;  
RESULT 452  
ID ADM87010 standard; cDNA; 11640 BP.  
DE Human protein encoding cDNA SEQ ID NO:103.  
PN WO2004009834-A2.  
PD 29-JAN-2004.  
PA (NUVE-) NUVELO INC.  
Query Match  
Best Local Similarity 5.3%; Score 52.4; DB 12; Length 11640;  
RESULT 453  
ID AAD55810 standard; DNA; 60196 BP.  
DE Micromonospora carbonacea polyketide synthase (PKS) type I gene cluster.  
PN CA2391131-A1.  
PD 19-NOV-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match  
Best Local Similarity 5.3%; Score 52.4; DB 10; Length 60196;  
RESULT 454  
ID AAC47161 standard; DNA; 738 BP.  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 52786.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 5.3%; Score 52.2; DB 3; Length 738;  
RESULT 455  
ID AAC47930 standard; DNA; 833 BP.  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 55635.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 5.3%; Score 52.2; DB 3; Length 833;  
RESULT 456  
ID AAT95356 standard; DNA; 2004 BP.  
DE Nephila clavipes spider silk protein 2 Kb DNA sequence.  
PN WO9708315-A1.  
PD 06-MAR-1997.  
PA (BASE/) BASEL R M.  
PA (ELIO/) ELION G R.  
Query Match  
Best Local Similarity 5.3%; Score 52.2; DB 2; Length 2004;  
RESULT 457  
ID ADSS6080 standard; cDNA; 2505 BP.  
DE Bacterial polynucleotide #8067.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.

PA (GOLD/) GOLDMAN B S.  
 Query Match 5.3%; Score 52.2; DB 13; Length 2505;  
 Best Local Similarity 48.3%; Pred. No. 7.5;  
 RESULT 458  
 ID ACA38157 standard; DNA; 2757 BP.  
 DE Prokaryotic essential gene #19814.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 5.3%; Score 52.2; DB 8; Length 2757;  
 Best Local Similarity 46.7%; Pred. No. 7.5;  
 RESULT 459  
 ID ADC30607 standard; cDNA; 4542 BP.  
 DE Human novel cDNA sequence, SEQ ID NO:689.  
 PN WO2003029271-A2.  
 PD 10-APR-2003.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 5.3%; Score 52.2; DB 10; Length 4542;  
 Best Local Similarity 47.8%; Pred. No. 7.4;  
 RESULT 460  
 ID AAD54236 standard; DNA; 6297 BP.  
 DE Streptomyces amphibiosporus lactimidomycin ORF6 DNA.  
 PN WO20028176-A2.  
 PD 07-NOV-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 5.3%; Score 52.2; DB 10; Length 6297;  
 Best Local Similarity 47.2%; Pred. No. 7.3;  
 RESULT 461  
 ID ABQ77491 standard; DNA; 67459 BP.  
 DE S. aurantiaca DNA containing sti gene cluster.  
 PN DE10128661-A1.  
 PD 19-DEC-2002.  
 PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
 Query Match 5.3%; Score 52.2; DB 8; Length 67459;  
 Best Local Similarity 43.5%; Pred. No. 6.9;  
 RESULT 462  
 ID ADO59147 standard; DNA; 70782 BP.  
 DE Angiococcus disciformis tubulysin biosynthesis cluster DNA.  
 PN DE10241152-A1.  
 PD 18-MAR-2004.  
 PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
 Query Match 5.3%; Score 52.2; DB 12; Length 70782;  
 Best Local Similarity 44.2%; Pred. No. 6.9;  
 RESULT 463  
 ID ACF06127 standard; DNA; 1218 BP.  
 DE Bacterial P450 enzyme encoding DNA SEQ ID NO:37.  
 PN WO2003052050-A2.  
 PD 26-JUN-2003.  
 PA (DIVE-) DIVERSA CORP.  
 Query Match 5.3%; Score 52; DB 9; Length 1218;  
 Best Local Similarity 50.6%; Pred. No. 8.3;  
 RESULT 464  
 ID ABD03077 standard; DNA; 1248 BP.  
 DE Pseudomonas aeruginosa polynucleotide #1691.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.3%; Score 52; DB 11; Length 1248;  
 Best Local Similarity 50.4%; Pred. No. 8.3;  
 RESULT 465  
 ID ABD02833 standard; DNA; 1302 BP.  
 DE Pseudomonas aeruginosa polynucleotide #1437.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.3%; Score 52; DB 11; Length 1302;  
 Best Local Similarity 50.4%; Pred. No. 8.3;  
 RESULT 466  
 ID ABL40020 standard; DNA; 1491 BP.  
 DE Synthetic gag polynucleotide sequence SEQ ID NO:99.  
 PN WO200204493-A2.  
 PD 17-JAN-2002.  
 PA (CHIR ) CHIRON CORP.

PA (UYST-) UNIV STELLENBOSCH.  
 Query Match 5.3%; Score 52; DB 6; Length 1491;  
 Best Local Similarity 46.4%; Pred. No. 8.2;  
 RESULT 467  
 ID ADM73833 standard; DNA; 1491 BP.  
 DE HIV-1 polynucleotide #68.  
 PN US2003223961-A1.  
 PD 04-DEC-2003.  
 PA (MEGE/) MEGEDE J Z.  
 PA (BARN/) BARNETT S W.  
 PA (ENGE/) ENGELBRECHT S.  
 PA (RENS/) RENSBURG E J V.  
 Query Match 5.3%; Score 52; DB 12; Length 1491;  
 Best Local Similarity 46.4%; Pred. No. 8.2;  
 RESULT 468  
 ID ABD02890 standard; DNA; 1956 BP.  
 DE Pseudomonas aeruginosa polynucleotide #1494.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.3%; Score 52; DB 11; Length 1956;  
 Best Local Similarity 50.4%; Pred. No. 8.2;  
 RESULT 469  
 ID ADP69917 standard; DNA; 3078 BP.  
 DE Mammalian codon optimised E. coli LacZ gene.  
 PN WO2004050872-A1.  
 PD 17-JUN-2004.  
 PA (WOME-) WOMEN'S & CHILDREN'S HOSPITAL.  
 Query Match 5.3%; Score 52; DB 12; Length 3078;  
 Best Local Similarity 45.4%; Pred. No. 8.1;  
 RESULT 470  
 ID ABD11785 standard; DNA; 498 BP.  
 DE Pseudomonas aeruginosa polynucleotide #10389.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.2%; Score 51.8; DB 11; Length 498;  
 Best Local Similarity 46.5%; Pred. No. 9.2;  
 RESULT 471  
 ID ABD11976 standard; DNA; 561 BP.  
 DE Pseudomonas aeruginosa polynucleotide #10580.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.2%; Score 51.8; DB 11; Length 561;  
 Best Local Similarity 46.5%; Pred. No. 9.1;  
 RESULT 472  
 ID ABD12080 standard; DNA; 1053 BP.  
 DE Pseudomonas aeruginosa polynucleotide #10684.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.2%; Score 51.8; DB 11; Length 1053;  
 Best Local Similarity 46.5%; Pred. No. 9;  
 RESULT 473  
 ID ACA27206 standard; DNA; 1227 BP.  
 DE Prokaryotic essential gene #8863.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 5.2%; Score 51.8; DB 8; Length 1227;  
 Best Local Similarity 46.9%; Pred. No. 8.9;  
 RESULT 474  
 ID ABD04500 standard; DNA; 1233 BP.  
 DE Pseudomonas aeruginosa polynucleotide #3104.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.2%; Score 51.8; DB 11; Length 1233;  
 Best Local Similarity 48.2%; Pred. No. 8.9;  
 RESULT 475  
 ID ACN44729 standard; cDNA; 1253 BP.  
 DE Mouse mRNA sequence mCT7005.



PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 5.2%; Score 51.8; DB 11; Length 1253;  
Best Local Similarity 47.6%; Pred. No. 8.9;  
RESULT 476  
ID ADT44764 standard; cDNA; 1347 BP.  
DE Bacterial polynucleotide #19515.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 5.2%; Score 51.8; DB 13; Length 1347;  
Best Local Similarity 46.3%; Pred. No. 8.9;  
RESULT 477  
ID ABD04263 standard; DNA; 1386 BP.  
DE Pseudomonas aeruginosa polynucleotide #2867.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.2%; Score 51.8; DB 11; Length 1386;  
Best Local Similarity 48.2%; Pred. No. 8.9;  
RESULT 478  
ID ADS64227 standard; cDNA; 1659 BP.  
DE Bacterial polynucleotide #16214.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 5.2%; Score 51.8; DB 13; Length 1659;  
Best Local Similarity 49.4%; Pred. No. 8.9;  
RESULT 479  
ID ADS63845 standard; cDNA; 1677 BP.  
DE Bacterial polynucleotide #15832.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 5.2%; Score 51.8; DB 13; Length 1677;  
Best Local Similarity 49.4%; Pred. No. 8.9;  
RESULT 480  
ID ADS63476 standard; cDNA; 1677 BP.  
DE Bacterial polynucleotide #15463.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 5.2%; Score 51.8; DB 13; Length 1677;  
Best Local Similarity 49.4%; Pred. No. 8.9;  
RESULT 481  
ID ABZ81830 standard; DNA; 2072 BP.  
DE Receptor FZD10 nucleic acid sequence.  
PN WO2003012082-A2.  
PD 13-FEB-2003.  
PA (AXOR-) AXORDIA LTD.  
Query Match 5.2%; Score 51.8; DB 8; Length 2072;  
Best Local Similarity 45.0%; Pred. No. 8.8;  
RESULT 482  
ID AAD17401 standard; DNA; 2075 BP.  
DE Human secreted Frizzled-related protein (sFRP) gene.  
PN WO200164717-A1.

PD 07-SEP-2001.  
PA (UYCO ) UNIV COLUMBIA NEW YORK.  
Query Match 5.2%; Score 51.8; DB 4; Length 2075;  
Best Local Similarity 45.0%; Pred. No. 8.8;  
RESULT 483  
ID ABV73022 standard; cDNA; 2075 BP.  
DE Human secreted Frizzled-related protein (sFRP)-1 encoding cDNA.  
PN WO200255547-A2.  
PD 18-JUL-2002.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA (SVIN-) ST VINCENTS INST MEDICAL RES.  
Query Match 5.2%; Score 51.8; DB 6; Length 2075;  
Best Local Similarity 45.0%; Pred. No. 8.8;  
RESULT 484  
ID ABX75330 standard; cDNA; 2075 BP.  
DE Human cDNA encoding Frizzled-8.  
PN WO200277204-A2.  
PD 03-OCT-2002.  
PA (AXOR-) AXORDIA LTD.  
Query Match 5.2%; Score 51.8; DB 8; Length 2075;  
Best Local Similarity 45.0%; Pred. No. 8.8;  
RESULT 485  
ID AAD52558 standard; DNA; 2075 BP.  
DE FRP DNA.  
PN WO200290992-A2.  
PD 14-NOV-2002.  
PA (AXOR-) AXORDIA LTD.  
Query Match 5.2%; Score 51.8; DB 8; Length 2075;  
Best Local Similarity 45.0%; Pred. No. 8.8;  
RESULT 486  
ID ADC71197 standard; cDNA; 2075 BP.  
DE Human secreted frizzled related protein (sFRP) cDNA.  
PN US6600018-B1.  
PD 29-JUL-2003.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 5.2%; Score 51.8; DB 10; Length 2075;  
Best Local Similarity 45.0%; Pred. No. 8.8;  
RESULT 487  
ID ADH43319 standard; cDNA; 2075 BP.  
DE Human secreted frizzled related protein 1 (sFRP-1) cDNA.  
PN US2003187223-A1.  
PD 02-OCT-2003.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA (UYMA-) UNIV MASSACHUSETTS.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 5.2%; Score 51.8; DB 12; Length 2075;  
Best Local Similarity 45.0%; Pred. No. 8.8;  
RESULT 488  
ID ACA43985 standard; DNA; 2145 BP.  
DE Prokaryotic essential gene #25642.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.2%; Score 51.8; DB 8; Length 2145;  
Best Local Similarity 44.4%; Pred. No. 8.8;  
RESULT 489  
ID AAK94307 standard; cDNA; 2525 BP.  
DE Human full-length cDNA, SEQ ID NO: 2971.  
PN EPI130094-A2.  
PD 05-SEP-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 5.2%; Score 51.8; DB 4; Length 2525;  
Best Local Similarity 43.0%; Pred. No. 8.8;  
RESULT 490  
ID ADL30938 standard; cDNA; 2525 BP.  
DE Full length human cDNA clone SeqID 2971.  
PN EPI1396543-A2.  
PD 10-MAR-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 5.2%; Score 51.8; DB 12; Length 2525;  
Best Local Similarity 43.0%; Pred. No. 8.8;  
RESULT 491  
ID ABS78645 standard; cDNA; 2597 BP.

DE Human cDNA encoding CGDD3, INCYTE 3089944CB1.  
 PN WO200272830-A2.  
 PD 19-SEP-2002.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Query Match 5.2%; Score 51.8; DB 6; Length 2597;  
 Best Local Similarity 43.0%; Pred. No. 8.8;  
 RESULT 492  
 ID ABX77526 standard; cDNA; 4462 BP.  
 DE Differentially expressed breast cancer associated cDNA #21.  
 PN US2002156263-A1.  
 PD 24-OCT-2002.  
 PA (CHEN/) CHEN H.  
 Query Match 5.2%; Score 51.8; DB 8; Length 4462;  
 Best Local Similarity 45.0%; Pred. No. 8.6;  
 RESULT 493  
 ID AAS12954 standard; cDNA; 4469 BP.  
 DE Human Frizzled Related Protein (FRP-1) cDNA.  
 PN WO200164949-A2.  
 PD 07-SEP-2003.  
 PA (ALCO-) ALCON LAB INC.  
 Query Match 5.2%; Score 51.8; DB 4; Length 4469;  
 Best Local Similarity 45.0%; Pred. No. 8.6;  
 RESULT 494  
 ID ABT10165 standard; cDNA; 4469 BP.  
 DE Human breast cancer associated coding sequence SEQ ID NO: 299.  
 PN WO200259271-A2.  
 PD 01-AUG-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Query Match 5.2%; Score 51.8; DB 6; Length 4469;  
 Best Local Similarity 45.0%; Pred. No. 8.6;  
 RESULT 495  
 ID ABZ34845 standard; cDNA; 4469 BP.  
 DE Coding sequence SEQ ID 203, differentially expressed in osteogenesis.  
 PN WO200281745-A2.  
 PD 17-OCT-2002.  
 PA (AVET-) AVENTIS PHARMA SA.  
 Query Match 5.2%; Score 51.8; DB 8; Length 4469;  
 Best Local Similarity 45.0%; Pred. No. 8.6;  
 RESULT 496  
 ID ADP21417 standard; DNA; 4469 BP.  
 DE Gene SFRP1 for screening for cardiac therapeutic preparation.  
 PN WO2004050894-A2.  
 PD 17-JUN-2004.  
 PA (ARTE-) ARTESIAN THERAPEUTICS INC.  
 Query Match 5.2%; Score 51.8; DB 12; Length 4469;  
 Best Local Similarity 45.0%; Pred. No. 8.6;  
 RESULT 497  
 ID ADR24996 standard; DNA; 4469 BP.  
 DE Breast cancer prognosis marker #857.  
 PN WO2004065545-A2.  
 PD 05-AUG-2004.  
 PA (ROSE-) ROSETTA INPHARMATICS LLC.  
 PA (NECA-) NETHERLANDS CANCER INST.  
 Query Match 5.2%; Score 51.8; DB 13; Length 4469;  
 Best Local Similarity 45.0%; Pred. No. 8.6;  
 RESULT 498  
 ID ADR99015 standard; DNA; 4469 BP.  
 DE Secreted frizzled-related protein 1, SFRP1, coding sequence, SEQ ID 21.  
 PN WO2004078035-A2.  
 PD 16-SEP-2004.  
 PA (FARB-) BAYER PHARM CORP.  
 Query Match 5.2%; Score 51.8; DB 13; Length 4469;  
 Best Local Similarity 45.0%; Pred. No. 8.6;  
 RESULT 499  
 ID AAA10594 standard; DNA; 10732 BP.  
 DE Gene encoding a subunit of cellulose synthase.  
 PN JP2000060568-A.  
 PD 29-FEB-2000.  
 PA (MIZU/) MIZUNO K.  
 PA (OJIP-) OJI PAPER CO.  
 Query Match 5.2%; Score 51.8; DB 3; Length 10732;  
 Best Local Similarity 13.2%; Pred. No. 8.4;  
 RESULT 500

ID AAL61170 standard; DNA; 14055 BP.  
 DE Actinosynnema pretiosum polyketide synthase (PKS) gene #1.  
 PN WO2003045312-A2.  
 PD 05-JUN-2003.  
 PA (UNIW-) UNIV WASHINGTON.  
 Query Match 5.2%; Score 51.8; DB 8; Length 14055;  
 Best Local Similarity 44.1%; Pred. No. 8.4;  
 RESULT 501  
 ID AAD54645 standard; DNA; 113193 BP.  
 DE Streptomyces nodosus amphoterin (amph) biosynthetic gene cluster.  
 PN WO200297082-A2.  
 PD 05-DEC-2002.  
 PA (YDU-) UNIV COLLEGE DUBLIN.  
 Query Match 5.2%; Score 51.8; DB 8; Length 113193;  
 Best Local Similarity 46.9%; Pred. No. 7.9;  
 RESULT 502  
 ID ACC00687 standard; cDNA; 893 BP.  
 DE Oryza sativa oil trait related cDNA sequence SEQ ID NO:123.  
 PN WO2003002751-A2.  
 PD 09-JAN-2003.  
 PA (DUPO-) DU PONT DE NEMOURS & CO E I.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Query Match 5.2%; Score 51.6; DB 8; Length 893;  
 Best Local Similarity 46.7%; Pred. No. 9.7;  
 RESULT 503  
 ID ADC3602 standard; cDNA; 893 BP.  
 DE cDNA encodes protein used to alter plant oil phenotype (SeqID 107).  
 PN WO2003001902-A2.  
 PD 09-JAN-2003.  
 PA (DUPO-) DU PONT DE NEMOURS & CO E I.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Query Match 5.2%; Score 51.6; DB 10; Length 893;  
 Best Local Similarity 46.7%; Pred. No. 9.7;  
 RESULT 504  
 ID ACA38013 standard; DNA; 1242 BP.  
 DE Prokaryotic essential gene #19670.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 5.2%; Score 51.6; DB 8; Length 1242;  
 Best Local Similarity 44.5%; Pred. No. 9.7;  
 RESULT 505  
 ID ABD15461 standard; DNA; 1311 BP.  
 DE Pseudomonas aeruginosa polynucleotide #14065.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.2%; Score 51.6; DB 11; Length 1311;  
 Best Local Similarity 43.9%; Pred. No. 9.6;  
 RESULT 506  
 ID ADS60055 standard; cDNA; 2055 BP.  
 DE Bacterial polynucleotide #12042.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match 5.2%; Score 51.6; DB 13; Length 2055;  
 Best Local Similarity 48.3%; Pred. No. 9.5;  
 RESULT 507  
 ID ABD15601 standard; DNA; 2850 BP.  
 DE Pseudomonas aeruginosa polynucleotide #14205.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.2%; Score 51.6; DB 11; Length 2850;  
 Best Local Similarity 43.9%; Pred. No. 9.4;  
 RESULT 508  
 ID ACA26098 standard; DNA; 2853 BP.  
 DE Prokaryotic essential gene #7755.  
 PN WO200277183-A2.

PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.2%; Score 51.6; DB 8; Length 2853;  
Best Local Similarity 45.4%; Pred. No. 9.4;  
RESULT 509  
ID ABX09933 standard; DNA; 2865 BP.  
DE DNA encoding maize Starch synthase Iia.  
PN WO200279410-A2.  
PD 10-OCT-2002.  
PA (BADI) BASF PLANT SCI GMBH.  
Query Match 5.2%; Score 51.6; DB 8; Length 2865;  
Best Local Similarity 49.6%; Pred. No. 9.4;  
RESULT 510  
ID ADG75175 standard; DNA; 9369 BP.  
DE Human herpesvirus 2 strain HG52 UL36 DNA - SEQ ID 247.  
PN WO2003086308-A2.  
PD 23-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 5.2%; Score 51.6; DB 10; Length 9369;  
Best Local Similarity 44.9%; Pred. No. 9.1;  
RESULT 511  
ID ADG75118 standard; DNA; 9369 BP.  
DE Human herpesvirus 2 UL36 ORF DNA - SEQ ID 190.  
PN WO2003086308-A2.  
PD 23-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 5.2%; Score 51.6; DB 10; Length 9369;  
Best Local Similarity 44.9%; Pred. No. 9.1;  
RESULT 512  
ID AAV62154 standard; DNA; 21034 BP.  
DE HSV-2 strain SB5 Contig ID 10 DNA sequence.  
PN WO9820016-A1.  
PD 14-MAY-1998.  
PA (SMIK) SMITHKLINE BEECHAM CORP.  
Query Match 5.2%; Score 51.6; DB 2; Length 21034;  
Best Local Similarity 44.9%; Pred. No. 8.9;  
RESULT 513  
ID AAV62134 standard; DNA; 26338 BP.  
DE HSV-2 strain SB5 Contig ID 104 DNA sequence.  
PN WO9820016-A1.  
PD 14-MAY-1998.  
PA (SMIK) SMITHKLINE BEECHAM CORP.  
Query Match 5.2%; Score 51.6; DB 2; Length 26338;  
Best Local Similarity 44.9%; Pred. No. 8.9;  
RESULT 514  
ID ADP64454 standard; DNA; 76994 BP.  
DE Sorangium cellulosum disorazole polyketide synthase gene cluster DNA.  
PN WO2004053065-A2.  
PD 24-JUN-2004.  
PA (KOGA-) KOSAN BIOSCIENCES INC.  
Query Match 5.2%; Score 51.6; DB 12; Length 76994;  
Best Local Similarity 44.5%; Pred. No. 8.6;  
RESULT 515  
ID AAD54645 standard; DNA; 113193 BP.  
DE Streptomyces nodosus amphotericin (amph) biosynthetic gene cluster.  
PN WO200297082-A2.  
PD 05-DEC-2002.  
PA (UYDU-) UNIV COLLEGE DUBLIN.  
Query Match 5.2%; Score 51.6; DB 8; Length 113193;  
Best Local Similarity 44.0%; Pred. No. 8.5;  
RESULT 516  
ID AAV62176 standard; DNA; 117213 BP.  
DE HSV-2 strain SB5 Contig ID 15 DNA sequence.  
Query Match 5.2%; Score 51.6; DB 2; Length 117213;  
Best Local Similarity 44.9%; Pred. No. 8.5;  
RESULT 517  
ID ABA99457 standard; DNA; 813 BP.  
DE Actinoplanes sp DNA encoding acarbose synthase AcbOasp.  
PN DE10021667-A1.  
PD 08-NOV-2001.  
PA (FARB) BAYER AG.  
Query Match 5.2%; Score 51.4; DB 6; Length 813;  
Best Local Similarity 44.7%; Pred. No. 11;

RESULT 518  
ID AAA29167 standard; cDNA; 1106 BP.  
DE Rice 4-hydroxyphenylpyruvate dioxygenase partial cDNA.  
PN WO200032757-A2.  
PD 08-JUN-2000.  
PA (DUPO) DU PONT DE NEMOURS & CO E I.  
Query Match 5.2%; Score 51.4; DB 3; Length 1106;  
Best Local Similarity 45.0%; Pred. No. 10;  
RESULT 519  
ID ADC36364 standard; DNA; 1197 BP.  
DE Weed controller metabolism associated gene SEQ ID NO:232.  
PN WO2003040370-A1.  
PD 15-MAY-2003.  
PA (SUMO) SUMITOMO CHEM CO LTD.  
Query Match 5.2%; Score 51.4; DB 10; Length 1197;  
Best Local Similarity 43.9%; Pred. No. 10;  
RESULT 520  
ID ADC36374 standard; DNA; 1411 BP.  
DE Weed controller metabolism associated gene SEQ ID NO:242.  
PN WO2003040370-A1.  
PD 15-MAY-2003.  
PA (SUMO) SUMITOMO CHEM CO LTD.  
Query Match 5.2%; Score 51.4; DB 10; Length 1411;  
Best Local Similarity 43.9%; Pred. No. 10;  
RESULT 521  
ID ADJ27276 standard; cDNA; 1926 BP.  
DE Mouse HSP70.3 coding sequence.  
PN WO2003061684-A2.  
PD 31-JUL-2003.  
PA (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.  
Query Match 5.2%; Score 51.4; DB 11; Length 1926;  
Best Local Similarity 44.1%; Pred. No. 10;  
RESULT 522  
ID AAS10678 standard; cDNA; 1929 BP.  
DE Murine hsp70 cDNA sequence.  
PN WO200151081-A1.  
PD 19-JUL-2001.  
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.  
Query Match 5.2%; Score 51.4; DB 4; Length 1929;  
Best Local Similarity 44.1%; Pred. No. 10;  
RESULT 523  
ID ACA23299 standard; DNA; 2307 BP.  
DE Prokaryotic essential gene #4956.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.2%; Score 51.4; DB 8; Length 2307;  
Best Local Similarity 49.8%; Pred. No. 10;  
RESULT 524  
ID ADQ18001 standard; DNA; 2526 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 818.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 5.2%; Score 51.4; DB 12; Length 2526;  
Best Local Similarity 44.1%; Pred. No. 10;  
RESULT 525  
ID ADQ22602 standard; DNA; 2652 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5422.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 5.2%; Score 51.4; DB 12; Length 2652;  
Best Local Similarity 44.1%; Pred. No. 10;  
RESULT 526  
ID AAD55818 standard; DNA; 4725 BP.  
DE Micromonospora carbonacea polyketide synthase (PKS) type I gene #8.  
PN CA2391131-A1.  
PD 19-NOV-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 5.2%; Score 51.4; DB 10; Length 4725;  
Best Local Similarity 50.6%; Pred. No. 10;

```

RESULT 527
ID AB211709 standard; cDNA; 7847 BP.
DE Human polynucleotide SEQ ID NO 591.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 5.2%; Score 51.4; DB 6; Length 7847;
Best Local Similarity 50.2%; Pred. No. 9.9;
RESULT 528
ID ADM44227 standard; cDNA; 7847 BP.
DE Novel human arginine-rich protein cDNA #591.
PN US2004053250-A1.
PD 18-MAR-2004.
PA (TANG/) TANG Y T.
PA (XUEA/) XUE A.
PA (DRWA/) DRMANAC R T.
Query Match 5.2%; Score 51.4; DB 12; Length 7847;
Best Local Similarity 50.2%; Pred. No. 9.9;
RESULT 529
ID ADP90617 standard; DNA; 34719 BP.
DE Micromonospora echinospora gentamycin biosynthesis gene SeqID 1.
PN JP2004180638-A.
PD 02-JUL-2004.
PA (MEIJ) MEIJI SEIKA KAISHA LTD.
Query Match 5.2%; Score 51.4; DB 12; Length 34719;
Best Local Similarity 47.1%; Pred. No. 9.5;
RESULT 530
ID ABA99469 standard; DNA; 38064 BP.
DE Actinoplanes sp SE 50/110 (CBS614.71) DNA encoding acarbose operon.
PN DE10021667-A1.
PD 08-NOV-2001.
PA (FARB) BAYER AG.
Query Match 5.2%; Score 51.4; DB 6; Length 38064;
Best Local Similarity 44.7%; Pred. No. 9.5;
RESULT 531
ID ABX04971 standard; DNA; 103599 BP.
DE S. cinnamomensis monensin type I polyketide synthase gene cluster.
PN WO200168867-A1.
PD 20-SEP-2001.
PA (BIOT-) BIOTICA TECHNOLOGY LTD.
Query Match 5.2%; Score 51.4; DB 4; Length 103599;
Best Local Similarity 44.8%; Pred. No. 9.2;
RESULT 532
ID ADP95323 standard; cDNA; 447 BP.
DE Cotton expressed sequence tag, EST, #4334.
PN US2004123338-A1.
PD 24-JUN-2004.
PA (FINC/) FINCHER K L.
Query Match 5.2%; Score 51.2; DB 12; Length 447;
Best Local Similarity 50.8%; Pred. No. 12;
RESULT 533
ID AB213934 standard; DNA; 699 BP.
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 1739.
PN WO200216655-A2.
PD 28-FEB-2002.
PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 5.2%; Score 51.2; DB 6; Length 699;
Best Local Similarity 47.5%; Pred. No. 11;
RESULT 534
ID ADG87603 standard; cDNA; 699 BP.
DE A. thaliana RPP7/RPP8-upregulated pathogen infection-related gene #45.
PN WO20022675-A2.
PD 21-MAR-2002.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
PA (UYNC-) UNIV NORTH CAROLINA.
PA (GLAZ/) GLAZEBROOK J.
PA (WANG/) WANG X.
PA (DANG/) DANG J L.
PA (EULG/) EULGEM T.
PA (ZHUT/) ZHU T.
Query Match 5.2%; Score 51.2; DB 6; Length 699;
Best Local Similarity 47.5%; Pred. No. 11;
RESULT 535
ID ADG87604 standard; cDNA; 699 BP.
DE A. thaliana RPP7/RPP8-upregulated pathogen infection-related gene #46.
PN WO20022675-A2.
PD 21-MAR-2002.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
PA (UYNC-) UNIV NORTH CAROLINA.
PA (GLAZ/) GLAZEBROOK J.
PA (WANG/) WANG X.
PA (DANG/) DANG J L.
PA (EULG/) EULGEM T.
PA (ZHUT/) ZHU T.
Query Match 5.2%; Score 51.2; DB 6; Length 699;
Best Local Similarity 47.5%; Pred. No. 11;
RESULT 536
ID ADA67907 standard; DNA; 699 BP.
DE Arabidopsis thaliana gene, SEQ ID 151.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 5.2%; Score 51.2; DB 8; Length 699;
Best Local Similarity 47.5%; Pred. No. 11;
RESULT 537
ID ABN99073 standard; DNA; 792 BP.
DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 841.
PN US2002023281-A1.
PD 21-FEB-2002.
PA (GORL/) GORLACH J.
PA (ANYV/) AN Y.
PA (HAML/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUYV/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHIEW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
Query Match 5.2%; Score 51.2; DB 6; Length 792;
Best Local Similarity 47.5%; Pred. No. 11;
RESULT 538
ID ACA36840 standard; DNA; 1107 BP.
DE Prokaryotic essential gene #8497.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.2%; Score 51.2; DB 8; Length 1107;
Best Local Similarity 45.2%; Pred. No. 11;
RESULT 539
ID AAD55811 standard; DNA; 1683 BP.
DE Micromonospora carbonacea polyketide synthase (PKS) type I gene #1.
PN CA2391131-A1.
PD 19-NOV-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 5.2%; Score 51.2; DB 10; Length 1683;
Best Local Similarity 48.3%; Pred. No. 11;
RESULT 540
ID AAS54365 standard; DNA; 2034 BP.
DE Pseudomonas aeruginosa DNA for cellular proliferation protein #496.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.2%; Score 51.2; DB 4; Length 2034;
Best Local Similarity 46.0%; Pred. No. 11;
RESULT 541

```

ID AAV13836 standard; cDNA; 2277 BP.  
 DE Homo sapiens mammalian codon-optimized telomerase protein p105 gene.  
 PN WO9801543-A1.  
 PD 15-JAN-1998.  
 PA (TULSA-) TULARIK INC.  
 Query Match 5.2%; Score 51.2; DB 2; Length 2277;  
 Best Local Similarity 46.4%; Pred. No. 11;  
 RESULT 542  
 ID AAV05372 standard; RNA; 2277 BP.  
 DE Human telomerase p105 subunit mammalian optimised synthetic RNA.  
 PN WO9801542-A1.  
 PD 15-JAN-1998.  
 PA (REGC ) UNIV CALIFORNIA.  
 Query Match 5.2%; Score 51.2; DB 2; Length 2277;  
 Best Local Similarity 46.4%; Pred. No. 11;  
 RESULT 543  
 ID AAA07385 standard; DNA; 4467 BP.  
 DE Heterosigma akashiwo Nat-ATPase gene.  
 PN JP2000050874-A.  
 PD 22-FEB-2000.  
 PA (NORQ ) NORINSUISANSHO KOKUSAI NORIN SUISANGYO.  
 Query Match 5.2%; Score 51.2; DB 3; Length 4467;  
 Best Local Similarity 44.1%; Pred. No. 11;  
 RESULT 544  
 ID AAA58471 standard; DNA; 58857 BP.  
 DE Nucleotide sequence of the bleomycin (BLM) gene cluster ORFs 8-30.  
 PN WO200040704-A1.  
 PD 13-JUL-2000.  
 PA (REGC ) UNIV CALIFORNIA.  
 Query Match 5.2%; Score 51.2; DB 3; Length 58857;  
 Best Local Similarity 45.2%; Pred. No. 10;  
 RESULT 545  
 ID ADP03244 standard; DNA; 473 BP.  
 DE S. tridiae IF012773 L-glutamine DOI aminotransferase partial DNA.  
 PN JP2004089151-A.  
 PD 25-MAR-2004.  
 PA (TOKO ) TOKYO INST TECHNOLOGY.  
 Query Match 5.2%; Score 51; DB 12; Length 473;  
 Best Local Similarity 44.4%; Pred. No. 12;  
 RESULT 546  
 ID ABD13343 standard; DNA; 501 BP.  
 DE Pseudomonas aeruginosa polynucleotide #11947.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.2%; Score 51; DB 11; Length 501;  
 Best Local Similarity 48.5%; Pred. No. 12;  
 RESULT 547  
 ID AAV55831 standard; DNA; 799 BP.  
 DE Nucleotide sequence of the stabilising sequence-encoding insert.  
 PN WO9822577-A1.  
 PD 28-MAY-1998.  
 PA (MASU/) MASUCCI M G.  
 Query Match 5.2%; Score 51; DB 2; Length 799;  
 Best Local Similarity 46.1%; Pred. No. 12;  
 RESULT 548  
 ID ACA37639 standard; DNA; 1497 BP.  
 DE Prokaryotic essential gene #19296.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 5.2%; Score 51; DB 8; Length 1497;  
 Best Local Similarity 48.0%; Pred. No. 12;  
 RESULT 549  
 ID ABD13303 standard; DNA; 1500 BP.  
 DE Pseudomonas aeruginosa polynucleotide #11907.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.2%; Score 51; DB 11; Length 1500;  
 Best Local Similarity 48.5%; Pred. No. 12;  
 RESULT 550  
 ID ADJ40244 standard; cDNA; 1503 BP.

DE Plant cDNA #1244.  
 PN US2004016025-A1.  
 PD 22-JAN-2004.  
 PA (BUDW/) BUDWORTH P.  
 PA (MOUG/) MOUGHAWER T.  
 PA (BRIG/) BRIGGS S P.  
 PA (COOP/) COOPER B.  
 PA (GLAZ/) GLAZEBROOK J.  
 PA (GOFF/) GOFF S A.  
 PA (KATA/) KATAGIRI F.  
 PA (KREP/) KREPS J.  
 PA (PROV/) PROVART N.  
 PA (RICK/) RIQUE D.  
 PA (ZHUT/) ZHU T.  
 Query Match 5.2%; Score 51; DB 12; Length 1503;  
 Best Local Similarity 47.6%; Pred. No. 12;  
 RESULT 551  
 ID AAL44275 standard; DNA; 1632 BP.  
 DE Micrococcus luteus crtI gene sequence.  
 PN WO200241833-A2.  
 PD 30-MAY-2002.  
 PA (CRGI ) CARGILL INC.  
 Query Match 5.2%; Score 51; DB 6; Length 1632;  
 Best Local Similarity 42.9%; Pred. No. 12;  
 RESULT 552  
 ID ADG93408 standard; DNA; 1632 BP.  
 DE Maize lipoxygenase (LOX) DNA #20.  
 PN US2003166855-A1.  
 PD 04-SEP-2003.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Query Match 5.2%; Score 51; DB 10; Length 1632;  
 Best Local Similarity 45.9%; Pred. No. 12;  
 RESULT 553  
 ID AAL61149 standard; DNA; 1713 BP.  
 DE Human mutant ARX gene #2.  
 PN WO2003045989-A1.  
 PD 05-JUN-2003.  
 PA (WOME-) WOMEN'S & CHILDREN'S HOSPITAL.  
 Query Match 5.2%; Score 51; DB 9; Length 1713;  
 Best Local Similarity 46.2%; Pred. No. 12;  
 RESULT 554  
 ID ADS56497 standard; cDNA; 1755 BP.  
 DE Bacterial polynucleotide #8484.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match 5.2%; Score 51; DB 13; Length 1755;  
 Best Local Similarity 47.9%; Pred. No. 12;  
 RESULT 555  
 ID ADG93406 standard; DNA; 1803 BP.  
 DE Maize lipoxygenase (LOX) DNA #19.  
 PN US2003166855-A1.  
 PD 04-SEP-2003.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Query Match 5.2%; Score 51; DB 10; Length 1803;  
 Best Local Similarity 45.9%; Pred. No. 12;  
 RESULT 556  
 ID AAH26500 standard; cDNA; 2561 BP.  
 DE Rabbit low density lipoprotein binding protein 2 (LBP-2) cDNA.  
 PN WO200164874-A2.  
 PD 07-SEP-2001.  
 PA (BOST-) BOSTON HEART FOUND INC.  
 Query Match 5.2%; Score 51; DB 5; Length 2561;  
 Best Local Similarity 47.3%; Pred. No. 12;  
 RESULT 557  
 ID ABN85324 standard; cDNA; 2710 BP.  
 DE Human cytoskeleton-associated protein, CSAP-15, coding sequence.  
 PN WO200253719-A2.  
 PD 11-JUL-2002.

PA (INCY-) INCYTE GENOMICS INC.  
 Query Match 5.1%; Score 51; DB 6; Length 2710;  
 Best Local Similarity 45.7%; Pred. No. 12;  
 RESULT 558  
 ID AAL44298 standard; DNA; 6941 BP.  
 DE Micrococcus luteus C50 carotenoid producing operon.  
 PN WO200241833-A2.  
 PD 30-MAY-2002.  
 PA (CRGI) CARGILL INC.  
 Query Match 5.2%; Score 51; DB 6; Length 6941;  
 Best Local Similarity 42.9%; Pred. No. 12;  
 RESULT 559  
 ID AAQ73500 standard; DNA; 8438 BP.  
 DE DNA encoding Pseudorabies virus large latency transcript.  
 PN US5352596-A.  
 PD 04-OCT-1994.  
 PA (USDA) US SEC OF AGRIC.  
 Query Match 5.2%; Score 51; DB 2; Length 8438;  
 Best Local Similarity 44.8%; Pred. No. 12;  
 RESULT 560  
 ID ABX56062 standard; DNA; 741 BP.  
 DE M. echinospira calicheamicin biosynthesis gene orf11.  
 PN WO200279465-A2.  
 PD 10-OCT-2002.  
 PA (SLOK) SLOAN KETTERING INST CANCER RES.  
 Query Match 5.1%; Score 50.8; DB 8; Length 741;  
 Best Local Similarity 45.8%; Pred. No. 13;  
 RESULT 561  
 ID ACA43508 standard; DNA; 1125 BP.  
 DE Prokaryotic essential gene #25165.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 5.1%; Score 50.8; DB 8; Length 1125;  
 Best Local Similarity 50.0%; Pred. No. 13;  
 RESULT 562  
 ID AAT91453 standard; DNA; 1155 BP.  
 DE Mycobacterium tuberculosis antigen Tbra28 encoding DNA.  
 PN WO9709429-A2.  
 PD 13-MAR-1997.  
 PA (CORI-) CORIXA CORP.  
 Query Match 5.1%; Score 50.8; DB 2; Length 1155;  
 Best Local Similarity 49.3%; Pred. No. 13;  
 RESULT 563  
 ID AAT91517 standard; DNA; 1155 BP.  
 DE Mycobacterium tuberculosis antigen Tbra28 encoding DNA.  
 PN WO9709428-A2.  
 PD 13-MAR-1997.  
 PA (CORI-) CORIXA CORP.  
 Query Match 5.1%; Score 50.8; DB 2; Length 1155;  
 Best Local Similarity 49.3%; Pred. No. 13;  
 RESULT 564  
 ID AAV44350 standard; DNA; 1155 BP.  
 DE Mycobacterium tuberculosis antigen Tbra28 DNA.  
 PN WO9816645-A2.  
 PD 23-APR-1998.  
 PA (CORI-) CORIXA CORP.  
 Query Match 5.1%; Score 50.8; DB 2; Length 1155;  
 Best Local Similarity 49.3%; Pred. No. 13;  
 RESULT 565  
 ID AAV64458 standard; DNA; 1155 BP.  
 DE M. tuberculosis immunogenic polypeptide Tbra28 DNA.  
 PN WO9816646-A2.  
 PD 23-APR-1998.  
 PA (CORI-) CORIXA CORP.  
 Query Match 5.1%; Score 50.8; DB 2; Length 1155;  
 Best Local Similarity 49.3%; Pred. No. 13;  
 RESULT 566  
 ID AAZ19048 standard; DNA; 1155 BP.  
 DE M. tuberculosis recombinant antigen DNA encoding Tbra28.  
 PN WO9942118-A2.  
 PD 26-AUG-1999.  
 PA (CORI-) CORIXA CORP.

Query Match 5.1%; Score 50.8; DB 2; Length 1155;  
 Best Local Similarity 49.3%; Pred. No. 13;  
 RESULT 567  
 ID AAZ19260 standard; DNA; 1155 BP.  
 DE M. tuberculosis antigen Tbra28 DNA sequence.  
 PN WO9942076-A2.  
 PD 26-AUG-1999.  
 PA (CORI-) CORIXA CORP.  
 Query Match 5.1%; Score 50.8; DB 2; Length 1155;  
 Best Local Similarity 49.3%; Pred. No. 13;  
 RESULT 568  
 ID ADA70376 standard; DNA; 1173 BP.  
 DE Rice gene, SEQ ID 3699.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Query Match 5.1%; Score 50.8; DB 8; Length 1173;  
 Best Local Similarity 43.9%; Pred. No. 13;  
 RESULT 569  
 ID ADJ39706 standard; cDNA; 1173 BP.  
 DE Plant cDNA #706.  
 PN US2004016025-A1.  
 PD 22-JAN-2004.  
 PA (BUDW/) BUDWORTH P.  
 PA (MOUG/) MOUGHAMER T.  
 PA (BRIG/) BRIGGS S P.  
 PA (COOP/) COOPER B.  
 PA (GLAZ/) GLAZEBROOK J.  
 PA (GORE/) GORE S A.  
 PA (KATA/) KATAGIRI F.  
 PA (KREP/) KREPS J.  
 PA (PROV/) PROVART N.  
 PA (RICK/) RICK D.  
 PA (ZHUT/) ZHU T.  
 Query Match 5.1%; Score 50.8; DB 12; Length 1173;  
 Best Local Similarity 43.9%; Pred. No. 13;  
 RESULT 570  
 ID AAS51566 standard; DNA; 1317 BP.  
 DE Pseudomonas aeruginosa DNA for cellular proliferation protein #151.  
 PN WO200170955-A2.  
 PD 27-SEP-2001.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 5.1%; Score 50.8; DB 4; Length 1317;  
 Best Local Similarity 51.0%; Pred. No. 13;  
 RESULT 571  
 ID ACA19467 standard; DNA; 1317 BP.  
 DE Prokaryotic essential gene #1124.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 5.1%; Score 50.8; DB 8; Length 1317;  
 Best Local Similarity 51.0%; Pred. No. 13;  
 RESULT 572  
 ID ADA71150 standard; DNA; 1479 BP.  
 DE Rice gene, SEQ ID 4473.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Query Match 5.1%; Score 50.8; DB 8; Length 1479;  
 Best Local Similarity 46.7%; Pred. No. 13;  
 RESULT 573  
 ID AAL51696 standard; cDNA; 1682 BP.  
 DE Argiopoie trifasciata epider silk protein coding sequence #1.  
 PN WO200299082-A2.  
 PD 12-DEC-2002.  
 PA (UYWY-) UNIV WYOMING.  
 Query Match 5.1%; Score 50.8; DB 8; Length 1682;  
 Best Local Similarity 45.8%; Pred. No. 13;  
 RESULT 574  
 ID ABS78661 standard; DNA; 5760 BP.  
 DE M. echinospira DNA encoding PKSE protein.  
 PN CA2387401-A1.  
 PD 04-SEP-2002.

PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 5.1%; Score 50.8; DB 6; Length 5760;  
Best Local Similarity 45.0%; Pred. No. 13;  
RESULT 575  
ID ABS63414 standard; cDNA; 508 BP.  
DE DNA encoding rice caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAFALSKI J A.  
Query Match 5.1%; Score 50.6; DB 6; Length 508;  
Best Local Similarity 54.6%; Pred. No. 15;  
RESULT 576  
ID AAF74867 standard; DNA; 1313 BP.  
DE Leishmania major PPG nucleotide sequence.  
PN CN1272542-A.  
PD 08-NOV-2000.  
PA (NANF-) NANFANG RES CENT STATE HUMAN GENE GROUP.  
Query Match 5.1%; Score 50.6; DB 4; Length 1313;  
Best Local Similarity 47.1%; Pred. No. 14;  
RESULT 577  
ID ACA37566 standard; DNA; 1371 BP.  
DE Prokaryotic essential gene #19223.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.1%; Score 50.6; DB 8; Length 1371;  
Best Local Similarity 43.7%; Pred. No. 14;  
RESULT 578  
ID AAI92870 standard; cDNA; 2564 BP.  
DE Human polynucleotide SEQ ID NO 12930.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.1%; Score 50.6; DB 4; Length 2564;  
Best Local Similarity 48.6%; Pred. No. 14;  
RESULT 579  
ID ADQ21323 standard; DNA; 4233 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4143.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 5.1%; Score 50.6; DB 12; Length 4233;  
Best Local Similarity 47.3%; Pred. No. 14;  
RESULT 580  
ID ADQ25196 standard; DNA; 4244 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 8016.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 5.1%; Score 50.6; DB 12; Length 4244;  
Best Local Similarity 47.3%; Pred. No. 14;  
RESULT 581  
ID ADQ91678 standard; DNA; 11740 BP.  
DE Polyketide synthase related DNA contig 1, SEQ ID 1.  
PN WO2004065401-A1.  
PD 05-AUG-2004.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 5.1%; Score 50.6; DB 13; Length 11740;  
Best Local Similarity 45.3%; Pred. No. 13;  
RESULT 582  
ID ADJ39239 standard; cDNA; 549 BP.  
DE Plant cDNA #239.  
PN US2004016025-A1.  
PD 22-JAN-2004.  
PA (BUDW/) BUDWORTH P.  
PA (MOUG/) MOUGHAMER T.  
PA (BRIG/) BRIGGS S P.  
PA (COOP/) COOPER B.  
PA (GLAZ/) GLAZEBROOK J.  
PA (GOFF/) GOFF S A.  
PA (KATA/) KATAGIRI F.

PA (KREP/) KREPS J.  
PA (PROV/) PROVART N.  
PA (RICK/) RICKS D.  
PA (ZHUT/) ZHU T.  
Query Match 5.1%; Score 50.4; DB 12; Length 549;  
Best Local Similarity 47.6%; Pred. No. 16;  
RESULT 583  
ID ABZ66752 standard; DNA; 669 BP.  
DE Orthosomycin biosynthetic polynucleotide SEQ ID NO 166.  
PN WO200279505-A2.  
PD 10-OCT-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 5.1%; Score 50.4; DB 10; Length 669;  
Best Local Similarity 44.7%; Pred. No. 16;  
RESULT 584  
ID AAV62138 standard; DNA; 980 BP.  
DE HSV-2 strain S85 Contig ID 53 DNA sequence.  
PN WO9820016-A1.  
PD 14-MAY-1998.  
PA (SMIK-) SMITHKLINE BEECHAM CORP.  
Query Match 5.1%; Score 50.4; DB 2; Length 980;  
Best Local Similarity 49.0%; Pred. No. 15;  
RESULT 585  
ID ADI42416 standard; DNA; 1159 BP.  
DE Plant transcription factor polynucleotide #544.  
PN US2004019927-A1.  
PD 29-JAN-2004.  
PA (SHER/) SHERMAN B K.  
PA (RIEC/) RIECHMANN J L.  
PA (JIAN/) JIANG C.  
PA (HEAR/) HEARD J E.  
PA (HAAK/) HAAKE V.  
PA (CREE/) CREELMAN R A.  
PA (RATC/) RATCLIFFE O.  
PA (ADAM/) ADAM L J.  
PA (REUB/) REUBER T L.  
PA (KEDD/) KEDDIE J.  
PA (BROU/) BROUN P E.  
PA (PILG/) PILGRIM M L.  
PA (DUBE/) DUBELL A N.  
PA (PINE/) PINEDA O.  
PA (YUGG/) YU G.  
Query Match 5.1%; Score 50.4; DB 12; Length 1159;  
Best Local Similarity 47.0%; Pred. No. 15;  
RESULT 586  
ID ADC36273 standard; DNA; 1209 BP.  
DE Weed controller metabolism associated gene SEQ ID NO:141.  
PN WO2003040370-A1.  
PD 15-MAY-2003.  
PA (SUMO-) SUMITOMO CHEM CO LTD.  
Query Match 5.1%; Score 50.4; DB 10; Length 1209;  
Best Local Similarity 47.0%; Pred. No. 15;  
RESULT 587  
ID ADC36278 standard; DNA; 1473 BP.  
DE Weed controller metabolism associated gene SEQ ID NO:146.  
PN WO2003040370-A1.  
PD 15-MAY-2003.  
PA (SUMO-) SUMITOMO CHEM CO LTD.  
Query Match 5.1%; Score 50.4; DB 10; Length 1473;  
Best Local Similarity 47.0%; Pred. No. 15;  
RESULT 588  
ID AAL61177 standard; DNA; 2247 BP.  
DE Actinosynnema pretiosum ABC transporter gene.  
PN WO2003045312-A2.  
PD 05-JUN-2003.  
PA (UNIW-) UNIV WASHINGTON.  
Query Match 5.1%; Score 50.4; DB 8; Length 2247;  
Best Local Similarity 43.7%; Pred. No. 15;  
RESULT 589  
ID ACN37449 standard; cDNA; 4755 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA323899, SEQ ID NO:338.  
PN WO2004030615-A2.  
PD 15-APR-2004.



PA (GETH ) GENENTECH INC.  
 Query Match 5.1%; Score 50.4; DB 13; Length 4755;  
 Best Local Similarity 51.3%; Pred. No. 15;  
 RESULT 590  
 ID ADS14589 standard; DNA; 6375 BP.  
 DE Pseudomonas aeruginosa quorum sensing controlled gene PA2302, SEQ ID 144.  
 PN WO2004083385-A2.  
 PD 30-SEP-2004.  
 PA (IOWA ) UNIV IOWA RES FOUND.  
 Query Match 5.1%; Score 50.4; DB 13; Length 6375;  
 Best Local Similarity 50.7%; Pred. No. 15;  
 RESULT 591  
 ID AAF81370 standard; DNA; 6390 BP.  
 DE Quorum sensing controlled gene qsc107 ORF.  
 PN WO200118248-A2.  
 PD 15-MAR-2001.  
 PA (IOWA ) UNIV IOWA RES FOUND.  
 PA (QUOR-) QUORUM SCI INC.  
 Query Match 5.1%; Score 50.4; DB 4; Length 6390;  
 Best Local Similarity 50.7%; Pred. No. 15;  
 RESULT 592  
 ID ABZ75344 standard; DNA; 23673 BP.  
 DE Human R1128 gene cluster.  
 PN US6340774-B1.  
 PD 22-JAN-2002.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 Query Match 5.1%; Score 50.4; DB 6; Length 23673;  
 Best Local Similarity 47.7%; Pred. No. 14;  
 RESULT 593  
 ID ABZ66808 standard; DNA; 45055 BP.  
 DE Orthosomycin biosynthetic gene cluster SEQ ID NO 277.  
 PN WO200279505-A2.  
 PD 10-OCT-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 5.1%; Score 50.4; DB 10; Length 45055;  
 Best Local Similarity 44.7%; Pred. No. 14;  
 RESULT 594  
 Query Match 5.1%; Score 50.4; DB 4; Length 110000;  
 Best Local Similarity 45.1%; Pred. No. 14;  
 RESULT 595  
 ID ADJ42262 standard; cDNA; 595 BP.  
 DE Plant cDNA #3262.  
 PN US2004016025-A1.  
 PD 22-JAN-2004.  
 PA (BUDW/) BUDWORTH P.  
 PA (MOUG/) MOUGHAMER T.  
 PA (BRIG/) BRIGGS S P.  
 PA (COOP/) COOPER B.  
 PA (GLAZ/) GLAZEBROOK J.  
 PA (GOFF/) GOFF S A.  
 PA (KATA/) KATAGIRI F.  
 PA (KREP/) KREPS J.  
 PA (PROV/) PROVART N.  
 PA (RICK/) RICKE D.  
 PA (ZHUT/) ZHU T.  
 Query Match 5.1%; Score 50.2; DB 12; Length 595;  
 Best Local Similarity 50.5%; Pred. No. 17;  
 RESULT 596  
 ID ACA26748 standard; DNA; 841 BP.  
 DE Prokaryotic essential gene #8405.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 5.1%; Score 50.2; DB 8; Length 841;  
 Best Local Similarity 46.7%; Pred. No. 17;  
 RESULT 597  
 ID ABD12328 standard; DNA; 864 BP.  
 DE Pseudomonas aeruginosa polynucleotide #10932.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.1%; Score 50.2; DB 11; Length 864;  
 Best Local Similarity 47.1%; Pred. No. 17;  
 RESULT 598  
 ID AAF61096 standard; DNA; 1545 BP.  
 DE P. putida KT2440-associated DNA ORF11200.  
 PN DE19935088-A1.  
 PD 01-FEB-2001.  
 PA (TIGR-) TIGR INST GENOMIC RES.  
 PA (QUIA-) QUIAGEN GMBH.  
 PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
 PA (DKF2-) DKFZ DEUT KREBSFORSCHUNGSZENTRUM.  
 PA (MEDI-) MEDIZINISCHE HOCHSCHULE HANNOVER.  
 Query Match 5.1%; Score 50.2; DB 4; Length 1545;  
 Best Local Similarity 44.2%; Pred. No. 16;  
 RESULT 599  
 ID ADQ91680 standard; DNA; 2160 BP.  
 DE Polyketide synthase related ORF1, SEQ ID 3.  
 PN WO2004065401-A1.  
 PD 05-AUG-2004.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 5.1%; Score 50.2; DB 13; Length 2160;  
 Best Local Similarity 45.3%; Pred. No. 16;  
 RESULT 600  
 ID ABD12652 standard; DNA; 2211 BP.  
 DE Pseudomonas aeruginosa polynucleotide #11256.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.1%; Score 50.2; DB 11; Length 2211;  
 Best Local Similarity 47.1%; Pred. No. 16;  
 RESULT 601  
 ID ABD12391 standard; DNA; 2289 BP.  
 DE Pseudomonas aeruginosa polynucleotide #10995.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.1%; Score 50.2; DB 11; Length 2289;  
 Best Local Similarity 47.1%; Pred. No. 16;  
 RESULT 602  
 ID ADT43953 standard; cDNA; 3039 BP.  
 DE Bacterial polynucleotide #18704.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOX/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATKIN S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match 5.1%; Score 50.2; DB 13; Length 3039;  
 Best Local Similarity 47.1%; Pred. No. 16;  
 RESULT 603  
 ID ADS34438 standard; DNA; 3263 BP.  
 DE POSH protein associated DNA #192.  
 PN WO2004078130-A2.  
 PD 16-SEP-2004.  
 PA (PROT-) PROTEOLOGICS INC.  
 Query Match 5.1%; Score 50.2; DB 13; Length 3263;  
 Best Local Similarity 47.6%; Pred. No. 16;  
 RESULT 604  
 ID AAH14472 standard; cDNA; 3269 BP.  
 DE Human cDNA sequence SEQ ID NO:11967.  
 PN EP1074617-A2.  
 PD 07-FEB-2001.  
 PA (HELI-) HELIX RES INST.  
 Query Match 5.1%; Score 50.2; DB 4; Length 3269;  
 Best Local Similarity 47.6%; Pred. No. 16;  
 RESULT 605  
 ID ACN40510 standard; cDNA; 3269 BP.  
 DE Tumour-associated antigenic target (TAT) cDNA DNA326614, SEQ ID NO:5332.  
 PN WO2004030615-A2.  
 PD 15-APR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 5.1%; Score 50.2; DB 13; Length 3269;  
 Best Local Similarity 47.6%; Pred. No. 16;  
 RESULT 606

ID ADS34443 standard; DNA; 3269 BP.  
 DE POSH protein associated DNA #197.  
 PN WO2004078130-A2.  
 PD 16-SEP-2004.  
 PA (PROT-) PROTEOLOGICS INC.  
 Query Match 5.1%; Score 50.2; DB 13; Length 3269;  
 Best Local Similarity 47.6%; Pred. No. 16;  
 RESULT 607  
 ID ADR31451 standard; DNA; 4826 BP.  
 DE Streptomyces aureofaciens NRRL2209 Sau3A I genomic DNA fragment.  
 PN US2004157303-A1.  
 PD 12-AUG-2004.  
 PA (MAHL/) MAHISHI L. H.  
 PA (TRIP/) TRIPATHI G.  
 PA (RAMC/) RAMCHANDER T V N.  
 PA (RAWA/) RAWAL S K.  
 Query Match 5.1%; Score 50.2; DB 13; Length 4826;  
 Best Local Similarity 43.9%; Pred. No. 16;  
 RESULT 608  
 ID AAL61173 standard; DNA; 9975 BP.  
 DE Actinosynnema pretiosum polyketide synthase (PKS) gene #4.  
 PN WO2003045312-A2.  
 PD 05-JUN-2003.  
 PA (UNIW ) UNIV WASHINGTON.  
 Query Match 5.1%; Score 50.2; DB 8; Length 9975;  
 Best Local Similarity 46.0%; Pred. No. 16;  
 RESULT 609  
 ID ABX48858 standard; cDNA; 390 BP.  
 DE Bovine EST associated with lactation/muscle/fat deposition #14023.  
 PN US2002137139-A1.  
 PD 26-SEP-2002.  
 PA (BYAT/) BYATT J C.  
 PA (MATH/) MATHIALAGAN N.  
 PA (TAON/) TAO N.  
 PA (WARR/) WARREN W C.  
 Query Match 5.1%; Score 50; DB 8; Length 390;  
 Best Local Similarity 52.2%; Pred. No. 18;  
 RESULT 610  
 ID AAZ52552 standard; cDNA; 888 BP.  
 DE Human secreted protein clone yd61\_1 nucleotide sequence SEQ ID NO:155.  
 PN WO9958642-A2.  
 PD 18-NOV-1999.  
 PA (GEMY ) GENETICS INST INC.  
 Query Match 5.1%; Score 50; DB 3; Length 888;  
 Best Local Similarity 49.4%; Pred. No. 18;  
 RESULT 611  
 ID ADO00480 standard; cDNA; 1149 BP.  
 DE Novel human cDNA sequence #1295.  
 PN WO2004038003-A2.  
 PD 06-MAY-2004.  
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
 Query Match 5.1%; Score 50; DB 12; Length 1149;  
 Best Local Similarity 47.8%; Pred. No. 18;  
 RESULT 612  
 ID ADN98911 standard; cDNA; 1149 BP.  
 DE Novel human cDNA sequence #511.  
 PN WO2004038003-A2.  
 PD 06-MAY-2004.  
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
 Query Match 5.1%; Score 50; DB 12; Length 1149;  
 Best Local Similarity 47.8%; Pred. No. 18;  
 RESULT 613  
 ID ADS55971 standard; cDNA; 1317 BP.  
 DE Bacterial polynucleotide #7958.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match 5.1%; Score 50; DB 13; Length 1317;  
 Best Local Similarity 46.2%; Pred. No. 18;

RESULT 614  
 ID ADT44554 standard; cDNA; 1337 BP.  
 DE Bacterial polynucleotide #19305.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match 5.1%; Score 50; DB 13; Length 1337;  
 Best Local Similarity 49.2%; Pred. No. 18;  
 RESULT 615  
 ID ACA25880 standard; DNA; 1365 BP.  
 DE Prokaryotic essential gene #7537.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 5.1%; Score 50; DB 8; Length 1365;  
 Best Local Similarity 45.4%; Pred. No. 18;  
 RESULT 616  
 ID ADP28824 standard; DNA; 1470 BP.  
 DE Human secreted protein encoding sequence SEQ ID #822.  
 PN WO2004035732-A2.  
 PD 29-APR-2004.  
 PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
 Query Match 5.1%; Score 50; DB 12; Length 1470;  
 Best Local Similarity 47.8%; Pred. No. 18;  
 RESULT 617  
 ID ADI23924 standard; DNA; 1806 BP.  
 DE Streptomyces refuineus 024A locus ORF2.  
 PN US2003198981-A1.  
 PD 23-OCT-2003.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 5.1%; Score 50; DB 10; Length 1806;  
 Best Local Similarity 46.3%; Pred. No. 18;  
 RESULT 618  
 ID ADG98257 standard; DNA; 1806 BP.  
 DE Acyl-specific C-domain DNA #13.  
 PN US2003211567-A1.  
 PD 13-NOV-2003.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 5.1%; Score 50; DB 12; Length 1806;  
 Best Local Similarity 46.3%; Pred. No. 18;  
 RESULT 619  
 ID ADT44505 standard; cDNA; 2148 BP.  
 DE Bacterial polynucleotide #19256.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match 5.1%; Score 50; DB 13; Length 2148;  
 Best Local Similarity 50.9%; Pred. No. 18;  
 RESULT 620  
 ID AAZ87297 standard; DNA; 13842 BP.  
 DE S. venezuelae macrolide biosynthetic gene pikAI, SEQ ID NO:30.  
 PN WO20000620-A2.  
 PD 06-JAN-2000.  
 PA (MINU ) UNIV MINNESOTA.  
 Query Match 5.1%; Score 50; DB 3; Length 13842;  
 Best Local Similarity 44.7%; Pred. No. 17;  
 RESULT 621  
 ID ADL91915 standard; DNA; 13842 BP.  
 DE Streptomyces macrolide biosynthetic protein (PikR2) coding sequence.  
 PN US2003194784-A1.  
 PD 16-OCT-2003.  
 PA (SHER/) SHERMAN D H.  
 PA (LIUH/) LIU H.  
 PA (XUEY/) XUE Y.  
 PA (ZHAO/) ZHAO L.

Query Match 5.1%; Score 50; DB 12; Length 13842;  
Best Local Similarity 44.7%; Pred. No. 17;  
RESULT 622  
ID ADI23898 standard; DNA; 15738 BP.  
DE Streptomyces fradiae A541 locus ORF5.  
PN US200319891-A1.  
PD 23-OCT-2003.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 5.1%; Score 50; DB 10; Length 15738;  
Best Local Similarity 43.1%; Pred. No. 17;  
RESULT 623  
ID ADO51695 standard; DNA; 32329 BP.  
DE Streptomyces cattleya NRRL 8057 thienamycin biosynthetic gene cluster.  
PN US2004038250-A1.  
PD 26-FEB-2004.  
PA (ASTU-) ASTUR-PHARMA SA.  
PA (UYOV-) UNIV OVIEDO.  
Query Match 5.1%; Score 50; DB 12; Length 32329;  
Best Local Similarity 48.5%; Pred. No. 16;  
RESULT 624  
ID AAZ87318 standard; DNA; 36778 BP.  
DE S. venezuelae pik (macrolide biosynthesis) gene cluster.  
PN WO200000620-A2.  
PD 06-JAN-2000.  
PA (MINU) UNIV MINNESOTA.  
Query Match 5.1%; Score 50; DB 3; Length 36778;  
Best Local Similarity 44.7%; Pred. No. 16;  
RESULT 625  
ID ADL91933 standard; DNA; 36778 BP.  
DE Streptomyces venezuelae pik gene cluster coding sequence.  
PN US2003194784-A1.  
PD 16-OCT-2003.  
PA (SHER/) SHERMAN D H.  
PA (LIUH/) LIU H.  
PA (XUEY/) XUE Y.  
PA (ZHAO/) ZHAO L.  
Query Match 5.1%; Score 50; DB 12; Length 36778;  
Best Local Similarity 44.7%; Pred. No. 16;  
RESULT 626  
ID ADI23892 standard; DNA; 37360 BP.  
DE Streptomyces fradiae A541 locus contig 2.  
PN US200319891-A1.  
PD 23-OCT-2003.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 5.1%; Score 50; DB 10; Length 37360;  
Best Local Similarity 43.1%; Pred. No. 16;  
RESULT 627  
ID AAZ87285 standard; DNA; 37948 BP.  
DE S. venezuelae pik (macrolide biosynthesis) gene cluster, SEQ ID NO:5.  
PN WO200000620-A2.  
PD 06-JAN-2000.  
PA (MINU) UNIV MINNESOTA.  
Query Match 5.1%; Score 50; DB 3; Length 37948;  
Best Local Similarity 44.7%; Pred. No. 16;  
RESULT 628  
ID AAA75633 standard; DNA; 38506 BP.  
DE Nucleotide sequence of the insert DNA in cosmid pKOS023-27.  
PN US6117659-A.  
PD 12-SEP-2000.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
Query Match 5.1%; Score 50; DB 3; Length 38506;  
Best Local Similarity 44.7%; Pred. No. 16;  
RESULT 629  
ID AAZ56001 standard; DNA; 38506 BP.  
DE Recombinant cosmid pKOS023-27 containing S. venezuelae PKS genes.  
PN WO961599-A2.  
PD 02-DEC-1999.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
Query Match 5.1%; Score 50; DB 3; Length 38506;  
Best Local Similarity 44.7%; Pred. No. 16;  
RESULT 630  
ID ADA09418 standard; DNA; 38506 BP.  
DE Cosmid pKOS023-27 containing S. venezuelae PKS gene cluster.

PN US6509455-B1.  
PD 21-JAN-2003.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
Query Match 5.1%; Score 50; DB 8; Length 38506;  
Best Local Similarity 44.7%; Pred. No. 16;  
RESULT 631  
ID ADH53462 standard; DNA; 38506 BP.  
DE S. venezuelae pKOS023-27 cosmid DNA.  
PN US2003162262-A1.  
PD 28-AUG-2003.  
PA (ASHL/) ASHLEY G.  
PA (BETL/) BETLACH M C.  
PA (BETL/) BETLACH M R.  
PA (MCDA/) MCDANIEL R.  
PA (TANG/) TANG L.  
Query Match 5.1%; Score 50; DB 10; Length 38506;  
Best Local Similarity 44.7%; Pred. No. 16;  
RESULT 632  
ID ABS56090 standard; DNA; 38506 BP.  
DE S. venezuelae DNA inserted into cosmid pKOS023-27.  
PN WO200297062-A2.  
PD 05-DEC-2002.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
Query Match 5.1%; Score 50; DB 10; Length 38506;  
Best Local Similarity 44.7%; Pred. No. 16;  
RESULT 633  
ID ABQ74179 standard; DNA; 229354 BP.  
DE Human cytomegalovirus strain AD169 genomic sequence SEQ ID NO:64.  
PN WO200257437-A2.  
PD 25-JUL-2002.  
PA (SCRI) SCRIPPS RES INST.  
Query Match 5.1%; Score 50; DB 6; Length 229354;  
Best Local Similarity 46.1%; Pred. No. 15;  
RESULT 634  
ID ABQ90211 standard; DNA; 825 BP.  
DE M. capesulatus gene #196 for DNA array.  
PN WO200255655-A2.  
PD 18-JUL-2002.  
PA (UNIF-) UNIFOB STIFTELSEN UNIV BERGEN.  
PA (TIGR-) TIGR.  
Query Match 5.0%; Score 49.8; DB 6; Length 825;  
Best Local Similarity 49.2%; Pred. No. 19;  
RESULT 635  
ID ABK34330 standard; cDNA; 856 BP.  
DE Human cDNA for novel secreted protein, SEQ ID 99.  
PN WO200177290-A2.  
PD 18-OCT-2001.  
PA (GEMY) GENETICS INST INC.  
Query Match 5.0%; Score 49.8; DB 6; Length 856;  
Best Local Similarity 50.5%; Pred. No. 19;  
RESULT 636  
ID ABZ66685 standard; DNA; 1272 BP.  
DE Orthosomycin biosynthetic polynucleotide SEQ ID NO 32.  
PN WO200279505-A2.  
PD 10-OCT-2002.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 5.0%; Score 49.8; DB 10; Length 1272;  
Best Local Similarity 45.5%; Pred. No. 19;  
RESULT 637  
ID AAD53025 standard; DNA; 1293 BP.  
DE Streptomyces platensis ema9 gene.  
PN WO200292801-A2.  
PD 21-NOV-2002.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 5.0%; Score 49.8; DB 8; Length 1293;  
Best Local Similarity 48.7%; Pred. No. 19;  
RESULT 638  
ID ACA26585 standard; DNA; 1374 BP.  
DE Prokaryotic essential gene #8242.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.0%; Score 49.8; DB 8; Length 1374;

Best Local Similarity 51.1%; Pred. No. 19;  
 RESULT 639  
 ID ADA70992 standard; DNA; 1458 BP.  
 DE Rice gene, SEQ ID 4315.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 Query Match 5.0%; Score 49.8; DB 8; Length 1458;  
 Best Local Similarity 48.1%; Pred. No. 19;  
 RESULT 640  
 ID ADI27212 standard; DNA; 1581 BP.  
 DE Rabbit LRP binding family protein DNA #1.  
 PN WO2003106657-A2.  
 PD 24-DEC-2003.  
 PA (STOW-) STOWERS INST MEDICAL RES.  
 Query Match 5.0%; Score 49.8; DB 12; Length 1581;  
 Best Local Similarity 46.2%; Pred. No. 19;  
 RESULT 641  
 ID ABV94776 standard; cDNA; 1814 BP.  
 DE Human pancreatic cancer expressed cDNA SEQ ID NO 182.  
 PN WO200260317-A2.  
 PD 08-AUG-2002.  
 PA (CORI-) CORIXA CORP.  
 Query Match 5.0%; Score 49.8; DB 6; Length 1814;  
 Best Local Similarity 47.5%; Pred. No. 19;  
 RESULT 642  
 ID ADPI0373 standard; DNA; 1837 BP.  
 DE Reference mRNA sequences for marker probe #50.  
 PN WO2004042346-A2.  
 PD 21-MAY-2004.  
 PA (EXPR-) EXPRESSION DIAGNOSTICS INC.  
 Query Match 5.0%; Score 49.8; DB 12; Length 1837;  
 Best Local Similarity 47.5%; Pred. No. 19;  
 RESULT 643  
 ID AAF26295 standard; DNA; 2048 BP.  
 DE Pseudomonas sp Type II (xcp) secretion system DNA ORF04962a.  
 PN WO200107622-A2.  
 PD 01-FEB-2001.  
 PA (TIGR-) TIGR INST GENOMIC RES.  
 PA (QUIA-) QUIAGEN GMBH.  
 PA (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
 PA (DKFZ-) DKFZ DEUT KREBSFORSCHUNGSZENTRUM.  
 PA (MEDI-) MEDIZINISCHE HOCHSCHULE HANNOVER.  
 Query Match 5.0%; Score 49.8; DB 4; Length 2048;  
 Best Local Similarity 43.1%; Pred. No. 19;  
 RESULT 644  
 ID ADA71072 standard; DNA; 2136 BP.  
 DE Rice gene, SEQ ID 4395.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 Query Match 5.0%; Score 49.8; DB 8; Length 2136;  
 Best Local Similarity 47.8%; Pred. No. 19;  
 RESULT 645  
 ID ABL61822 standard; DNA; 2520 BP.  
 DE Colon adenocarcinoma related gene sequence SEQ ID NO:159.  
 PN WO200194629-A2.  
 PD 13-DEC-2001.  
 PA (AVAL-) AVALON PHARM.  
 Query Match 5.0%; Score 49.8; DB 6; Length 2520;  
 Best Local Similarity 48.7%; Pred. No. 19;  
 RESULT 646  
 ID ABR84011 standard; cDNA; 2520 BP.  
 DE Human cDNA differentially expressed in granulocytic cells #582.  
 PN WO200228999-A2.  
 PD 11-APR-2002.  
 PA (GENE-) GENE LOGIC INC.  
 Query Match 5.0%; Score 49.8; DB 6; Length 2520;  
 Best Local Similarity 48.7%; Pred. No. 19;  
 RESULT 647  
 ID ABD16186 standard; DNA; 3003 BP.  
 DE Pseudomonas aeruginosa polynucleotide #14790.  
 PN US6551795-B1.

PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.0%; Score 49.8; DB 11; Length 3003;  
 Best Local Similarity 49.1%; Pred. No. 19;  
 RESULT 648  
 ID AAD28566 standard; DNA; 3113 BP.  
 DE Herpes simplex virus type 2 UL46fragFl1F5 DNA.  
 PN WO200202131-A2.  
 PD 10-JAN-2002.  
 PA (CORI-) CORIXA CORP.  
 Query Match 5.0%; Score 49.8; DB 6; Length 3113;  
 Best Local Similarity 43.8%; Pred. No. 19;  
 RESULT 649  
 ID ADG74980 standard; DNA; 3113 BP.  
 DE Human herpesvirus 2 isolated clone insert DNA - SEQ ID 52.  
 PN WO2003086308-A2.  
 PD 23-OCT-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match 5.0%; Score 49.8; DB 10; Length 3113;  
 Best Local Similarity 43.8%; Pred. No. 19;  
 RESULT 650  
 ID ABD15936 standard; DNA; 3132 BP.  
 DE Pseudomonas aeruginosa polynucleotide #14540.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.0%; Score 49.8; DB 11; Length 3132;  
 Best Local Similarity 49.1%; Pred. No. 19;  
 RESULT 651  
 ID AAT86704 standard; DNA; 3147 BP.  
 DE DNA encoding thermostable esterase Tspa E101.  
 PN WO9725058-A1.  
 PD 17-JUL-1997.  
 PA (THER-) THERMOGEN INC.  
 Query Match 5.0%; Score 49.8; DB 2; Length 3147;  
 Best Local Similarity 46.4%; Pred. No. 19;  
 RESULT 652  
 ID AAO3399 standard; DNA; 3147 BP.  
 DE Thermus DNA encoding a thermostable esterase, Tspa/E101.  
 PN US6218163-B1.  
 PD 17-APR-2001.  
 PA (THER-) THERMOGEN INC.  
 Query Match 5.0%; Score 49.8; DB 4; Length 3147;  
 Best Local Similarity 46.4%; Pred. No. 19;  
 RESULT 653  
 ID AAD28565 standard; DNA; 3345 BP.  
 DE Herpes simplex virus type 2 full length HSV-2 UL37 gene.  
 PN WO200202131-A2.  
 PD 10-JAN-2002.  
 PA (CORI-) CORIXA CORP.  
 Query Match 5.0%; Score 49.8; DB 6; Length 3345;  
 Best Local Similarity 43.8%; Pred. No. 19;  
 RESULT 654  
 ID ADG75117 standard; DNA; 3345 BP.  
 DE Human herpesvirus 2 UL37 ORF DNA - SEQ ID 189.  
 PN WO2003086308-A2.  
 PD 23-OCT-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match 5.0%; Score 49.8; DB 10; Length 3345;  
 Best Local Similarity 43.8%; Pred. No. 19;  
 RESULT 655  
 ID ADG74977 standard; DNA; 3345 BP.  
 DE Human herpesvirus 2 UL37 DNA - SEQ ID 49.  
 PN WO2003086308-A2.  
 PD 23-OCT-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match 5.0%; Score 49.8; DB 10; Length 3345;  
 Best Local Similarity 43.8%; Pred. No. 19;  
 RESULT 656  
 ID ABD16219 standard; DNA; 3411 BP.  
 DE Pseudomonas aeruginosa polynucleotide #14823.  
 PN US6551795-B1.  
 PD 22-APR-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.0%; Score 49.8; DB 11; Length 3411;  
 Best Local Similarity 49.1%; Pred. No. 19;  
 RESULT 657  
 ID ADO85407 standard; DNA; 3540 BP.  
 DE Streptomyces Phox/Phor operon containing DNA fragment, seq id 1.  
 PN FR2848567-A1.  
 PD 18-JUN-2004.  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 Query Match 5.0%; Score 49.8; DB 12; Length 3540;  
 Best Local Similarity 44.5%; Pred. No. 19;  
 RESULT 658  
 ID AAV62148 standard; DNA; 3663 BP.  
 DE HSV-2 strain SB5 Contig ID 94 DNA sequence.  
 PN WO9820016-A1.  
 PD 14-MAY-1998.  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 Query Match 5.0%; Score 49.8; DB 2; Length 3663;  
 Best Local Similarity 43.8%; Pred. No. 19;  
 RESULT 659  
 ID ACA38707 standard; DNA; 4323 BP.  
 DE Prokaryotic essential gene #20364.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 5.0%; Score 49.8; DB 8; Length 4323;  
 Best Local Similarity 43.3%; Pred. No. 19;  
 RESULT 660  
 ID ADO85409 standard; DNA; 4440 BP.  
 DE Streptomyces phor::omegaaac mutant, seq id 4.  
 PN FR2848567-A1.  
 PD 18-JUN-2004.  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 Query Match 5.0%; Score 49.8; DB 12; Length 4440;  
 Best Local Similarity 44.5%; Pred. No. 19;  
 RESULT 661  
 ID ADQ91711 standard; DNA; 9684 BP.  
 DE Polyketide synthase ORF16, SEQ ID 34.  
 PN WO2004065401-A1.  
 PD 05-AUG-2004.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 5.0%; Score 49.8; DB 13; Length 9684;  
 Best Local Similarity 45.5%; Pred. No. 18;  
 RESULT 662  
 ID ABZ66810 standard; DNA; 37116 BP.  
 DE Orthosomycin biosynthetic gene cluster SEQ ID NO 279.  
 PN WO200279505-A2.  
 PD 10-OCT-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 5.0%; Score 49.8; DB 10; Length 37116;  
 Best Local Similarity 45.5%; Pred. No. 18;  
 RESULT 663  
 ID AAD17184 standard; DNA; 65140 BP.  
 DE Streptomyces noursei nysl DNA of nystatin PKS gene cluster.  
 PN WO200159126-A2.  
 PD 16-AUG-2001.  
 PA (UYNO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.  
 PA (SNTF ) SINTEF STIFTELSEN IND TEK FORSK.  
 PA (ALPH-) ALPHARMA AS.  
 PA (SINV-) SINVENT AS.  
 PA (DZIE/) DZIEGLEWSKA H.  
 PA (ZOTC/) ZOTCHEV S B.  
 PA (SEKU/) SEKUROVA O N.  
 PA (FJAE/) FJAERVIK E.  
 PA (BRAU/) BRAUTASET T.  
 PA (STRO/) STROM A R.  
 PA (VALL/) VALLA S.  
 Query Match 5.0%; Score 49.8; DB 4; Length 65140;  
 Best Local Similarity 46.4%; Pred. No. 17;  
 RESULT 664  
 ID AAD17186 standard; DNA; 125401 BP.  
 DE Streptomyces noursei nystatin PKS gene cluster DNA.  
 PN WO200159126-A2.

PD 16-AUG-2001.  
 PA (UYNO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.  
 PA (SNTF ) SINTEF STIFTELSEN IND TEK FORSK.  
 PA (ALPH-) ALPHARMA AS.  
 PA (SINV-) SINVENT AS.  
 PA (DZIE/) DZIEGLEWSKA H.  
 PA (ZOTC/) ZOTCHEV S B.  
 PA (SEKU/) SEKUROVA O N.  
 PA (FJAE/) FJAERVIK E.  
 PA (BRAU/) BRAUTASET T.  
 PA (STRO/) STROM A R.  
 PA (VALL/) VALLA S.  
 Query Match 5.0%; Score 49.8; DB 4; Length 125401;  
 Best Local Similarity 46.4%; Pred. No. 17;  
 RESULT 665  
 ID ADQ91695 standard; DNA; 164051 BP.  
 DE Polyketide synthase related DNA contig 2, SEQ ID 18.  
 PN WO2004065401-A1.  
 PD 05-AUG-2004.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 5.0%; Score 49.8; DB 13; Length 164051;  
 Best Local Similarity 45.5%; Pred. No. 17;  
 RESULT 666  
 ID ADS65765 standard; cDNA; 242 BP.  
 DE Corn seedling-derived polynucleotide (cpds), SEQ ID 781.  
 PN US2003237110-A9.  
 PD 25-DEC-2003.  
 PA (INCY-) INCVTE PHARM INC.  
 Query Match 5.0%; Score 49.6; DB 7; Length 242;  
 Best Local Similarity 54.0%; Pred. No. 22;  
 RESULT 667  
 ID ABD03617 standard; DNA; 678 BP.  
 DE Pseudomonas aeruginosa polynucleotide #2221.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.0%; Score 49.6; DB 11; Length 678;  
 Best Local Similarity 44.8%; Pred. No. 21;  
 RESULT 668  
 ID ABD03778 standard; DNA; 753 BP.  
 DE Pseudomonas aeruginosa polynucleotide #2382.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.0%; Score 49.6; DB 11; Length 753;  
 Best Local Similarity 44.8%; Pred. No. 21;  
 RESULT 669  
 ID ACA45724 standard; DNA; 1362 BP.  
 DE Prokaryotic essential gene #27381.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 5.0%; Score 49.6; DB 8; Length 1362;  
 Best Local Similarity 48.3%; Pred. No. 21;  
 RESULT 670  
 ID ADS56076 standard; cDNA; 1404 BP.  
 DE Bacterial polynucleotide #8063.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match 5.0%; Score 49.6; DB 13; Length 1404;  
 Best Local Similarity 45.9%; Pred. No. 21;  
 RESULT 671  
 ID ADB58045 standard; DNA; 1531 BP.  
 DE Toxicity-related gene, SEQ ID 3071.  
 PN WO2003064624-A2.  
 PD 07-AUG-2003.  
 PA (GENE-) GENE LOGIC INC.  
 Query Match 5.0%; Score 49.6; DB 10; Length 1531;

Best Local Similarity 47.2%; Pred. No. 21;  
 RESULT 672  
 ID ADB52519 standard; DNA; 1531 BP.  
 DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3061.  
 PN WO2003065993-A2.  
 PD 14-AUG-2003.  
 PA (GENE-) GENE LOGIC INC.  
 Query Match 5.0%; Score 49.6; DB 10; Length 1531;  
 Best Local Similarity 47.2%; Pred. No. 21;  
 RESULT 673  
 ID AAQ13305 standard; DNA; 1591 BP.  
 DE Rat catechol-O-methyltransferase gene.  
 PN WO9111513-A.  
 PD 08-AUG-1991.  
 PA (ORIN ) ORION YHTYMAE OY.  
 Query Match 5.0%; Score 49.6; DB 2; Length 1591;  
 Best Local Similarity 47.2%; Pred. No. 21;  
 RESULT 674  
 ID ADR25526 standard; DNA; 1743 BP.  
 DE Breast cancer prognosis marker #1387.  
 PN WO2004065545-A2.  
 PD 05-AUG-2004.  
 PA (ROSE-) ROSETTA INPHARMATICS LLC.  
 PA (NECA-) NETHERLANDS CANCER INST.  
 Query Match 5.0%; Score 49.6; DB 13; Length 1743;  
 Best Local Similarity 49.6%; Pred. No. 21;  
 RESULT 675  
 ID ADG75153 standard; DNA; 1765 BP.  
 DE Human herpesvirus 2 isolated clone insert DNA - SEQ ID 225.  
 PN WO2003086308-A2.  
 PD 23-OCT-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match 5.0%; Score 49.6; DB 10; Length 1765;  
 Best Local Similarity 45.6%; Pred. No. 21;  
 RESULT 676  
 ID AAS51445 standard; DNA; 2040 BP.  
 DE Pseudomonas aeruginosa DNA for cellular proliferation protein #30.  
 PN WO200170955-A2.  
 PD 27-SEP-2001.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 5.0%; Score 49.6; DB 4; Length 2040;  
 Best Local Similarity 44.6%; Pred. No. 21;  
 RESULT 677  
 ID ACA19446 standard; DNA; 2040 BP.  
 DE Prokaryotic essential gene #1103.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 5.0%; Score 49.6; DB 8; Length 2040;  
 Best Local Similarity 44.6%; Pred. No. 21;  
 RESULT 678  
 ID ADM03489 standard; cDNA; 2218 BP.  
 DE Human cDNA of the invention SEQ ID NO:2174.  
 PN EP1347046-A1.  
 PD 24-SEP-2003.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 Query Match 5.0%; Score 49.6; DB 11; Length 2218;  
 Best Local Similarity 43.5%; Pred. No. 20;  
 RESULT 679  
 ID ABZ35021 standard; cDNA; 2271 BP.  
 DE Human gene expression profile polynucleotide SEQ ID NO 133.  
 PN WO200274979-A2.  
 PD 26-SEP-2002.  
 PA (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.  
 Query Match 5.0%; Score 49.6; DB 6; Length 2271;  
 Best Local Similarity 47.2%; Pred. No. 20;  
 RESULT 680  
 ID ADB75311 standard; cDNA; 2487 BP.  
 DE Prostate cancer marker cDNA.  
 PN WO2003009814-A2.  
 PD 06-FEB-2003.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 5.0%; Score 49.6; DB 10; Length 2487;  
 Best Local Similarity 44.7%; Pred. No. 20;  
 RESULT 681  
 ID ADR25184 standard; DNA; 2487 BP.  
 DE Breast cancer prognosis marker #1045.  
 PN WO2004065545-A2.  
 PD 05-AUG-2004.  
 PA (ROSE-) ROSETTA INPHARMATICS LLC.  
 PA (NECA-) NETHERLANDS CANCER INST.  
 Query Match 5.0%; Score 49.6; DB 13; Length 2487;  
 Best Local Similarity 47.2%; Pred. No. 20;  
 RESULT 682  
 ID AAS51581 standard; DNA; 2742 BP.  
 DE Pseudomonas aeruginosa DNA for cellular proliferation protein #166.  
 PN WO200170955-A2.  
 PD 27-SEP-2001.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 5.0%; Score 49.6; DB 4; Length 2742;  
 Best Local Similarity 44.8%; Pred. No. 20;  
 RESULT 683  
 ID ACA19538 standard; DNA; 2742 BP.  
 DE Prokaryotic essential gene #1195.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 5.0%; Score 49.6; DB 8; Length 2742;  
 Best Local Similarity 44.8%; Pred. No. 20;  
 RESULT 684  
 ID ABD03933 standard; DNA; 2814 BP.  
 DE Pseudomonas aeruginosa polynucleotide #2537.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.0%; Score 49.6; DB 11; Length 2814;  
 Best Local Similarity 44.8%; Pred. No. 20;  
 RESULT 685  
 ID ADS55878 standard; cDNA; 3459 BP.  
 DE Bacterial polynucleotide #7865.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match 5.0%; Score 49.6; DB 13; Length 3459;  
 Best Local Similarity 45.7%; Pred. No. 20;  
 RESULT 686  
 ID ADJ67856 standard; DNA; 3729 BP.  
 DE T. thermophilus dnaE gene.  
 PN US2004038289-A1.  
 PD 26-FEB-2004.  
 PA (ODON/) O'DONNELL M E.  
 PA (YUZH/) YUZHAKOV A.  
 PA (YURI/) YURIEVA O.  
 PA (JERU/) JERUZALMI D.  
 PA (BRUC/) BRUCK I.  
 PA (KURI/) KURIYAN J.  
 Query Match 5.0%; Score 49.6; DB 12; Length 3729;  
 Best Local Similarity 44.7%; Pred. No. 20;  
 RESULT 687  
 ID ADJ68068 standard; DNA; 3729 BP.  
 DE T. thermophilus dnaE gene.  
 PN US2004038290-A1.  
 PD 26-FEB-2004.  
 PA (ODON/) O'DONNELL M E.  
 PA (YUZH/) YUZHAKOV A.  
 PA (YURI/) YURIEVA O.  
 PA (JERU/) JERUZALMI D.  
 PA (BRUC/) BRUCK I.  
 PA (KURI/) KURIYAN J.  
 Query Match 5.0%; Score 49.6; DB 12; Length 3729;  
 Best Local Similarity 44.7%; Pred. No. 20;  
 RESULT 688

ID ADK01146 standard; DNA; 3729 BP.  
DE DNA polymerase III-type enzyme subunit DNA #6.  
PN US2004043415-A1.  
PD 04-MAR-2004.  
PA (ODON/) O'DONNELL M E.  
PA (YUZH/) YUZHAKOV A.  
PA (YURI/) YURIEVA O.  
PA (JERU/) JERUZALMI D.  
PA (BRUC/) BRUCK I.  
PA (KURI/) KURIYAN J.  
Query Match 5.0%; Score 49.6; DB 12; Length 3729;  
Best Local Similarity 44.7%; Pred. No. 20;  
RESULT 689  
ID ADJ79365 standard; DNA; 3729 BP.  
DE T. thermophilus dnaE gene.  
PN US2004043414-A1.  
PD 04-MAR-2004.  
PA (ODON/) O'DONNELL M E.  
PA (YUZH/) YUZHAKOV A.  
PA (YURI/) YURIEVA O.  
PA (JERU/) JERUZALMI D.  
PA (BRUC/) BRUCK I.  
PA (KURI/) KURIYAN J.  
Query Match 5.0%; Score 49.6; DB 12; Length 3729;  
Best Local Similarity 44.7%; Pred. No. 20;  
RESULT 690  
ID ADJ84805 standard; DNA; 3729 BP.  
DE T. thermophilus DNA polymerase III alpha subunit gene.  
PN US2004048309-A1.  
PD 11-MAR-2004.  
PA (ODON/) O'DONNELL M E.  
PA (YUZH/) YUZHAKOV A.  
PA (YURI/) YURIEVA O.  
PA (JERU/) JERUZALMI D.  
PA (BRUC/) BRUCK I.  
PA (KURI/) KURIYAN J.  
Query Match 5.0%; Score 49.6; DB 12; Length 3729;  
Best Local Similarity 44.7%; Pred. No. 20;  
RESULT 691  
ID ADJ7593 standard; DNA; 3729 BP.  
DE DNA polymerase III-type enzyme related polynucleotide #4.  
PN US2004077012-A1.  
PD 22-APR-2004.  
PA (ODON/) O'DONNELL M E.  
PA (YUZH/) YUZHAKOV A.  
PA (YURI/) YURIEVA O.  
PA (JERU/) JERUZALMI D.  
PA (BRUC/) BRUCK I.  
PA (KURI/) KURIYAN J.  
Query Match 5.0%; Score 49.6; DB 12; Length 3729;  
Best Local Similarity 44.7%; Pred. No. 20;  
RESULT 692  
ID ADM66260 standard; DNA; 3729 BP.  
DE T. thermophilus dnaE gene.  
PN US2004081995-A1.  
PD 29-APR-2004.  
PA (ODON/) O'DONNELL M E.  
PA (YUZH/) YUZHAKOV A.  
PA (YURI/) YURIEVA O.  
PA (JERU/) JERUZALMI D.  
PA (BRUC/) BRUCK I.  
PA (KURI/) KURIYAN J.  
Query Match 5.0%; Score 49.6; DB 12; Length 3729;  
Best Local Similarity 44.7%; Pred. No. 20;  
RESULT 693  
ID ADO04313 standard; DNA; 3729 BP.  
DE T. thermophilus DNA polymerase III dnaE gene.  
PN US2004106137-A1.  
PD 03-JUN-2004.  
PA (ODON/) O'DONNELL M E.  
PA (YUZH/) YUZHAKOV A.  
PA (YURI/) YURIEVA O.  
PA (JERU/) JERUZALMI D.  
PA (BRUC/) BRUCK I.  
PA (KURI/) KURIYAN J.  
Query Match 5.0%; Score 49.6; DB 12; Length 3729;  
Best Local Similarity 44.7%; Pred. No. 20;

PA (BRUC/) BRUCK I.  
PA (KURI/) KURIYAN J.  
Query Match 5.0%; Score 49.6; DB 12; Length 3729;  
Best Local Similarity 44.7%; Pred. No. 20;  
RESULT 694  
ID ADP82390 standard; DNA; 3729 BP.  
DE Thermus thermophilus dnaE gene.  
PN US2004110210-A1.  
PD 10-JUN-2004.  
PA (ODON/) O'DONNELL M E.  
PA (YUZH/) YUZHAKOV A.  
PA (YURI/) YURIEVA O.  
PA (JERU/) JERUZALMI D.  
PA (BRUC/) BRUCK I.  
PA (KURI/) KURIYAN J.  
Query Match 5.0%; Score 49.6; DB 12; Length 3729;  
Best Local Similarity 44.7%; Pred. No. 20;  
RESULT 695  
ID ABN59919 standard; cDNA; 5080 BP.  
DE Novel human coding sequence SEQ ID NO: 330.  
PN WO200222660-A2.  
PD 21-MAR-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.0%; Score 49.6; DB 6; Length 5080;  
Best Local Similarity 44.2%; Pred. No. 20;  
RESULT 696  
ID ADF82340 standard; DNA; 5081 BP.  
DE Leukaemia-related DNA sequence #2896.  
PN WO2003039443-A2.  
PD 15-MAY-2003.  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.  
PA (HAPE/) HAERLACH T.  
PA (SCHO/) SCHOCH C.  
PA (KEEN/) KERN W.  
Query Match 5.0%; Score 49.6; DB 10; Length 5081;  
Best Local Similarity 44.2%; Pred. No. 20;  
RESULT 697  
ID ABL68935 standard; DNA; 5181 BP.  
DE Kidney cancer related gene sequence SEQ ID NO: 7272.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Query Match 5.0%; Score 49.6; DB 6; Length 5181;  
Best Local Similarity 47.2%; Pred. No. 20;  
RESULT 698  
ID ADJ11677 standard; DNA; 951 BP.  
DE Rice DNA modulated by post-transcriptional gene silencing SeqID 313.  
PN US2003135888-A1.  
PD 17-JUL-2003.  
PA (ZHUT/) ZHU T.  
PA (WANG/) WANG X.  
PA (CHAN/) CHANG H.  
PA (BRIG/) BRIGGS S P.  
PA (COOP/) COOPER B.  
PA (GLAZ/) GLAZEBROOK J.  
PA (GOFF/) GOFF S A.  
PA (KATA/) KATAGIRI F.  
PA (KREP/) KREPS J.  
PA (MOUG/) MOUGHAMER T.  
PA (PROV/) PROVART N.  
PA (RICK/) RICHE D.  
Query Match 5.0%; Score 49.4; DB 11; Length 951;  
Best Local Similarity 44.3%; Pred. No. 23;  
RESULT 699  
ID ADR01286 standard; DNA; 978 BP.  
DE Farnesyl dibenzodiazepinone biosynthetic ORF37 protein UNIQ DNA.  
PN WO2004065591-A1.  
PD 05-AUG-2004.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 5.0%; Score 49.4; DB 13; Length 978;  
Best Local Similarity 49.4%; Pred. No. 23;  
RESULT 700



ID ABZ37556 standard; DNA; 1029 BP.  
DE Streptomyces viridochromogenes AvigT4 encoding polynucleotide.  
PN WO200268436-A1.  
PD 06-SEP-2002.  
PA (COMB-) COMBINATURE BIOPHARM AG.  
Query Match 5.0%; Score 49.4; DB 8; Length 1029;  
Best Local Similarity 47.8%; Pred. No. 23;  
RESULT 701  
ID ADP88594 standard; DNA; 1149 BP.  
DE Human POU domain factor Brn3a gene exon 2.  
PN WO2004052186-A2.  
PD 24-JUN-2004.  
PA (FORS-) FORSYTH INST.  
Query Match 5.0%; Score 49.4; DB 12; Length 1149;  
Best Local Similarity 46.7%; Pred. No. 23;  
RESULT 702  
ID ACA38093 standard; DNA; 1173 BP.  
DE Prokaryotic essential gene #19750.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.0%; Score 49.4; DB 8; Length 1173;  
Best Local Similarity 45.2%; Pred. No. 23;  
RESULT 703  
ID ACA27337 standard; DNA; 1191 BP.  
DE Prokaryotic essential gene #8994.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.0%; Score 49.4; DB 8; Length 1191;  
Best Local Similarity 53.8%; Pred. No. 22;  
RESULT 704  
ID AAX09010 standard; cDNA; 1272 BP.  
DE Brn-3a polynucleotide.  
PN WO9905272-A1.  
PD 04-FEB-1999.  
PA (UNLO) UNIV COLLEGE LONDON.  
Query Match 5.0%; Score 49.4; DB 2; Length 1272;  
Best Local Similarity 46.7%; Pred. No. 22;  
RESULT 705  
ID AAA29006 standard; cDNA; 1272 BP.  
DE Human transcription factor Brn-3a coding sequence.  
PN WO200034466-A1.  
PD 15-JUN-2000.  
PA (UNLO) UNIV COLLEGE LONDON.  
Query Match 5.0%; Score 49.4; DB 3; Length 1272;  
Best Local Similarity 46.7%; Pred. No. 22;  
RESULT 706  
ID ADM80093 standard; DNA; 1398 BP.  
DE Spiramycin biosynthesis orf13c, SEQ ID 60.  
PN FR2845394-A1.  
PD 09-APR-2004.  
PA (AVET) AVENTIS PHARMA SA.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
Query Match 5.0%; Score 49.4; DB 12; Length 1398;  
Best Local Similarity 45.0%; Pred. No. 22;  
RESULT 707  
ID ADN97609 standard; DNA; 1398 BP.  
DE S ambotaciens spiramycin biosynthetic gene ORF13c.  
PN WO2004033689-A2.  
PD 22-APR-2004.  
PA (AVET) AVENTIS PHARMA SA.  
PA (CNRS) CNRS.  
Query Match 5.0%; Score 49.4; DB 12; Length 1398;  
Best Local Similarity 45.0%; Pred. No. 22;  
RESULT 708  
ID ABD01548 standard; DNA; 1419 BP.  
DE Pseudomonas aeruginosa polynucleotide #152.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.0%; Score 49.4; DB 11; Length 1419;  
Best Local Similarity 46.2%; Pred. No. 22;

RESULT 709  
ID ACA40703 standard; DNA; 1587 BP.  
DE Prokaryotic essential gene #22360.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.0%; Score 49.4; DB 8; Length 1587;  
Best Local Similarity 47.6%; Pred. No. 22;  
RESULT 710  
ID ACA38400 standard; DNA; 1590 BP.  
DE Prokaryotic essential Gene #20057.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.0%; Score 49.4; DB 8; Length 1590;  
Best Local Similarity 47.6%; Pred. No. 22;  
RESULT 711  
ID ABD01553 standard; DNA; 1692 BP.  
DE Pseudomonas aeruginosa polynucleotide #157.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.0%; Score 49.4; DB 11; Length 1692;  
Best Local Similarity 46.2%; Pred. No. 22;  
RESULT 712  
ID ABD01582 standard; DNA; 1698 BP.  
DE Pseudomonas aeruginosa polynucleotide #186.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 5.0%; Score 49.4; DB 11; Length 1698;  
Best Local Similarity 46.2%; Pred. No. 22;  
RESULT 713  
ID AAT40082 standard; DNA; 1724 BP.  
DE M. tuberculosis RNA polymerase Group I sigma subunit sigA gene.  
PN GB2298862-A.  
PD 18-SEP-1996.  
PA (ASTR) ASTRA AB.  
Query Match 5.0%; Score 49.4; DB 2; Length 1724;  
Best Local Similarity 47.6%; Pred. No. 22;  
RESULT 714  
ID ADG75006 standard; DNA; 2091 BP.  
DE Human herpesvirus 2 UL47 DNA - SEQ ID 78.  
PN WO2003086308-A2.  
PD 23-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 5.0%; Score 49.4; DB 10; Length 2091;  
Best Local Similarity 45.8%; Pred. No. 22;  
RESULT 715  
ID ADG75154 standard; DNA; 2091 BP.  
DE Human herpesvirus 2 strain HG52 UL47 DNA - SEQ ID 226.  
PN WO2003086308-A2.  
PD 23-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 5.0%; Score 49.4; DB 10; Length 2091;  
Best Local Similarity 45.8%; Pred. No. 22;  
RESULT 716  
ID ADG75015 standard; DNA; 2118 BP.  
DE Human herpesvirus 2 UL47 coding region DNA - SEQ ID 87.  
PN WO2003086308-A2.  
PD 23-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 5.0%; Score 49.4; DB 10; Length 2118;  
Best Local Similarity 45.8%; Pred. No. 22;  
RESULT 717  
ID ADG75014 standard; DNA; 2211 BP.  
DE Human herpesvirus 2 UL47-His construct DNA - SEQ ID 86.  
PN WO2003086308-A2.  
PD 23-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 5.0%; Score 49.4; DB 10; Length 2211;  
Best Local Similarity 45.8%; Pred. No. 22;  
RESULT 718

ID AAV22682 standard; DNA; 2214 BP.  
DE New DNA sequence isolated from Pinctada fucata.  
PN JF1080285-A.  
PD 31-MAR-1998.  
PA (MIKI-) MIKIMOTO SEIYAKU KK.  
Query Match 5.0%; Score 49.4; DB 2; Length 2214;  
Best Local Similarity 47.1%; Pred. No. 22;  
RESULT 719  
ID ADC30095 standard; cDNA; 2382 BP.  
DE Human novel cDNA sequence, SEQ ID NO:177.  
PN WO2003029271-A2.  
PD 10-APR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 5.0%; Score 49.4; DB 10; Length 2382;  
Best Local Similarity 45.6%; Pred. No. 22;  
RESULT 720  
ID ACA30032 standard; DNA; 2502 BP.  
DE Prokaryotic essential gene #11689.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.0%; Score 49.4; DB 8; Length 2502;  
Best Local Similarity 55.6%; Pred. No. 22;  
RESULT 721  
ID ADT44784 standard; cDNA; 2517 BP.  
DE Bacterial polynucleotide #19535.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 5.0%; Score 49.4; DB 13; Length 2517;  
Best Local Similarity 46.4%; Pred. No. 22;  
RESULT 722  
ID AAQ92657 standard; DNA; 2745 BP.  
DE Virulence determinant rpov gene.  
PN WO9517511-A2.  
PD 29-JUN-1995.  
PA (AGRE-) AGRESEARCH NEW ZEALAND PASTORAL AGRIC.  
PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.  
Query Match 5.0%; Score 49.4; DB 2; Length 2745;  
Best Local Similarity 47.6%; Pred. No. 22;  
RESULT 723  
ID AAQ92656 standard; DNA; 2745 BP.  
DE Virulence determinant rpov gene.  
PN WO9517511-A2.  
PD 29-JUN-1995.  
PA (AGRE-) AGRESEARCH NEW ZEALAND PASTORAL AGRIC.  
PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.  
Query Match 5.0%; Score 49.4; DB 2; Length 2745;  
Best Local Similarity 47.6%; Pred. No. 22;  
RESULT 724  
ID AAV38109 standard; DNA; 2745 BP.  
DE Mycobacterium bovis large ORF WAG9200 DNA sequence.  
PN US5783386-A.  
PD 21-JUL-1998.  
PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.  
PA (AGRE-) AGRESEARCH NEW ZEALAND PASTORAL AGRIC.  
Query Match 5.0%; Score 49.4; DB 2; Length 2745;  
Best Local Similarity 47.6%; Pred. No. 22;  
RESULT 725  
ID AAV38108 standard; DNA; 2745 BP.  
DE Mycobacterium bovis virulence restoring DNA sequence.  
PN US5783386-A.  
PD 21-JUL-1998.  
PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.  
PA (AGRE-) AGRESEARCH NEW ZEALAND PASTORAL AGRIC.  
Query Match 5.0%; Score 49.4; DB 2; Length 2745;  
Best Local Similarity 47.6%; Pred. No. 22;  
RESULT 726  
ID AAS14697 standard; DNA; 3038 BP.

DE Human cDNA encoding neuroendocrine VGF.  
PN WO200174298-A2.  
PD 11-OCT-2001.  
PA (UYBR-) UNIV BROWN RESEARCH FOUND.  
PA (HUGH-) HUGHES HOWARD MED INST.  
Query Match 5.0%; Score 49.4; DB 4; Length 3038;  
Best Local Similarity 44.2%; Pred. No. 22;  
RESULT 727  
ID ADD14800 standard; cDNA; 3038 BP.  
DE Human src biomarker polynucleotide SEQ ID NO:194.  
PN WO2003062395-A2.  
PD 31-JUL-2003.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
Query Match 5.0%; Score 49.4; DB 10; Length 3038;  
Best Local Similarity 44.2%; Pred. No. 22;  
RESULT 728  
ID AAV22683 standard; cDNA to mRNA; 3331 BP.  
DE New DNA sequence isolated from Pinctada fucata.  
PN JF1080285-A.  
PD 31-MAR-1998.  
PA (MIKI-) MIKIMOTO SEIYAKU KK.  
Query Match 5.0%; Score 49.4; DB 2; Length 3331;  
Best Local Similarity 47.1%; Pred. No. 22;  
RESULT 729  
ID AAZ32021 standard; DNA; 3331 BP.  
DE Human METH1 related EST D86074.  
PN WO937660-A1.  
PD 29-JUL-1999.  
PA (IRUE/) IRUELA-ARISPE L.  
PA (HAST/) HASTINGS G A.  
PA (RUBE/) RUBEN S M.  
Query Match 5.0%; Score 49.4; DB 2; Length 3331;  
Best Local Similarity 47.1%; Pred. No. 22;  
RESULT 730  
ID AAC90078 standard; DNA; 3331 BP.  
DE D86074 cDNA clone.  
PN WO200071577-A1.  
PD 30-NOV-2000.  
PA (HUNA-) HUMAN GENOME SCI INC.  
PA (SMIK) SMITHKLINE BEECHAM CORP.  
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.  
PA (IRUE/) IRUELA-ARISPE L.  
PA (HAST/) HASTINGS G A.  
PA (RUBE/) RUBEN S M.  
PA (JONA/) JONAK Z L.  
PA (TRUL/) TRULLI S H.  
PA (FORN/) FORNWALD J A.  
PA (TERR/) TERRETT J A.  
Query Match 5.0%; Score 49.4; DB 5; Length 3331;  
Best Local Similarity 47.1%; Pred. No. 22;  
RESULT 731  
ID AAA30290 standard; DNA; 3489 BP.  
DE Kaposi's sarcoma-associated herpesvirus LANA gene.  
PN WO200029626-A1.  
PD 25-MAY-2000.  
PA (KIEF/) KIEFF E D.  
PA (BALI/) BALLESTAS M E.  
PA (KAYE/) KAYE K M.  
Query Match 5.0%; Score 49.4; DB 3; Length 3489;  
Best Local Similarity 42.9%; Pred. No. 22;  
RESULT 732  
ID AAF82901 standard; DNA; 3489 BP.  
DE Nucleotide sequence of KSHV tethering protein, LANA.  
PN WO200125484-A2.  
PD 12-APR-2001.  
PA (UNMI) UNIV MICHIGAN.  
Query Match 5.0%; Score 49.4; DB 4; Length 3489;  
Best Local Similarity 42.9%; Pred. No. 22;  
RESULT 733  
ID ABA93487 standard; DNA; 3489 BP.  
DE Kaposi's sarcoma-associated herpesvirus LANA protein encoding DNA.  
PN US6322792-B1.  
PD 27-NOV-2001.

PA (KIEFF/) KIEFF E D.  
Query Match 5.0%; Score 49.4; DB 6; Length 3489;  
Best Local Similarity 42.9%; Pred. No. 22;  
RESULT 734  
ID ADJ65095 standard; DNA; 3489 BP.  
DE HHV8 DNA encoding latency-associated nuclear antigen, LANNA.  
PN US2004037847-A1.  
PD 26-FEB-2004.  
PA (KIEFF/) KIEFF E D.  
PA (BALL/) BALLESTAS M E.  
PA (KAYE/) KAYE K M.  
Query Match 5.0%; Score 49.4; DB 12; Length 3489;  
Best Local Similarity 42.9%; Pred. No. 22;  
RESULT 735  
ID ACA27005 standard; DNA; 4255 BP.  
DE Prokaryotic essential gene #8662.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 5.0%; Score 49.4; DB 8; Length 4255;  
Best Local Similarity 45.5%; Pred. No. 22;  
RESULT 736  
ID ADS19485 standard; DNA; 4353 BP.  
DE Modified HIV-1 GagPol polynucleotide sequence.  
PN US2004037780-A1.  
PD 26-FEB-2004.  
PA (PARS/) PARSONS D.  
PA (ANSO/) ANSON D.  
PA (LIMB/) LIMBERIS M.  
PA (FULL/) FULLER M.  
Query Match 5.0%; Score 49.4; DB 13; Length 4353;  
Best Local Similarity 48.1%; Pred. No. 22;  
RESULT 737  
ID AAV33912 standard; cDNA; 4524 BP.  
DE Nucleotide sequence of the SIAX DP2-64 (Oct-T1) gene.  
PN WO9849299-A1.  
PD 05-NOV-1998.  
PA (LUDW-) LUDWIG INST CANCER RES.  
Query Match 5.0%; Score 49.4; DB 2; Length 4524;  
Best Local Similarity 47.5%; Pred. No. 22;  
RESULT 738  
ID ADRO1282 standard; DNA; 9762 BP.  
DE Farnesyl dibenzodiazepinone biosynthetic locus Contig 3, SEQ ID 73.  
PN WO2004065591-A1.  
PD 05-AUG-2004.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 5.0%; Score 49.4; DB 13; Length 9762;  
Best Local Similarity 49.4%; Pred. No. 21;  
RESULT 739  
ID AAV62152 standard; DNA; 10211 BP.  
DE HSV-2 strain 8B5 Contig ID 99 DNA sequence.  
PN WO9820016-A1.  
PD 14-MAY-1998.  
PA (SMIK-) SMITKLINE BEECHAM CORP.  
Query Match 5.0%; Score 49.4; DB 2; Length 10211;  
Best Local Similarity 45.8%; Pred. No. 21;  
RESULT 740  
ID ABV99363 standard; DNA; 14061 BP.  
DE Human NOVI3b coding sequence.  
PN WO200272771-A2.  
PD 19-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 5.0%; Score 49.4; DB 6; Length 14061;  
Best Local Similarity 44.7%; Pred. No. 21;  
RESULT 741  
ID AAV73805 standard; DNA; 32207 BP.  
DE KSHV LUR DNA (nucleotides 105,301-137,507).  
PN US5849564-A.  
PD 15-DEC-1998.  
PA (UYCO-) UNIV COLUMBIA NEW YORK.  
Query Match 5.0%; Score 49.4; DB 2; Length 32207;  
Best Local Similarity 42.9%; Pred. No. 21;  
RESULT 742

ID ADR67012 standard; DNA; 32229 BP.  
DE Human cancer associated gene genomic sequence SEQ ID NO:58.  
PN WO2004074321-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 5.0%; Score 49.4; DB 13; Length 32229;  
Best Local Similarity 45.0%; Pred. No. 21;  
RESULT 743  
ID ADO51695 standard; DNA; 32329 BP.  
DE Streptomyces cattleya NRRL 8057 thienamycin biosynthetic gene cluster.  
PN US2004038250-A1.  
PD 26-FEB-2004.  
PA (ASTU-) ASTUR-PHARMA SA.  
PA (UYOV-) UNIV OVIEDO.  
Query Match 5.0%; Score 49.4; DB 12; Length 32329;  
Best Local Similarity 44.7%; Pred. No. 21;  
RESULT 744  
ID ABZ37516 standard; DNA; 59816 BP.  
DE Streptomyces viridochromogenes Avi gene cluster sense strand.  
PN WO200268436-A1.  
PD 06-SEP-2002.  
PA (COMB-) COMBINATURE BIOPHARM AG.  
Query Match 5.0%; Score 49.4; DB 8; Length 59816;  
Best Local Similarity 47.8%; Pred. No. 20;  
RESULT 745  
ID ABZ37515 standard; DNA; 59816 BP.  
DE Streptomyces viridochromogenes Avi gene cluster sense strand.  
PN WO200268436-A1.  
PD 06-SEP-2002.  
PA (COMB-) COMBINATURE BIOPHARM AG.  
Query Match 5.0%; Score 49.4; DB 8; Length 59816;  
Best Local Similarity 47.8%; Pred. No. 20;  
RESULT 746  
ID ABX04971 standard; DNA; 103599 BP.  
DE S. cinamonensis monensin type I polyketide synthase gene cluster.  
PN WO200168867-A1.  
PD 20-SEP-2001.  
PA (BIOT-) BIOTICA TECHNOLOGY LTD.  
Query Match 5.0%; Score 49.4; DB 4; Length 103599;  
Best Local Similarity 47.8%; Pred. No. 20;  
RESULT 747  
ID AAS08693 standard; DNA; 109519 BP.  
DE Micromonospora DNA encoding biosynthetic enzymes for Everninomycin.  
Query Match 5.0%; Score 49.4; DB 5; Length 109519;  
Best Local Similarity 47.8%; Pred. No. 20;  
RESULT 748  
Query Match 5.0%; Score 49.4; DB 4; Length 110000;  
Best Local Similarity 47.6%; Pred. No. 20;  
RESULT 749  
Query Match 5.0%; Score 49.4; DB 4; Length 110000;  
Best Local Similarity 47.6%; Pred. No. 20;  
RESULT 750  
ID AAV19941 standard; DNA; 137507 BP.  
DE KSHV long unique coding region and terminal repeat.  
PN WO9804576-A1.  
PD 05-FEB-1998.  
PA (UYCO-) UNIV COLUMBIA NEW YORK.  
Query Match 5.0%; Score 49.4; DB 2; Length 137507;  
Best Local Similarity 42.9%; Pred. No. 20;  
RESULT 751  
ID ADNI2162 standard; DNA; 137508 BP.  
DE Human herpesvirus 8.  
PN WO2004027036-A2.  
PD 01-APR-2004.  
PA (UYJO-) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
Query Match 5.0%; Score 49.4; DB 12; Length 137508;  
Best Local Similarity 42.9%; Pred. No. 20;  
RESULT 752  
ID ABD17309 standard; DNA; 789 BP.  
DE Pseudomonas aeruginosa polynucleotide #15913.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.

Query Match 5.0%; Score 49.2; DB 11; Length 789;  
 Best Local Similarity 48.3%; Pred. No. 25;  
 RESULT 753  
 ID ABD13248 standard; DNA; 795 BP.  
 DE Pseudomonas aeruginosa polynucleotide #11852.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.0%; Score 49.2; DB 11; Length 795;  
 Best Local Similarity 46.1%; Pred. No. 25;  
 RESULT 754  
 ID ABD17908 standard; DNA; 888 BP.  
 DE Pseudomonas aeruginosa polynucleotide #16512.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.0%; Score 49.2; DB 11; Length 888;  
 Best Local Similarity 50.7%; Pred. No. 24;  
 RESULT 755  
 ID ADS5666 standard; cDNA; 972 BP.  
 DE Bacterial polynucleotide #8653.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOV/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match 5.0%; Score 49.2; DB 13; Length 972;  
 Best Local Similarity 47.2%; Pred. No. 24;  
 RESULT 756  
 ID AAS72681 standard; cDNA; 1074 BP.  
 DE DNA encoding novel human diagnostic protein #8485.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 5.0%; Score 49.2; DB 5; Length 1074;  
 Best Local Similarity 42.4%; Pred. No. 24;  
 RESULT 757  
 ID ABD12927 standard; DNA; 1221 BP.  
 DE Pseudomonas aeruginosa polynucleotide #11531.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.0%; Score 49.2; DB 11; Length 1221;  
 Best Local Similarity 46.1%; Pred. No. 24;  
 RESULT 758  
 ID ABD15054 standard; DNA; 1263 BP.  
 DE Pseudomonas aeruginosa polynucleotide #13658.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.0%; Score 49.2; DB 11; Length 1263;  
 Best Local Similarity 45.8%; Pred. No. 24;  
 RESULT 759  
 ID ABD14863 standard; DNA; 1263 BP.  
 DE Pseudomonas aeruginosa polynucleotide #13467.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.0%; Score 49.2; DB 11; Length 1263;  
 Best Local Similarity 45.6%; Pred. No. 24;  
 RESULT 760  
 ID AAX09011 standard; cDNA; 1266 BP.  
 DE Brn-3a polynucleotide.  
 PN WO9905272-A1.  
 PD 04-FEB-1999.  
 PA (UNLO-) UNIV COLLEGE LONDON.  
 Query Match 5.0%; Score 49.2; DB 2; Length 1266;  
 Best Local Similarity 47.4%; Pred. No. 24;  
 RESULT 761  
 ID AAA29007 standard; cDNA; 1266 BP.  
 DE Murine transcription factor Brn-3a coding sequence.

PN WO200034466-A1.  
 PD 15-JUN-2000.  
 PA (UNLO-) UNIV COLLEGE LONDON.  
 Query Match 5.0%; Score 49.2; DB 3; Length 1266;  
 Best Local Similarity 47.4%; Pred. No. 24;  
 RESULT 762  
 ID ABD17488 standard; DNA; 1512 BP.  
 DE Pseudomonas aeruginosa polynucleotide #16092.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.0%; Score 49.2; DB 11; Length 1512;  
 Best Local Similarity 50.7%; Pred. No. 24;  
 RESULT 763  
 ID ABD17174 standard; DNA; 1521 BP.  
 DE Pseudomonas aeruginosa polynucleotide #15778.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.0%; Score 49.2; DB 11; Length 1521;  
 Best Local Similarity 48.3%; Pred. No. 24;  
 RESULT 764  
 ID ABD17253 standard; DNA; 1569 BP.  
 DE Pseudomonas aeruginosa polynucleotide #15857.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 5.0%; Score 49.2; DB 11; Length 1569;  
 Best Local Similarity 48.3%; Pred. No. 24;  
 RESULT 765  
 ID AAD11112 standard; DNA; 1602 BP.  
 DE Human small cell lung cancer associated gene, ZIC2.  
 PN WO200153349-A2.  
 PD 26-JUL-2001.  
 PA (LUDM-) LUDWIG INST CANCER RES.  
 PA (SLOK-) SLOAN KETTERING INST CANCER RES.  
 PA (CORR-) CORNELL RES FOUND INC.  
 Query Match 5.0%; Score 49.2; DB 4; Length 1602;  
 Best Local Similarity 53.0%; Pred. No. 24;  
 RESULT 766  
 ID AAS61863 standard; cDNA; 1602 BP.  
 DE Lung small cell carcinoma antigen, cDNA #404.  
 PN WO200177168-A2.  
 PD 18-OCT-2001.  
 PA (CORI-) CORIXA CORP.  
 Query Match 5.0%; Score 49.2; DB 6; Length 1602;  
 Best Local Similarity 53.0%; Pred. No. 24;  
 RESULT 767  
 ID ADD15207 standard; DNA; 1602 BP.  
 DE DNA encoding the human zinc finger protein ZIC2.  
 PN WO2003039490-A2.  
 PD 15-MAY-2003.  
 PA (UYTE-) UNIV OFFICE TECHNOLOGY LICENSING STANFORD.  
 Query Match 5.0%; Score 49.2; DB 10; Length 1602;  
 Best Local Similarity 53.0%; Pred. No. 24;  
 RESULT 768  
 ID ADQ03085 standard; DNA; 1713 BP.  
 DE P. aeruginosa virulence gene, VIR17.  
 PN US2004122212-A1.  
 PD 24-JUN-2004.  
 PA (COSS/) COSSON P.  
 PA (KOHL/) KOHLER T.  
 PA (BENG/) BENGHEZAL M.  
 PA (MARC/) MARCHETTI A.  
 PA (DELD/) DELDEN C V.  
 Query Match 5.0%; Score 49.2; DB 12; Length 1713;  
 Best Local Similarity 43.8%; Pred. No. 24;  
 RESULT 769  
 ID ADP88591 standard; DNA; 2160 BP.  
 DE Murine class V POU transcription factor Brn3a gene.  
 PN WO2004052186-A2.  
 PD 24-JUN-2004.  
 PA (FORS-) FORSYTH INST.

Query Match  
Best Local Similarity 5.0%; Score 49.2; DB 12; Length 2160;  
RESULT 770  
ID ABD17387 standard; DNA; 2400 BP.  
DE Pseudomonas aeruginosa polynucleotide #15991.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENE-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 5.0%; Score 49.2; DB 11; Length 2400;  
RESULT 771  
ID ABK63479 standard; cDNA; 2455 BP.  
DE Rat sequence differentially expressed in response to a hepatotoxin #1386.  
PN WO200210453-A2.  
PD 07-FEB-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match  
Best Local Similarity 5.0%; Score 49.2; DB 6; Length 2455;  
RESULT 772  
ID ADB5687 standard; DNA; 2455 BP.  
DE Toxicity-related gene, SEQ ID 3713.  
PN WO2003084624-A2.  
PD 07-AUG-2003.  
PA (GENE-) GENE LOGIC INC.  
Query Match  
Best Local Similarity 5.0%; Score 49.2; DB 10; Length 2455;  
RESULT 773  
ID ADB53374 standard; DNA; 2455 BP.  
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3916.  
PN WO2003065993-A2.  
PD 14-AUG-2003.  
PA (GENE-) GENE LOGIC INC.  
Query Match  
Best Local Similarity 5.0%; Score 49.2; DB 10; Length 2455;  
RESULT 774  
ID ADF30464 standard; cDNA; 2455 BP.  
DE Rat angio genesis modulating protein cDNA #9.  
PN US2003162706-A1.  
PD 28-AUG-2003.  
PA (PROC ) PROCTER & GAMBLE CO.  
Query Match  
Best Local Similarity 5.0%; Score 49.2; DB 10; Length 2455;  
RESULT 775  
ID ABT42262 standard; DNA; 2455 BP.  
DE Toxicity modelling related rat gene SEQ ID NO 1964.  
PN WO200295000-A2.  
PD 28-NOV-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match  
Best Local Similarity 5.0%; Score 49.2; DB 10; Length 2455;  
RESULT 776  
ID ADP72601 standard; DNA; 2455 BP.  
DE Renal toxin progression gene marker #1190.  
PN WO2004048598-A2.  
PD 10-JUN-2004.  
PA (GENE-) GENE LOGIC INC.  
Query Match  
Best Local Similarity 5.0%; Score 49.2; DB 12; Length 2455;  
RESULT 777  
ID ADE25609 standard; cDNA; 2607 BP.  
DE Human cDNA differentially expressed in foam cells #13.  
PN US2003194721-A1.  
PD 16-OCT-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match  
Best Local Similarity 5.0%; Score 49.2; DB 10; Length 2607;  
RESULT 778  
ID ADK70215 standard; cDNA; 2680 BP.  
DE Human oesophageal cancer antigen cDNA SEQ ID NO:11.  
PN JP2003259872-A.  
PD 16-SEP-2003.  
PA (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.  
Query Match  
Best Local Similarity 5.0%; Score 49.2; DB 12; Length 2680;

Best Local Similarity 53.0%; Pred. No. 24;  
RESULT 779  
ID ADQ25191 standard; DNA; 2717 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 8011.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match  
Best Local Similarity 5.0%; Score 49.2; DB 12; Length 2717;  
RESULT 780  
ID ABA02191 standard; cDNA; 3318 BP.  
DE Human C/EBP alpha-encoding cDNA.  
PN US6306655-B1.  
PD 23-OCT-2001.  
PA (ISIS-) ISIS PHARM INC.  
Query Match  
Best Local Similarity 5.0%; Score 49.2; DB 6; Length 3318;  
RESULT 781  
ID ADS56329 standard; cDNA; 3540 BP.  
DE Bacterial polynucleotide #8316.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match  
Best Local Similarity 5.0%; Score 49.2; DB 13; Length 3540;  
RESULT 782  
ID ADI39068 standard; DNA; 3597 BP.  
DE S. coelicolor meth DNA.  
PN WO2003087386-A2.  
PD 23-OCT-2003.  
PA (BADI ) BASF AG.  
Query Match  
Best Local Similarity 5.0%; Score 49.2; DB 10; Length 3597;  
RESULT 783  
ID ADI39145 standard; DNA; 8787 BP.  
DE Plasmid pCPhsdh meth\_SC DNA.  
PN WO2003087386-A2.  
PD 23-OCT-2003.  
PA (BADI ) BASF AG.  
Query Match  
Best Local Similarity 5.0%; Score 49.2; DB 10; Length 8787;  
RESULT 784  
ID ABL50991 standard; DNA; 35133 BP.  
DE Thermus caldophilus GK24 cosmid clone 3 nucleotide sequence.  
PN KR2001019888-A.  
PD 15-MAR-2001.  
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.  
Query Match  
Best Local Similarity 5.0%; Score 49.2; DB 4; Length 35133;  
RESULT 785  
ID ABL50990 standard; DNA; 35134 BP.  
DE Thermus caldophilus GK24 cosmid clone 3 SEQ ID NO:1.  
PN KR2001019888-A.  
PD 15-MAR-2001.  
PA (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.  
Query Match  
Best Local Similarity 5.0%; Score 49.2; DB 4; Length 35134;  
RESULT 786  
ID ADP74816 standard; DNA; 137560 BP.  
DE Parapoxvirus ovis genome DNA sequence SeqID1.  
PN WO200202099-A1.  
PD 20-APR-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Query Match  
Best Local Similarity 5.0%; Score 49.2; DB 12; Length 137560;  
RESULT 787  
ID AA68100 standard; DNA; 399 BP.  
DE E. grandis caffeoyl CoA methyl transferase DNA sequence SEQ ID NO:193.  
PN WO200202099-A1.  
PD 20-APR-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.

Query Match 5.0%; Score 49; DB 3; Length 399;  
 Best Local Similarity 57.5%; Pred. No. 27;  
 RESULT 788  
 ID ADD41850 standard; DNA; 399 BP.  
 DE Caffeoyl CoA methyl transferase DNA #1.  
 PN US200311373-A1.  
 PD 10-JUL-2003.  
 PA (BLOK/) BLOKSBERG L N.  
 PA (HAVU/) HAVUKKALA I.  
 Query Match 5.0%; Score 49; DB 10; Length 399;  
 Best Local Similarity 57.5%; Pred. No. 27;  
 RESULT 789  
 ID ACA37827 standard; DNA; 717 BP.  
 DE Prokaryotic essential gene #19484.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 5.0%; Score 49; DB 8; Length 717;  
 Best Local Similarity 44.8%; Pred. No. 27;  
 RESULT 790  
 ID ABX56042 standard; DNA; 843 BP.  
 DE M. echinospira calicheamicin biosynthesis gene calr.  
 PN WO200279465-A2.  
 PD 10-OCT-2002.  
 PA (SLOK-) SLOAN KETTERING INST CANCER RES.  
 Query Match 5.0%; Score 49; DB 8; Length 843;  
 Best Local Similarity 47.9%; Pred. No. 26;  
 RESULT 791  
 ID AAZ51697 standard; DNA; 1044 BP.  
 DE Burkholderia cepacia reca gene (1).  
 PN WO200014274-A1.  
 PD 16-MAR-2000.  
 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 Query Match 5.0%; Score 49; DB 3; Length 1044;  
 Best Local Similarity 43.8%; Pred. No. 26;  
 RESULT 792  
 ID AAT44494 standard; cDNA; 1355 BP.  
 DE Murine cyclin-dependent kinase inhibitor p57KIP2 cDNA.  
 PN WO9631534-A1.  
 PD 10-OCT-1996.  
 PA (SLOK-) SLOAN KETTERING INST CANCER RES.  
 Query Match 5.0%; Score 49; DB 2; Length 1355;  
 Best Local Similarity 50.2%; Pred. No. 26;  
 RESULT 793  
 ID AAI72395 standard; cDNA; 1355 BP.  
 DE p57-KIP2 cDNA.  
 PN WO200204605-A2.  
 PD 17-JAN-2002.  
 PA (OTOG-) OTOGENE USA INC.  
 PA (OTOG-) OTOGENE AG.  
 Query Match 5.0%; Score 49; DB 6; Length 1355;  
 Best Local Similarity 50.2%; Pred. No. 26;  
 RESULT 794  
 ID AAH26499 standard; DNA; 1614 BP.  
 DE Human low density lipoprotein binding protein 2 (LBP-2) DNA.  
 PN WO200164874-A2.  
 PD 07-SEP-2001.  
 PA (BOST-) BOSTON HEART FOUND INC.  
 Query Match 5.0%; Score 49; DB 5; Length 1614;  
 Best Local Similarity 43.7%; Pred. No. 26;  
 RESULT 795  
 ID ABS58306 standard; cDNA; 1852 BP.  
 DE Spider dragline cDNA repetitive nucleotide sequence.  
 PN US2002137211-A1.  
 PD 26-SEP-2002.  
 PA (UYSI-) UNIV SICHUAN TIANYOU BIOLOGIC ENG CO LTD.  
 Query Match 5.0%; Score 49; DB 10; Length 1852;  
 Best Local Similarity 46.6%; Pred. No. 26;  
 RESULT 796  
 ID ADM47862 standard; DNA; 1891 BP.  
 DE Polynucleotide sequence #280 useful in producing transgenic plants.  
 PN US2003233670-A1.  
 PD 18-DEC-2003.

PA (EDGE/) EDGERTON M D.  
 PA (CHOM/) CHOMET P S.  
 PA (LACC/) LACCETTI L B.  
 Query Match 5.0%; Score 49; DB 12; Length 1891;  
 Best Local Similarity 50.6%; Pred. No. 26;  
 RESULT 797  
 ID ADA71938 standard; DNA; 2000 BP.  
 DE Rice gene, SEQ ID 5263.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN-) SYNGENTA PARTICIPATIONS AG.  
 Query Match 5.0%; Score 49; DB 8; Length 2000;  
 Best Local Similarity 9.7%; Pred. No. 26;  
 RESULT 798  
 ID ADS10050 standard; DNA; 3070 BP.  
 DE Human therapeutic DNA - SEQ ID 287.  
 PN WO2004080148-A2.  
 PD 23-SEP-2004.  
 PA (NUVE-) NUVELO INC.  
 Query Match 5.0%; Score 49; DB 13; Length 3070;  
 Best Local Similarity 49.1%; Pred. No. 26;  
 RESULT 799  
 ID AAH98717 standard; cDNA; 4486 BP.  
 DE Human EST-derived coding sequence SEQ ID NO: 574.  
 PN WO200154477-A2.  
 PD 02-AUG-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 5.0%; Score 49; DB 4; Length 4486;  
 Best Local Similarity 47.5%; Pred. No. 25;  
 RESULT 800  
 ID AAV62153 standard; DNA; 7361 BP.  
 DE HSV-2 strain SB5 Contig ID 1 DNA sequence.  
 PN WO9820016-A1.  
 PD 14-MAY-1998.  
 PA (SMIX-) SMITHKLINE BEECHAM CORP.  
 Query Match 5.0%; Score 49; DB 2; Length 7361;  
 Best Local Similarity 42.8%; Pred. No. 25;  
 RESULT 801  
 ID AAV62130 standard; DNA; 8952 BP.  
 DE HSV-2 strain SB5 Contig ID 100 DNA sequence.  
 PN WO9820016-A1.  
 PD 14-MAY-1998.  
 PA (SMIX-) SMITHKLINE BEECHAM CORP.  
 Query Match 5.0%; Score 49; DB 2; Length 8952;  
 Best Local Similarity 42.8%; Pred. No. 25;  
 RESULT 802  
 ID AAL61171 standard; DNA; 9222 BP.  
 DE Actinosynnema pretiosum polyketide synthase (PKS) gene #2.  
 PN WO2003045312-A2.  
 PD 05-JUN-2003.  
 PA (UNIW-) UNIV WASHINGTON.  
 Query Match 5.0%; Score 49; DB 8; Length 9222;  
 Best Local Similarity 46.0%; Pred. No. 25;  
 RESULT 803  
 ID AAH26495 standard; DNA; 12425 BP.  
 DE Human low density lipoprotein binding protein 2 (LBP-2) gene.  
 PN WO200164874-A2.  
 PD 07-SEP-2001.  
 PA (BOST-) BOSTON HEART FOUND INC.  
 Query Match 5.0%; Score 49; DB 5; Length 12425;  
 Best Local Similarity 43.7%; Pred. No. 25;  
 RESULT 804  
 ID AAA14651 standard; DNA; 77536 BP.  
 DE Nucleotide sequence of the PK-520 biosynthetic gene cluster.  
 Query Match 5.0%; Score 49; DB 3; Length 77536;  
 Best Local Similarity 44.4%; Pred. No. 23;  
 RESULT 805  
 Query Match 5.0%; Score 49; DB 4; Length 110000;  
 Best Local Similarity 50.6%; Pred. No. 23;  
 RESULT 806  
 Query Match 5.0%; Score 49; DB 4; Length 110000;  
 Best Local Similarity 45.0%; Pred. No. 23;  
 RESULT 807

Query Match 5.0%; Score 49; DB 4; Length 110000;  
 Best Local Similarity 45.0%; Pred. No. 23;  
 RESULT 808  
 ID AAV62176 standard; DNA; 117213 BP.  
 DE HSV-2 strain S95 Contig ID 15 DNA sequence.  
 Query Match 5.0%; Score 49; DB 2; Length 117213;  
 Best Local Similarity 42.8%; Pred. No. 23;  
 RESULT 809  
 ID ABD09003 standard; DNA; 852 BP.  
 DE Pseudomonas aeruginosa polynucleotide #7607.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.9%; Score 48.8; DB 11; Length 852;  
 Best Local Similarity 49.2%; Pred. No. 29;  
 RESULT 810  
 ID ABD10213 standard; DNA; 1083 BP.  
 DE Pseudomonas aeruginosa polynucleotide #8817.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.9%; Score 48.8; DB 11; Length 1083;  
 Best Local Similarity 50.3%; Pred. No. 28;  
 RESULT 811  
 ID ADQ87326 standard; cDNA; 1149 BP.  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #4203.  
 PN WO2004060270-A2.  
 PD 22-JUL-2004.  
 PA (GETH ) GENENTECH INC.  
 PA (WUTD/) WU T D.  
 PA (ZHOU/) ZHOU Y.  
 Query Match 4.9%; Score 48.8; DB 13; Length 1149;  
 Best Local Similarity 49.6%; Pred. No. 28;  
 RESULT 812  
 ID ADQ87564 standard; cDNA; 1149 BP.  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #4442.  
 PN WO2004060270-A2.  
 PD 22-JUL-2004.  
 PA (GETH ) GENENTECH INC.  
 PA (WUTD/) WU T D.  
 PA (ZHOU/) ZHOU Y.  
 Query Match 4.9%; Score 48.8; DB 13; Length 1149;  
 Best Local Similarity 49.6%; Pred. No. 28;  
 RESULT 813  
 ID ADC36141 standard; DNA; 1188 BP.  
 DE Weed controller metabolism associated gene SEQ ID NO:8.  
 PN WO2003040370-A1.  
 PD 15-MAY-2003.  
 PA (SUMO ) SUMITOMO CHEM CO LTD.  
 Query Match 4.9%; Score 48.8; DB 10; Length 1188;  
 Best Local Similarity 47.1%; Pred. No. 28;  
 RESULT 814  
 ID ACF06125 standard; DNA; 1194 BP.  
 DE Bacterial P450 enzyme encoding DNA SEQ ID NO:33.  
 PN WO2003052050-A2.  
 PD 26-JUN-2003.  
 PA (DIVE-) DIVERSA CORP.  
 Query Match 4.9%; Score 48.8; DB 9; Length 1194;  
 Best Local Similarity 44.8%; Pred. No. 28;  
 RESULT 815  
 ID AAS09830 standard; DNA; 1209 BP.  
 DE Pseudorabies virus DNA encoding glycoprotein 50, gp50.  
 PN US6251634-B1.  
 PD 26-JUN-2001.  
 PA (PHAA ) PHARMACIA & UPJOHN CO.  
 Query Match 4.9%; Score 48.8; DB 4; Length 1209;  
 Best Local Similarity 44.9%; Pred. No. 28;  
 RESULT 816  
 ID ABD10628 standard; DNA; 1227 BP.  
 DE Pseudomonas aeruginosa polynucleotide #9232.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.

Query Match 4.9%; Score 48.8; DB 11; Length 1227;  
 Best Local Similarity 50.3%; Pred. No. 28;  
 RESULT 817  
 ID ABZ66800 standard; DNA; 1272 BP.  
 DE Orthosomycin biosynthetic polynucleotide SEQ ID NO 262.  
 PN WO200279505-A2.  
 PD 10-OCT-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 4.9%; Score 48.8; DB 10; Length 1272;  
 Best Local Similarity 47.6%; Pred. No. 28;  
 RESULT 818  
 ID ABD10546 standard; DNA; 1296 BP.  
 DE Pseudomonas aeruginosa polynucleotide #9150.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.9%; Score 48.8; DB 11; Length 1296;  
 Best Local Similarity 50.3%; Pred. No. 28;  
 RESULT 819  
 ID ADC36144 standard; DNA; 1418 BP.  
 DE Weed controller metabolism associated gene SEQ ID NO:11.  
 PN WO2003040370-A1.  
 PD 15-MAY-2003.  
 PA (SUMO ) SUMITOMO CHEM CO LTD.  
 Query Match 4.9%; Score 48.8; DB 10; Length 1418;  
 Best Local Similarity 47.1%; Pred. No. 28;  
 RESULT 820  
 ID ADC36202 standard; DNA; 1418 BP.  
 DE Weed controller metabolism associated gene SEQ ID NO:69.  
 PN WO2003040370-A1.  
 PD 15-MAY-2003.  
 PA (SUMO ) SUMITOMO CHEM CO LTD.  
 Query Match 4.9%; Score 48.8; DB 10; Length 1418;  
 Best Local Similarity 47.1%; Pred. No. 28;  
 RESULT 821  
 ID ACC47259 standard; cDNA; 1427 BP.  
 DE Human SCAP encoding cDNA-Incyte Id. 6891852CB1.  
 PN WO2003008625-A2.  
 PD 30-JAN-2003.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Query Match 4.9%; Score 48.8; DB 8; Length 1427;  
 Best Local Similarity 48.0%; Pred. No. 28;  
 RESULT 822  
 ID ABD13152 standard; DNA; 2232 BP.  
 DE Pseudomonas aeruginosa polynucleotide #11756.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.9%; Score 48.8; DB 11; Length 2232;  
 Best Local Similarity 43.4%; Pred. No. 28;  
 RESULT 823  
 ID ABD13005 standard; DNA; 2274 BP.  
 DE Pseudomonas aeruginosa polynucleotide #11609.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.9%; Score 48.8; DB 11; Length 2274;  
 Best Local Similarity 43.4%; Pred. No. 28;  
 RESULT 824  
 ID ABD13232 standard; DNA; 2613 BP.  
 DE Pseudomonas aeruginosa polynucleotide #11836.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.9%; Score 48.8; DB 11; Length 2613;  
 Best Local Similarity 43.4%; Pred. No. 28;  
 RESULT 825  
 ID ABD10111 standard; DNA; 2715 BP.  
 DE Pseudomonas aeruginosa polynucleotide #8715.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.9%; Score 48.8; DB 11; Length 2715;



```

Best Local Similarity 50.3%; Pred. No. 28;
RESULT 826
ID ABK93509 standard; DNA; 4826 BP.
DE DNA fragment containing poly-beta-hydroxybutyrate, PHB, synthesis genes.
PN US2002146785-A1.
PD 10-OCT-2002.
PA (MAHI/) MAHISHI L H.
PA (TRIP/) TRIPATHI G.
PA (RAMC/) RAMCHANDER T V N.
PA (RAWA/) RAWAL S K.
Query Match 4.9%; Score 48.8; DB 8; Length 4826;
Best Local Similarity 45.7%; Pred. No. 27;
RESULT 827
ID ABK91609 standard; DNA; 7897 BP.
DE Modified HIV protein-encoding plasmid DNA #161.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match 4.9%; Score 48.8; DB 6; Length 7897;
Best Local Similarity 47.9%; Pred. No. 27;
RESULT 828
ID ABK91616 standard; DNA; 9166 BP.
DE Modified HIV protein-encoding plasmid DNA #168.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match 4.9%; Score 48.8; DB 6; Length 9166;
Best Local Similarity 47.9%; Pred. No. 27;
RESULT 829
ID ABK91619 standard; DNA; 9167 BP.
DE Modified HIV protein-encoding plasmid DNA #171.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match 4.9%; Score 48.8; DB 6; Length 9167;
Best Local Similarity 47.9%; Pred. No. 27;
RESULT 830
ID ABK91617 standard; DNA; 9169 BP.
DE Modified HIV protein-encoding plasmid DNA #169.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match 4.9%; Score 48.8; DB 6; Length 9169;
Best Local Similarity 47.9%; Pred. No. 27;
RESULT 831
ID ABK91614 standard; DNA; 9170 BP.
DE Modified HIV protein-encoding plasmid DNA #166.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match 4.9%; Score 48.8; DB 6; Length 9170;
Best Local Similarity 47.9%; Pred. No. 27;
RESULT 832
ID ABK91607 standard; DNA; 9189 BP.
DE Modified HIV protein-encoding plasmid DNA #159.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match 4.9%; Score 48.8; DB 6; Length 9189;
Best Local Similarity 47.9%; Pred. No. 27;
RESULT 833
ID ABK91612 standard; DNA; 9194 BP.
DE Modified HIV protein-encoding plasmid DNA #164.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match 4.9%; Score 48.8; DB 6; Length 9194;
Best Local Similarity 47.9%; Pred. No. 27;
RESULT 834
ID ABK91611 standard; DNA; 9194 BP.
DE Modified HIV protein-encoding plasmid DNA #163.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match 4.9%; Score 48.8; DB 6; Length 9194;
Best Local Similarity 47.9%; Pred. No. 27;
RESULT 835
ID ABK91623 standard; DNA; 9407 BP.
DE Modified HIV protein-encoding plasmid DNA #175.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match 4.9%; Score 48.8; DB 6; Length 9407;
Best Local Similarity 47.9%; Pred. No. 27;
RESULT 836
ID ABK91621 standard; DNA; 9782 BP.
DE Modified HIV protein-encoding plasmid DNA #173.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match 4.9%; Score 48.8; DB 6; Length 9782;
Best Local Similarity 47.9%; Pred. No. 27;
RESULT 837
ID ABK91620 standard; DNA; 9783 BP.
DE Modified HIV protein-encoding plasmid DNA #172.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match 4.9%; Score 48.8; DB 6; Length 9783;
Best Local Similarity 47.9%; Pred. No. 27;
RESULT 838
ID ABK91624 standard; DNA; 9785 BP.
DE Modified HIV protein-encoding plasmid DNA #176.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match 4.9%; Score 48.8; DB 6; Length 9785;
Best Local Similarity 47.9%; Pred. No. 27;
RESULT 839
ID ABK91622 standard; DNA; 9788 BP.
DE Modified HIV protein-encoding plasmid DNA #174.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match 4.9%; Score 48.8; DB 6; Length 9788;
Best Local Similarity 47.9%; Pred. No. 27;
RESULT 840
ID ABK91618 standard; DNA; 9792 BP.
DE Modified HIV protein-encoding plasmid DNA #170.
PN WO200232943-A2.
PD 25-APR-2002.
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (CHAD/) CHADRABARTI B K.
Query Match 4.9%; Score 48.8; DB 6; Length 9792;
Best Local Similarity 47.9%; Pred. No. 27;
RESULT 841
ID ABZ66813 standard; DNA; 10035 BP.
DE Orthosomycin biosynthetic gene cluster SEQ ID NO 282.
PN WO200279505-A2.
PD 10-OCT-2002.
PA (ECOP-) ECOPIA BIOSCIENCES INC.
Query Match 4.9%; Score 48.8; DB 10; Length 10035;
Best Local Similarity 47.6%; Pred. No. 27;

```

RESULT 842  
ID ADQ91701 standard; DNA; 10287 BP.  
DE Polyketide synthase ORF1, SEQ ID 24.  
PN WO2004065401-A1.  
PD 05-AUG-2004.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 4.9%; Score 48.8; DB 13; Length 10287;  
Best Local Similarity 47.4%; Pred. No. 27;  
RESULT 843  
ID ABK91613 standard; DNA; 12411 BP.  
DE Modified HIV protein-encoding plasmid DNA #165.  
PN WO2002323943-A2.  
PD 25-APR-2002.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA (CHAD/) CHADRABARTI B K.  
Query Match 4.9%; Score 48.8; DB 6; Length 12411;  
Best Local Similarity 47.9%; Pred. No. 27;  
RESULT 844  
ID ABX34289 standard; DNA; 135638 BP.  
DE S. atroolivaceus leinamycin biosynthesis gene cluster.  
PN WO200277173-A2.  
PD 03-OCT-2002.  
PA (REGC ) UNIV CALIFORNIA.  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
Query Match 4.9%; Score 48.8; DB 10; Length 135638;  
Best Local Similarity 44.7%; Pred. No. 25;  
RESULT 845  
ID ABS63423 standard; cDNA; 528 BP.  
DE DNA encoding soybean caffeoyl-CoA O-methyltransferase (CCOMT).  
PN US2002081693-A1.  
PD 27-JUN-2002.  
PA (CAHO/) CAHOON R E.  
PA (FADE/) FADER G M.  
PA (RAFA/) RAFALSKI J A.  
Query Match 4.9%; Score 48.6; DB 6; Length 528;  
Best Local Similarity 50.2%; Pred. No. 31;  
RESULT 846  
ID ACA38429 standard; DNA; 687 BP.  
DE Prokaryotic essential gene #20086.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.9%; Score 48.6; DB 8; Length 687;  
Best Local Similarity 45.3%; Pred. No. 31;  
RESULT 847  
ID ACA40639 standard; DNA; 690 BP.  
DE Prokaryotic essential gene #22296.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.9%; Score 48.6; DB 8; Length 690;  
Best Local Similarity 45.3%; Pred. No. 31;  
RESULT 848  
ID ADS58740 standard; cDNA; 1203 BP.  
DE Bacterial polynucleotide #10727.  
PN US2002323675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 4.9%; Score 48.6; DB 13; Length 1203;  
Best Local Similarity 46.6%; Pred. No. 31;  
RESULT 849  
ID ABX56068 standard; DNA; 1320 BP.  
DE M. echinospira calicheamicin biosynthesis gene orfVIII.  
PN WO200279465-A2.  
PD 10-OCT-2002.  
PA (SLOK ) SLOAN KETTERING INST CANCER RES.  
Query Match 4.9%; Score 48.6; DB 8; Length 1320;  
Best Local Similarity 45.1%; Pred. No. 30;  
RESULT 850

ID ACC92989 standard; DNA; 1397 BP.  
DE HIV-1 subtype C isolate Dui51 reverse transcriptase codon optimised DNA.  
PN WO2003037919-A2.  
PD 08-MAY-2003.  
PA (SAME-) SOUTH AFRICAN MEDICAL RES COUNCIL.  
PA (UYCA-) UNIV CAPE TOWN.  
Query Match 4.9%; Score 48.6; DB 8; Length 1397;  
Best Local Similarity 47.8%; Pred. No. 30;  
RESULT 851  
ID AAT90471 standard; cDNA; 1479 BP.  
DE Human agrin cDNA.  
PN WO9721811-A2.  
PD 19-JUN-1997.  
PA (REG-) REGENERON PHARM INC.  
Query Match 4.9%; Score 48.6; DB 2; Length 1479;  
Best Local Similarity 43.8%; Pred. No. 30;  
RESULT 852  
ID ADL61985 standard; DNA; 1533 BP.  
DE Human ovarian cancer DNA marker #20197.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 4.9%; Score 48.6; DB 5; Length 1533;  
Best Local Similarity 48.4%; Pred. No. 30;  
RESULT 853  
ID ABD12608 standard; DNA; 1575 BP.  
DE Pseudomonas aeruginosa polynucleotide #11212.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48.6; DB 11; Length 1575;  
Best Local Similarity 46.6%; Pred. No. 30;  
RESULT 854  
ID ABD12542 standard; DNA; 1620 BP.  
DE Pseudomonas aeruginosa polynucleotide #11146.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48.6; DB 11; Length 1620;  
Best Local Similarity 46.6%; Pred. No. 30;  
RESULT 855  
ID AAT62137 standard; DNA; 2040 BP.  
DE Leishmania braziliensis Lbhsp83 antigen cDNA.  
PN WO9711180-A1.  
PD 27-MAR-1997.  
PA (CORI-) CORIXA CORP.  
Query Match 4.9%; Score 48.6; DB 2; Length 2040;  
Best Local Similarity 44.4%; Pred. No. 30;  
RESULT 856  
ID AAV47557 standard; DNA; 2040 BP.  
DE Leishmania antigen Lbhsp83 coding sequence.  
PN WO9835045-A2.  
PD 13-AUG-1998.  
PA (CORI-) CORIXA CORP.  
Query Match 4.9%; Score 48.6; DB 2; Length 2040;  
Best Local Similarity 44.4%; Pred. No. 30;  
RESULT 857  
ID AAD47114 standard; DNA; 2040 BP.  
DE Leishmania sp. 6H (Lbhsp83) DNA.  
PN WO200272792-A2.  
PD 19-SEP-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 4.9%; Score 48.6; DB 6; Length 2040;  
Best Local Similarity 44.4%; Pred. No. 30;  
RESULT 858  
ID AAD40284 standard; DNA; 2040 BP.  
DE Leishmania braziliensis hsp83 antigenic protein encoding DNA.  
PN US6375955-B1.  
PD 23-APR-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 4.9%; Score 48.6; DB 6; Length 2040;  
Best Local Similarity 44.4%; Pred. No. 30;  
RESULT 859

ID AAS96021 standard; cDNA; 2040 BP.  
 DE Leishmania antigen Lbhsp83 DNA.  
 PN WO200179276-A2.  
 PD 25-OCT-2001.  
 PA (CORI-) CORIXA CORP.  
 Query Match 4.9%; Score 48.6; DB 6; Length 2040;  
 Best Local Similarity 44.4%; Pred. No. 30;  
 RESULT 860  
 ID ABK81732 standard; cDNA; 2040 BP.  
 DE Leishmania antigenic polynucleotide #3.  
 PN US6365165-B1.  
 PD 02-APR-2002.  
 PA (CORI-) CORIXA CORP.  
 Query Match 4.9%; Score 48.6; DB 6; Length 2040;  
 Best Local Similarity 44.4%; Pred. No. 30;  
 RESULT 861  
 ID AAF89523 standard; DNA; 2040 BP.  
 DE L. braziliensis Hsp83 antigen DNA SEQ ID 5.  
 PN US2002081320-A1.  
 PA (REED/) REED S G.  
 PA (CAMP/) CAMPOS-NETO A.  
 PA (WEBB/) WEBB J R.  
 PA (DILL/) DILLON D C.  
 PA (SKEI/) SKEIKY Y A W.  
 PA (BHAT/) BHATIA A.  
 PA (COLE/) COLER R N.  
 PA (PROB/) PROBST P.  
 PA (BRAN/) BRANNON M.  
 Query Match 4.9%; Score 48.6; DB 6; Length 2040;  
 Best Local Similarity 44.4%; Pred. No. 30;  
 RESULT 862  
 ID ADB78768 standard; cDNA; 2040 BP.  
 DE Leishmania DNA encoding antigen Lbhsp83.  
 PN US2002189285-A1.  
 PD 14-NOV-2002.  
 PA (REED/) REED S G.  
 PA (CAMP/) CAMPOS-NETO A.  
 PA (WEBB/) WEBB J R.  
 PA (DILL/) DILLON D C.  
 Query Match 4.9%; Score 48.6; DB 9; Length 2040;  
 Best Local Similarity 44.4%; Pred. No. 30;  
 RESULT 863  
 ID AAH14403 standard; cDNA; 2279 BP.  
 DE Human cDNA sequence SEQ ID NO:11841.  
 PN EP1074617-A2.  
 PD 07-FEB-2001.  
 PA (HELI-) HELIX RES INST.  
 Query Match 4.9%; Score 48.6; DB 4; Length 2279;  
 Best Local Similarity 47.3%; Pred. No. 30;  
 RESULT 864  
 ID ABX08845 standard; cDNA; 2279 BP.  
 DE Angiogenesis-associated human polynucleotide sequence #107.  
 PN WO200279492-A2.  
 PD 10-OCT-2002.  
 PA (BOSB-) EOS BIOTECHNOLOGY INC.  
 Query Match 4.9%; Score 48.6; DB 10; Length 2279;  
 Best Local Similarity 47.3%; Pred. No. 30;  
 RESULT 865  
 ID ADS34446 standard; DNA; 2279 BP.  
 DE POSH protein associated DNA #200.  
 PN WO2004078130-A2.  
 PD 16-SEP-2004.  
 PA (PROT-) PROTEOLOGICS INC.  
 Query Match 4.9%; Score 48.6; DB 13; Length 2279;  
 Best Local Similarity 47.3%; Pred. No. 30;  
 RESULT 866  
 ID AAH17825 standard; cDNA; 2454 BP.  
 DE Human cDNA sequence SEQ ID NO:17498.  
 PN EP1074617-A2.  
 PD 07-FEB-2001.  
 PA (HELI-) HELIX RES INST.  
 Query Match 4.9%; Score 48.6; DB 4; Length 2454;

Best Local Similarity 47.3%; Pred. No. 30;  
 RESULT 867  
 ID ADS34445 standard; DNA; 2454 BP.  
 DE POSH protein associated DNA #199.  
 PN WO2004078130-A2.  
 PD 16-SEP-2004.  
 PA (PROT-) PROTEOLOGICS INC.  
 Query Match 4.9%; Score 48.6; DB 13; Length 2454;  
 Best Local Similarity 47.3%; Pred. No. 30;  
 RESULT 868  
 ID ABD12439 standard; DNA; 2472 BP.  
 DE Pseudomonas aeruginosa polynucleotide #11043.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.9%; Score 48.6; DB 11; Length 2472;  
 Best Local Similarity 46.6%; Pred. No. 30;  
 RESULT 869  
 ID ADS34441 standard; DNA; 2544 BP.  
 DE POSH protein associated DNA #195.  
 PN WO2004078130-A2.  
 PD 16-SEP-2004.  
 PA (PROT-) PROTEOLOGICS INC.  
 Query Match 4.9%; Score 48.6; DB 13; Length 2544;  
 Best Local Similarity 47.3%; Pred. No. 30;  
 RESULT 870  
 ID AAL41592 standard; DNA; 2577 BP.  
 DE HIV-1 subtype C isolate Du151 pol gene.  
 PN WO200204494-A2.  
 PD 17-JAN-2002.  
 PA (MEDI-) MEDICAL RES COUNCIL.  
 PA (UYCA-) UNIV CAPE TOWN.  
 PA (UYNC-) UNIV NORTH CAROLINA.  
 Query Match 4.9%; Score 48.6; DB 6; Length 2577;  
 Best Local Similarity 47.8%; Pred. No. 30;  
 RESULT 871  
 ID AAZ06825 standard; DNA; 2712 BP.  
 DE Streptomyces albidoflavus endochitinase DNA.  
 PN WO9942594-A1.  
 PD 26-AUG-1999.  
 PA (CORR-) CORNELL RES FOUND INC.  
 Query Match 4.9%; Score 48.6; DB 2; Length 2712;  
 Best Local Similarity 47.8%; Pred. No. 30;  
 RESULT 872  
 ID AAH74538 standard; DNA; 2712 BP.  
 DE Nucleotide sequence of an endochitinase polypeptide.  
 PN WO200146387-A1.  
 PD 28-JUN-2001.  
 PA (CORR-) CORNELL RES FOUND INC.  
 Query Match 4.9%; Score 48.6; DB 4; Length 2712;  
 Best Local Similarity 47.6%; Pred. No. 30;  
 RESULT 873  
 ID ADS34444 standard; DNA; 3003 BP.  
 DE POSH protein associated DNA #198.  
 PN WO2004078130-A2.  
 PD 16-SEP-2004.  
 PA (PROT-) PROTEOLOGICS INC.  
 Query Match 4.9%; Score 48.6; DB 13; Length 3003;  
 Best Local Similarity 47.3%; Pred. No. 30;  
 RESULT 874  
 ID ADQ85699 standard; cDNA; 3268 BP.  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #2513.  
 PN WO2004060270-A2.  
 PD 22-JUL-2004.  
 PA (GETH-) GENENTECH INC.  
 PA (WUTD/) WU T D.  
 PA (ZHOU/) ZHOU Y.  
 Query Match 4.9%; Score 48.6; DB 12; Length 3268;  
 Best Local Similarity 47.3%; Pred. No. 30;  
 RESULT 875  
 ID ADQ86774 standard; cDNA; 3268 BP.  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #3649.  
 PN WO2004060270-A2.

PD 22-JUL-2004.  
PA (GETH ) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Query Match 4.9%; Score 48.6; DB 13; Length 3268;  
Best Local Similarity 47.3%; Pred. No. 30;  
RESULT 876  
ID ADS34439 standard; DNA; 3292 BP.  
DE POSH protein associated DNA #193.  
PN WO2004078130-A2.  
PD 16-SEP-2004.  
PA (PROT-) PROTEOLOGICS INC.  
Query Match 4.9%; Score 48.6; DB 13; Length 3292;  
Best Local Similarity 47.3%; Pred. No. 30;  
RESULT 877  
ID ABA95198 standard; cDNA; 3298 BP.  
DE Human MICAPTUB-2 polypeptide encoding cDNA (clone ID: 1593855CB1).  
PN WO200216587-A2.  
PD 28-FEB-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 4.9%; Score 48.6; DB 6; Length 3298;  
Best Local Similarity 47.3%; Pred. No. 30;  
RESULT 878  
ID ACC82987 standard; DNA; 3687 BP.  
DE HIV-1 Gtttnc DNA construct.  
PN WO2003037919-A2.  
PD 08-MAY-2003.  
PA (SAME-) SOUTH AFRICAN MEDICAL RES COUNCIL.  
PA (UYCA-) UNIV CAPE TOWN.  
Query Match 4.9%; Score 48.6; DB 8; Length 3687;  
Best Local Similarity 47.8%; Pred. No. 30;  
RESULT 879  
ID ADO85410 standard; DNA; 3720 BP.  
DE Streptomycetes phoK/phoR::omegaaac double mutant, seq id 5.  
PN FR2848567-A1.  
PD 18-JUN-2004.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 4.9%; Score 48.6; DB 12; Length 3720;  
Best Local Similarity 49.4%; Pred. No. 30;  
RESULT 880  
ID ADQ85245 standard; cDNA; 4405 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #2059.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH ) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Query Match 4.9%; Score 48.6; DB 13; Length 4405;  
Best Local Similarity 47.5%; Pred. No. 29;  
RESULT 881  
ID ADC39155 standard; cDNA; 4760 BP.  
DE Novel human NOVX polypeptide coding sequence SEQ ID NO: 97.  
PN WO2003010327-A2.  
PD 06-FEB-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 4.9%; Score 48.6; DB 10; Length 4760;  
Best Local Similarity 43.8%; Pred. No. 29;  
RESULT 882  
ID ADH72283 standard; DNA; 4760 BP.  
DE Human gene of the invention NOV60d SEQ ID NO:1179.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 4.9%; Score 48.6; DB 12; Length 4760;  
Best Local Similarity 43.8%; Pred. No. 29;  
RESULT 883  
ID ADO85408 standard; DNA; 4860 BP.  
DE Streptomycetes phoK::omegaaac mutant, seq id 3.  
PN FR2848567-A1.  
PD 18-JUN-2004.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 4.9%; Score 48.6; DB 12; Length 4860;  
Best Local Similarity 49.4%; Pred. No. 29;

RESULT 884  
ID AAH48730 standard; cDNA; 5065 BP.  
DE Human HCN4 cDNA.  
PN WO200159153-A2.  
PD 16-AUG-2001.  
PA (AVET ) AVENTIS PHARMA DEUT GMBH.  
Query Match 4.9%; Score 48.6; DB 4; Length 5065;  
Best Local Similarity 50.6%; Pred. No. 29;  
RESULT 885  
ID ADR86593 standard; cDNA; 5065 BP.  
DE Human HCN4 gene.  
PN JP2004254628-A.  
PD 16-SEP-2004.  
PA (KIMU/) KIMURA A.  
Query Match 4.9%; Score 48.6; DB 13; Length 5065;  
Best Local Similarity 50.6%; Pred. No. 29;  
RESULT 886  
ID ABA09197 standard; cDNA; 5499 BP.  
DE Human cation channel hHCN4 homologue cDNA, SEQ ID NO:973.  
PN WO200157188-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.9%; Score 48.6; DB 4; Length 5499;  
Best Local Similarity 50.6%; Pred. No. 29;  
RESULT 887  
ID ADC39153 standard; cDNA; 6224 BP.  
DE Novel human NOVX polypeptide coding sequence SEQ ID NO: 95.  
PN WO2003010327-A2.  
PD 06-FEB-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 4.9%; Score 48.6; DB 10; Length 6224;  
Best Local Similarity 43.8%; Pred. No. 29;  
RESULT 888  
ID ADH72277 standard; DNA; 6224 BP.  
DE Human gene of the invention NOV60a SEQ ID NO:1173.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 4.9%; Score 48.6; DB 12; Length 6224;  
Best Local Similarity 43.8%; Pred. No. 29;  
RESULT 889  
ID ADM74234 standard; DNA; 6224 BP.  
DE Human NOV8A gene sequence SeqID73.  
PN WO2004015079-A2.  
PD 19-FEB-2004.  
PA (CURA-) CURAGEN CORP.  
Query Match 4.9%; Score 48.6; DB 12; Length 6224;  
Best Local Similarity 43.8%; Pred. No. 29;  
RESULT 890  
ID ADC39163 standard; cDNA; 6494 BP.  
DE Novel human NOVX polypeptide coding sequence SEQ ID NO: 105.  
PN WO2003010327-A2.  
PD 06-FEB-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 4.9%; Score 48.6; DB 10; Length 6494;  
Best Local Similarity 43.8%; Pred. No. 29;  
RESULT 891  
ID ADH72291 standard; DNA; 6494 BP.  
DE Human gene of the invention NOV60h SEQ ID NO:1187.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 4.9%; Score 48.6; DB 12; Length 6494;  
Best Local Similarity 43.8%; Pred. No. 29;  
RESULT 892  
ID AAV23873 standard; DNA; 562 BP.  
DE Plant OMT enzyme DNA sequence.  
PN WO9811205-A2.  
PD 19-MAR-1998.  
PA (GENE-) GENESIS RES & DEV CORP LTD.

PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Query Match 4.9%; Score 48.4; DB 2; Length 562;  
Best Local Similarity 49.2%; Pred. No. 34;  
RESULT 894  
ID AAZ06876 standard; cDNA; 562 BP.  
DE Pine O-methyl transferase (OMT) partial cDNA 2.  
PN US5952486-A.  
PD 14-SEP-1999.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
Query Match 4.9%; Score 48.4; DB 2; Length 562;  
Best Local Similarity 49.2%; Pred. No. 34;  
RESULT 895  
ID AAA69580 standard; cDNA; 562 BP.  
DE Pinus radiata O-methyltransferase cDNA SEQ ID NO:54.  
PN WO200036081-A2.  
PD 22-JUN-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Query Match 4.9%; Score 48.4; DB 3; Length 562;  
Best Local Similarity 49.2%; Pred. No. 34;  
RESULT 896  
ID AAA67960 standard; DNA; 562 BP.  
DE Pinus radiata OMT nucleotide sequence SEQ ID NO:53.  
PN WO200022099-A1.  
PD 20-APR-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Query Match 4.9%; Score 48.4; DB 3; Length 562;  
Best Local Similarity 49.2%; Pred. No. 34;  
RESULT 897  
ID ADD41710 standard; DNA; 562 BP.  
DE O-methyl transferase DNA #6.  
PN US2003131373-A1.  
PD 10-JUL-2003.  
PA (BLOK/) BLOKSBERG L N.  
PA (HAVU/) HAVUKKALA I.  
Query Match 4.9%; Score 48.4; DB 10; Length 562;  
Best Local Similarity 49.2%; Pred. No. 34;  
RESULT 898  
ID ADO52096 standard; DNA; 633 BP.  
DE Novel canine microarray-related DNA sequence SeqID33398.  
PN WO2004063324-A2.  
PD 29-JUL-2004.  
PA (GENE-) GENE LOGIC INC.  
PA (PFIZ) PFIZER PROD INC.  
Query Match 4.9%; Score 48.4; DB 13; Length 633;  
Best Local Similarity 49.8%; Pred. No. 34;  
RESULT 899  
ID AAQ43032 standard; DNA; 756 BP.  
DE Collagen-like polymer DCP3-C2 (AB12)C2 coding sequence.  
PN WO9310154-A1.  
PD 27-MAY-1993.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 4.9%; Score 48.4; DB 2; Length 756;  
Best Local Similarity 44.3%; Pred. No. 33;  
RESULT 900  
ID AAT16766 standard; DNA; 756 BP.  
DE Collagen-like polymer sequence D gene 2 encoding unit C2A24C2.  
PN US5496712-A.  
PD 05-MAR-1996.  
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
Query Match 4.9%; Score 48.4; DB 2; Length 756;  
Best Local Similarity 44.3%; Pred. No. 33;  
RESULT 901  
ID AAQ2484 standard; cDNA; 1000 BP.  
DE Human colon cancer cell line polynucleotide sequence SEQ ID NO:2475.  
PN WO9558675-A2.  
PD 18-NOV-1999.  
PA (CHIR) CHIRON CORP.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.9%; Score 48.4; DB 3; Length 1000;  
Best Local Similarity 33.5%; Pred. No. 33;

RESULT 902  
ID ADA70207 standard; DNA; 1059 BP.  
DE Rice gene, SEQ ID 3530.  
PN WO2003000898-A1.  
PD 03-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 4.9%; Score 48.4; DB 8; Length 1059;  
Best Local Similarity 43.8%; Pred. No. 33;  
RESULT 903  
ID ADJ11579 standard; DNA; 1059 BP.  
DE Rice DNA modulated by post-transcriptional gene silencing SeqID 215.  
PN US2003135888-A1.  
PD 17-JUL-2003.  
PA (ZHUT/) ZHU T.  
PA (WANG/) WANG X.  
PA (CHAN/) CHANG H.  
PA (BRIG/) BRIGGS S P.  
PA (COOP/) COOPER B.  
PA (GLAZ/) GLAZEBROOK J.  
PA (GOFF/) GOFF S A.  
PA (KATA/) KATAGIRI F.  
PA (KREP/) KREPS J.  
PA (MOUG/) MOUGHAMER T.  
PA (PROV/) PROVART N.  
PA (RICK/) RIQUE D.  
Query Match 4.9%; Score 48.4; DB 11; Length 1059;  
Best Local Similarity 43.8%; Pred. No. 33;  
RESULT 904  
ID ADA71187 standard; DNA; 1482 BP.  
DE Rice gene, SEQ ID 4510.  
PN WO2003000898-A1.  
PD 03-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 4.9%; Score 48.4; DB 8; Length 1482;  
Best Local Similarity 44.0%; Pred. No. 33;  
RESULT 905  
ID AAZ35999 standard; DNA; 1646 BP.  
DE S. kitatoensis macrolide antibiotic acylation enzyme gene.  
PN JP11285384-A.  
PD 19-OCT-1999.  
PA (ASAH) ASAH KASEI KOGYO KK.  
Query Match 4.9%; Score 48.4; DB 3; Length 1646;  
Best Local Similarity 50.4%; Pred. No. 33;  
RESULT 906  
ID ACA37821 standard; DNA; 1650 BP.  
DE Prokaryotic essential gene #19478.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.9%; Score 48.4; DB 8; Length 1650;  
Best Local Similarity 45.0%; Pred. No. 33;  
RESULT 907  
ID ACA27358 standard; DNA; 2523 BP.  
DE Prokaryotic essential gene #9015.  
PN WO20027183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.9%; Score 48.4; DB 8; Length 2523;  
Best Local Similarity 47.4%; Pred. No. 32;  
RESULT 908  
ID ADA70538 standard; DNA; 2562 BP.  
DE Rice gene, SEQ ID 3861.  
PN WO2003000898-A1.  
PD 03-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 4.9%; Score 48.4; DB 8; Length 2562;  
Best Local Similarity 47.3%; Pred. No. 32;  
RESULT 909  
ID AAS06333 standard; cDNA; 2898 BP.  
DE RNA encoding human glutamate receptor-like protein, MEM2.  
PN WO200144473-A2.  
PD 21-JUN-2001.  
PA (CURA-) CURAGEN CORP.

Query Match 4.9%; Score 48.4; DB 4; Length 2898;  
 Best Local Similarity 43.0%; Pred. No. 32;  
 RESULT 910  
 ID AAD07033 standard; DNA; 3690 BP.  
 DE Methylobacterium extorquens PHA synthase DNA.  
 PN WO200123596-A2.  
 PD 05-APR-2001.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 PA (DUPO) DU PONT DE NEMOURS & CO E I.  
 Query Match 4.9%; Score 48.4; DB 4; Length 3690;  
 Best Local Similarity 48.2%; Pred. No. 32;  
 RESULT 911  
 ID AAZ09496 standard; DNA; 4751 BP.  
 DE Human heart tissue Ih ion channel DNA.  
 PN WO9942574-A1.  
 PD 26-AUG-1999.  
 PA (KERJ) FORSCHUNGSZENTRUM JUELICH OMBH.  
 Query Match 4.9%; Score 48.4; DB 2; Length 4751;  
 Best Local Similarity 53.8%; Pred. No. 32;  
 RESULT 912  
 ID AAD29757 standard; DNA; 4751 BP.  
 DE Human hyperpolarisation-activated cyclic nucleotide-gated channel 4 DNA.  
 PN WO200202630-A2.  
 PD 10-JAN-2002.  
 PA (SMIK) SMITHKLINE BEECHAM PLC.  
 Query Match 4.9%; Score 48.4; DB 6; Length 4751;  
 Best Local Similarity 53.8%; Pred. No. 32;  
 RESULT 913  
 ID ACA37735 standard; DNA; 4833 BP.  
 DE Prokaryotic essential gene #19392.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.9%; Score 48.4; DB 8; Length 4833;  
 Best Local Similarity 50.3%; Pred. No. 32;  
 RESULT 914  
 ID AAD54223 standard; DNA; 24081 BP.  
 DE Streptomyces platensis subspecies rosaceus dorrigocin ORF6 DNA.  
 PN WO200288176-A2.  
 PD 07-NOV-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 4.9%; Score 48.4; DB 10; Length 24081;  
 Best Local Similarity 51.1%; Pred. No. 30;  
 RESULT 915  
 ID ACA37577 standard; DNA; 31263 BP.  
 DE Prokaryotic essential gene #19234.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.9%; Score 48.4; DB 8; Length 31263;  
 Best Local Similarity 46.2%; Pred. No. 30;  
 RESULT 916  
 ID AAD54217 standard; DNA; 52101 BP.  
 DE Streptomyces platensis subspecies rosaceus dorrigocin DNA.  
 PN WO200288176-A2.  
 PD 07-NOV-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 4.9%; Score 48.4; DB 10; Length 52101;  
 Best Local Similarity 51.1%; Pred. No. 30;  
 RESULT 917  
 ID AAD54217 standard; DNA; 52101 BP.  
 DE Streptomyces platensis subspecies rosaceus dorrigocin DNA.  
 PN WO200288176-A2.  
 PD 07-NOV-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 4.9%; Score 48.4; DB 4; Length 110000;  
 Best Local Similarity 45.6%; Pred. No. 29;  
 RESULT 918  
 ID ADQ54676 standard; DNA; 489 BP.  
 DE Novel canine microarray-related DNA sequence SeqID5978.  
 PN WO2004063324-A2.  
 PD 29-JUL-2004.  
 PA (GENE-) GENE LOGIC INC.  
 PA (PFIZ) PFIZER PROD INC.  
 Query Match 4.9%; Score 48.2; DB 13; Length 489;  
 Best Local Similarity 52.7%; Pred. No. 37;  
 RESULT 919  
 ID AAD57189 standard; DNA; 600 BP.

DE Mycobacterium avium subspecies paratuberculosis protein gene #2.  
 PN WO2003058248-A2.  
 PD 17-JUL-2003.  
 PA (IDLE-) ID-LELYSTAD INST DIERHOUDERIJ EN DIERGEZ.  
 Query Match 4.9%; Score 48.2; DB 9; Length 600;  
 Best Local Similarity 48.4%; Pred. No. 36;  
 RESULT 920  
 ID ADC30820 standard; cDNA; 663 BP.  
 DE Human novel cDNA sequence, SEQ ID NO:902.  
 PN WO2003029271-A2.  
 PD 10-APR-2003.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 4.9%; Score 48.2; DB 10; Length 663;  
 Best Local Similarity 52.7%; Pred. No. 36;  
 RESULT 921  
 ID ADK52175 standard; cDNA; 663 BP.  
 DE Full length cDNA clone MasP1 clone 3.  
 PN WO2004016651-A2.  
 PD 26-FEB-2004.  
 PA (UYVO-) UNIV YORK.  
 Query Match 4.9%; Score 48.2; DB 12; Length 663;  
 Best Local Similarity 44.0%; Pred. No. 36;  
 RESULT 922  
 ID ADJ39458 standard; cDNA; 786 BP.  
 DE Plant cDNA #458.  
 PN US2004016025-A1.  
 PD 22-JAN-2004.  
 PA (BUDW) BUDWORTH P.  
 PA (MOUG) MOUGHAMER T.  
 PA (BRIG) BRIGGS S P.  
 PA (COOP) COOPER B.  
 PA (GLAZ) GLAZERBOOK J.  
 PA (GOFF) GOFF S A.  
 PA (KATA) KATAGIRI F.  
 PA (KREP) KREPS J.  
 PA (PROV) PROVART N.  
 PA (RICK) RIQUE D.  
 PA (ZHUT) ZHU T.  
 Query Match 4.9%; Score 48.2; DB 12; Length 786;  
 Best Local Similarity 49.8%; Pred. No. 36;  
 RESULT 923  
 ID ACC68993 standard; cDNA; 811 BP.  
 DE Human neurotransmission-associated protein NTRAN-15 cDNA SEQ ID NO:40.  
 PN WO2003025129-A2.  
 PD 27-MAR-2003.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Query Match 4.9%; Score 48.2; DB 10; Length 811;  
 Best Local Similarity 52.7%; Pred. No. 36;  
 RESULT 924  
 ID ABD13103 standard; DNA; 822 BP.  
 DE Pseudomonas aeruginosa polynucleotide #11707.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.9%; Score 48.2; DB 11; Length 822;  
 Best Local Similarity 46.5%; Pred. No. 36;  
 RESULT 925  
 ID ADG10464 standard; cDNA; 823 BP.  
 DE Human STAT6-activating protein-encoding cDNA, SEQ ID NO:54.  
 PN WO200296943-A1.  
 PD 05-DEC-2002.  
 PA (ASAH) ASAH KASEI KOGYO KK.  
 Query Match 4.9%; Score 48.2; DB 10; Length 823;  
 Best Local Similarity 52.7%; Pred. No. 36;  
 RESULT 926  
 ID ADG10466 standard; cDNA; 823 BP.  
 DE Human STAT6-activating protein-encoding cDNA, SEQ ID NO:56.  
 PN WO200296943-A1.  
 PD 05-DEC-2002.  
 PA (ASAH) ASAH KASEI KOGYO KK.  
 Query Match 4.9%; Score 48.2; DB 10; Length 823;  
 Best Local Similarity 52.7%; Pred. No. 36;  
 RESULT 927

ID ACA37950 standard; DNA; 825 BP.  
DE Prokaryotic essential gene #19607.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.9%; Score 48.2; DB 8; Length 825;  
Best Local Similarity 48.9%; Pred. No. 36;  
RESULT 928  
ID AAI58255 standard; cDNA; 920 BP.  
DE Human polynucleotide SEQ ID NO 458.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSSEQ INC.  
Query Match 4.9%; Score 48.2; DB 4; Length 920;  
Best Local Similarity 52.7%; Pred. No. 36;  
RESULT 929  
ID ADQ98462 standard; cDNA; 920 BP.  
DE DNA encoding human GPCR-like protein seqid 132.  
PN US659662-B1.  
PD 27-MAY-2003.  
PA (HYSE-) HYSSEQ INC.  
Query Match 4.9%; Score 48.2; DB 5; Length 920;  
Best Local Similarity 52.7%; Pred. No. 36;  
RESULT 930  
ID ADB48222 standard; cDNA; 920 BP.  
DE Novel human cDNA SEQ ID NO 132.  
PN US2003104529-A1.  
PD 05-JUN-2003.  
PA (ZHOU/) ZHOU P.  
PA (TANG/) TANG Y T.  
PA (LIUC/) LIU C.  
PA (ASUN/) ASUNDI V.  
PA (DRMA/) DRMANAC R T.  
Query Match 4.9%; Score 48.2; DB 9; Length 920;  
Best Local Similarity 52.7%; Pred. No. 36;  
RESULT 931  
ID ACA42680 standard; DNA; 930 BP.  
DE Prokaryotic essential gene #24337.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.9%; Score 48.2; DB 8; Length 930;  
Best Local Similarity 48.1%; Pred. No. 36;  
RESULT 932  
ID ABK51403 standard; DNA; 969 BP.  
DE DNA encoding human CCAAT enhancer binding protein beta-2.  
PN WO200160973-A2.  
PD 23-AUG-2001.  
PA (UYVA-) UNIV VANDERBILT.  
Query Match 4.9%; Score 48.2; DB 4; Length 969;  
Best Local Similarity 47.2%; Pred. No. 36;  
RESULT 933  
ID RAD19181 standard; DNA; 969 BP.  
DE Human CCAAT/enhancer binding protein (C/EBP) beta-2 isoform DNA.  
PN WO200160320-A2.  
PD 23-AUG-2001.  
PA (UYVA-) UNIV VANDERBILT.  
Query Match 4.9%; Score 48.2; DB 4; Length 969;  
Best Local Similarity 47.2%; Pred. No. 36;  
RESULT 934  
ID ADQ83726 standard; cDNA; 972 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #540.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Query Match 4.9%; Score 48.2; DB 12; Length 972;  
Best Local Similarity 52.7%; Pred. No. 36;  
RESULT 935  
ID ADQ87027 standard; cDNA; 972 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3903.  
PN WO2004060270-A2.

PD 22-JUL-2004.  
PA (GETH) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Query Match 4.9%; Score 48.2; DB 13; Length 972;  
Best Local Similarity 52.7%; Pred. No. 36;  
RESULT 936  
ID ABK51402 standard; DNA; 1038 BP.  
DE DNA encoding human CCAAT enhancer binding protein beta-1.  
PN WO200160973-A2.  
PD 23-AUG-2001.  
PA (UYVA-) UNIV VANDERBILT.  
Query Match 4.9%; Score 48.2; DB 4; Length 1038;  
Best Local Similarity 47.2%; Pred. No. 36;  
RESULT 937  
ID RAD19380 standard; DNA; 1038 BP.  
DE Human CCAAT/enhancer binding protein (C/EBP) beta-1 isoform DNA.  
PN WO200160320-A2.  
PD 23-AUG-2001.  
PA (UYVA-) UNIV VANDERBILT.  
Query Match 4.9%; Score 48.2; DB 4; Length 1038;  
Best Local Similarity 47.2%; Pred. No. 36;  
RESULT 938  
ID AAS14696 standard; DNA; 1038 BP.  
DE Human cDNA encoding transcription factor C/EBPbeta.  
PN WO200174298-A2.  
PD 11-OCT-2001.  
PA (UYBR-) UNIV BROWN RESEARCH FOUND.  
PA (HUGH-) HUGHES HOWARD MED INST.  
Query Match 4.9%; Score 48.2; DB 4; Length 1038;  
Best Local Similarity 47.2%; Pred. No. 36;  
RESULT 939  
ID AAL44084 standard; DNA; 1038 BP.  
DE Human C/EBP-beta protein coding sequence 3.  
PN WO200254938-A2.  
PD 18-JUL-2002.  
PA (REGC) UNIV CALIFORNIA.  
Query Match 4.9%; Score 48.2; DB 6; Length 1038;  
Best Local Similarity 47.2%; Pred. No. 36;  
RESULT 940  
ID ABK51997 standard; DNA; 1038 BP.  
DE DNA encoding wild-type human C/EBPbeta protein #3.  
PN WO200246218-A2.  
PD 13-JUN-2002.  
PA (REGC) UNIV CALIFORNIA.  
Query Match 4.9%; Score 48.2; DB 6; Length 1038;  
Best Local Similarity 47.2%; Pred. No. 36;  
RESULT 941  
ID ACF36516 standard; DNA; 1038 BP.  
DE Human wild-type C/EBPbeta polypeptide encoding DNA.  
PN WO2003072031-A2.  
PD 04-SEP-2003.  
PA (REGC) UNIV CALIFORNIA.  
Query Match 4.9%; Score 48.2; DB 10; Length 1038;  
Best Local Similarity 47.2%; Pred. No. 36;  
RESULT 942  
ID ACN40795 standard; cDNA; 1038 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA326852, SEQ ID NO:5808.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 4.9%; Score 48.2; DB 13; Length 1038;  
Best Local Similarity 47.2%; Pred. No. 36;  
RESULT 943  
ID ABK51410 standard; DNA; 1042 BP.  
DE Human CCAAT enhancer binding protein (C/EBPB) gene mutant.  
PN WO200160973-A2.  
PD 23-AUG-2001.  
PA (UYVA-) UNIV VANDERBILT.  
Query Match 4.9%; Score 48.2; DB 4; Length 1042;  
Best Local Similarity 47.2%; Pred. No. 36;  
RESULT 944  
ID ADS14749 standard; DNA; 1059 BP.

DE Pseudomonas aeruginosa quorum sensing controlled gene PA5161, SEQ ID 304.  
PN WO2004083385-A2.  
PD 30-SEP-2004.  
PA (IOWA ) UNIV IOWA RES FOUND.  
Query Match 4.9%; Score 48.2; DB 13; Length 1059;  
Best Local Similarity 47.5%; Pred. No. 36;  
RESULT 945  
ID ADK71964 standard; DNA; 1260 BP.  
DE Human I Kappa B kinase (IKK) gamma DNA SeqID 22.  
PN WO2004016781-A1.  
PD 26-FEB-2004.  
PA (RIKE ) RIKEN KK.  
PA (KAZU-) KAZUSA DNA RES INST.  
Query Match 4.9%; Score 48.2; DB 12; Length 1260;  
Best Local Similarity 47.8%; Pred. No. 36;  
RESULT 946  
ID AAD55721 standard; DNA; 1336 BP.  
DE Argiope trifasciata major ampullate spidroin 2 (MaSp2) DNA.  
PN WO2003020916-A2.  
PD 13-MAR-2003.  
PA (UYWY-) UNIV WYOMING.  
Query Match 4.9%; Score 48.2; DB 8; Length 1336;  
Best Local Similarity 43.2%; Pred. No. 36;  
RESULT 947  
ID ADP09651 standard; DNA; 1413 BP.  
DE Rice cinnamic acid 5-hydroxylase ORF DNA without the T-DNA insert Seq 42.  
PN WO2004046357-A1.  
PD 03-JUN-2004.  
PA (POSC-) POSCO.  
PA (POST-) POSTECH FOUND.  
Query Match 4.9%; Score 48.2; DB 12; Length 1413;  
Best Local Similarity 49.8%; Pred. No. 35;  
RESULT 948  
ID ADP75211 standard; cDNA; 1701 BP.  
DE Human ADAMTS2 cDNA splice variant 2.  
PN WO2003031594-A2.  
PD 17-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48.2; DB 11; Length 1701;  
Best Local Similarity 44.0%; Pred. No. 35;  
RESULT 949  
ID AAA35065 standard; DNA; 1910 BP.  
DE Human adenosine receptor related polynucleotide SEQ ID NO:2754.  
PN WO200009525-A2.  
PD 24-FEB-2000.  
PA (UYEC-) UNIV EAST CAROLINA.  
Query Match 4.9%; Score 48.2; DB 3; Length 1910;  
Best Local Similarity 47.2%; Pred. No. 35;  
RESULT 950  
ID AAF21187 standard; DNA; 1910 BP.  
DE Human low adenosine antisense oligonucleotide related sequence #2754.  
PN WO200062736-A2.  
PD 26-OCT-2000.  
PA (UYEC-) UNIV EAST CAROLINA.  
PA (NYCE-) NYCE J W.  
Query Match 4.9%; Score 48.2; DB 3; Length 1910;  
Best Local Similarity 47.2%; Pred. No. 35;  
RESULT 951  
ID ABK51401 standard; DNA; 1910 BP.  
DE Human CCAAT enhancer binding protein (C/EBPB) gene.  
PN WO200160973-A2.  
PD 23-AUG-2001.  
PA (UYVA-) UNIV VANDERBILT.  
Query Match 4.9%; Score 48.2; DB 4; Length 1910;  
Best Local Similarity 47.2%; Pred. No. 35;  
RESULT 952  
ID AAD19379 standard; DNA; 1910 BP.  
DE Human CCAAT/enhancer binding protein (C/EBP) beta DNA.  
PN WO200160320-A2.  
PD 23-AUG-2001.  
PA (UYVA-) UNIV VANDERBILT.  
Query Match 4.9%; Score 48.2; DB 4; Length 1910;  
Best Local Similarity 47.2%; Pred. No. 35;

RESULT 953  
ID AAL44083 standard; DNA; 1910 BP.  
DE Human C/EBP-beta protein coding sequence 2.  
PN WO200254938-A2.  
PD 18-JUL-2002.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 4.9%; Score 48.2; DB 6; Length 1910;  
Best Local Similarity 47.2%; Pred. No. 35;  
RESULT 954  
ID ABK84563 standard; cDNA; 1910 BP.  
DE Human cDNA differentially expressed in granulocytic cells #1134.  
PN WO200228999-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 4.9%; Score 48.2; DB 6; Length 1910;  
Best Local Similarity 47.2%; Pred. No. 35;  
RESULT 955  
ID ABL94237 standard; cDNA; 1910 BP.  
DE Human C/EBP beta-encoding cDNA, SEQ ID NO:3.  
PN US6271030-B1.  
PD 07-AUG-2001.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 4.9%; Score 48.2; DB 6; Length 1910;  
Best Local Similarity 47.2%; Pred. No. 35;  
RESULT 956  
ID ABK51996 standard; DNA; 1910 BP.  
DE DNA encoding wild-type human C/EBPbeta protein #2.  
PN WO200246218-A2.  
PD 13-JUN-2002.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 4.9%; Score 48.2; DB 6; Length 1910;  
Best Local Similarity 47.2%; Pred. No. 35;  
RESULT 957  
ID ACF36515 standard; DNA; 1910 BP.  
DE Human wild-type C/EBPbeta polypeptide encoding DNA.  
PN WO2003072031-A2.  
PD 04-SEP-2003.  
PA (REGC ) UNIV CALIFORNIA.  
Query Match 4.9%; Score 48.2; DB 10; Length 1910;  
Best Local Similarity 47.2%; Pred. No. 35;  
RESULT 958  
ID ABZ96881 standard; DNA; 1910 BP.  
DE Human nucleic acid sequence.  
PN WO200285308-A2.  
PD 31-OCT-2002.  
PA (EPIG-) EPIGENESIS PHARM INC.  
Query Match 4.9%; Score 48.2; DB 10; Length 1910;  
Best Local Similarity 47.2%; Pred. No. 35;  
RESULT 959  
ID ABD20730 standard; DNA; 1910 BP.  
DE Human pulmonary and inflammatory target DNA #341.  
PN WO200285309-A2.  
PD 31-OCT-2002.  
PA (EPIG-) EPIGENESIS PHARM INC.  
Query Match 4.9%; Score 48.2; DB 11; Length 1910;  
Best Local Similarity 47.2%; Pred. No. 35;  
RESULT 960  
ID AAQ15015 standard; DNA; 1913 BP.  
DE Nuclear factor C/EBP2 DNA.  
PN JP03236782-A.  
PD 22-OCT-1991.  
PA (CHUZ-) CHUZO KISH IMOTO.  
Query Match 4.9%; Score 48.2; DB 2; Length 1913;  
Best Local Similarity 47.2%; Pred. No. 35;  
RESULT 961  
ID ADQ87415 standard; cDNA; 1967 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #4292.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH ) GENENTECH INC.  
PA (WUTD/) WU T D.  
PA (ZHOU/) ZHOU Y.  
Query Match 4.9%; Score 48.2; DB 13; Length 1967;



Best Local Similarity 47.8%; Pred. No. 35;  
 RESULT 962  
 ID A086256 standard; cDNA; 1967 BP.  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #3128.  
 PN WO2004060270-A2.  
 PD 22-JUL-2004.  
 PA (GETH) GENENTECH INC.  
 PA (WUTD) WU T D.  
 PA (ZHOU) ZHOU Y.  
 Query Match 4.9%; Score 48.2; DB 13; Length 1967;  
 Best Local Similarity 47.8%; Pred. No. 35;  
 RESULT 963  
 ID ADA44712 standard; DNA; 1975 BP.  
 DE Human inhibitor-kappa B kinase-gamma encoding DNA #SEQ ID 10.  
 PN WO2003031576-A2.  
 PD 17-APR-2003.  
 PA (ISIS-) ISIS PHARM INC.  
 Query Match 4.9%; Score 48.2; DB 8; Length 1975;  
 Best Local Similarity 47.8%; Pred. No. 35;  
 RESULT 964  
 ID AAC81426 standard; cDNA; 1994 BP.  
 DE Human I-kappa-B kinase gamma-subunit (IKK-gamma) cDNA.  
 PN JP2000253884-A.  
 PD 19-SEP-2000.  
 PA (TOAG) TOA GOSHI CHEM IND LTD.  
 Query Match 4.9%; Score 48.2; DB 3; Length 1994;  
 Best Local Similarity 47.8%; Pred. No. 35;  
 RESULT 965  
 ID AAA35027 standard; DNA; 1994 BP.  
 DE Human adenosine receptor related polynucleotide SEQ ID NO:2716.  
 PN WO200009525-A2.  
 PD 24-FEB-2000.  
 PA (UYEC-) UNIV EAST CAROLINA.  
 Query Match 4.9%; Score 48.2; DB 3; Length 1994;  
 Best Local Similarity 47.8%; Pred. No. 35;  
 RESULT 966  
 ID AAF21149 standard; DNA; 1994 BP.  
 DE Human low adenosine antisense oligonucleotide related sequence #2716.  
 PN WO200062736-A2.  
 PD 26-OCT-2000.  
 PA (UYEC-) UNIV EAST CAROLINA.  
 PA (NYCE/) NYCE J W.  
 Query Match 4.9%; Score 48.2; DB 3; Length 1994;  
 Best Local Similarity 47.8%; Pred. No. 35;  
 RESULT 967  
 ID ADA44705 standard; DNA; 1994 BP.  
 DE Human inhibitor-kappa B kinase-gamma encoding DNA #SEQ ID 3.  
 PN WO2003031576-A2.  
 PD 17-APR-2003.  
 PA (ISIS-) ISIS PHARM INC.  
 Query Match 4.9%; Score 48.2; DB 8; Length 1994;  
 Best Local Similarity 47.8%; Pred. No. 35;  
 RESULT 968  
 ID ABZ96843 standard; DNA; 1994 BP.  
 DE Human nucleic acid sequence.  
 PN WO200285308-A2.  
 PD 31-OCT-2002.  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 Query Match 4.9%; Score 48.2; DB 10; Length 1994;  
 Best Local Similarity 47.8%; Pred. No. 35;  
 RESULT 969  
 ID ABV75393 standard; DNA; 1994 BP.  
 DE Human NEMO polypeptide encoding DNA.  
 PN WO200292761-A2.  
 PD 21-NOV-2002.  
 PA (IMMV) IMMUNEX CORP.  
 Query Match 4.9%; Score 48.2; DB 10; Length 1994;  
 Best Local Similarity 47.8%; Pred. No. 35;  
 RESULT 970  
 ID ABD20692 standard; DNA; 1994 BP.  
 DE Human pulmonary and inflammatory target DNA #303.  
 PN WO200285309-A2.  
 PD 31-OCT-2002.

PA (EPIG-) EPIGENESIS PHARM INC.  
 Query Match 4.9%; Score 48.2; DB 11; Length 1994;  
 Best Local Similarity 47.8%; Pred. No. 35;  
 RESULT 971  
 ID AAZ07513 standard; DNA; 2009 BP.  
 DE Human RIP-associated protein (RAP-2) encoding DNA.  
 PN WO9947672-A1.  
 PD 23-SEP-1999.  
 PA (YED) YEDA RES & DEV CO LTD.  
 PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.  
 Query Match 4.9%; Score 48.2; DB 2; Length 2009;  
 Best Local Similarity 47.8%; Pred. No. 35;  
 RESULT 972  
 ID AAV06593 standard; cDNA; 2023 BP.  
 DE Human N-proteinase (short form) cDNA.  
 PN WO9800555-A1.  
 PD 08-JAN-1998.  
 PA (PROC/) PROCKOP D J.  
 PA (COLI/) COLIGE A.  
 PA (LAPI/) LAPIERE C.  
 Query Match 4.9%; Score 48.2; DB 2; Length 2023;  
 Best Local Similarity 44.0%; Pred. No. 35;  
 RESULT 973  
 ID ABS57455 standard; cDNA; 2023 BP.  
 DE Human short form N-proteinase cDNA.  
 PN US6428998-B1.  
 PD 06-AUG-2002.  
 PA (UYLI-) UNIV LIEGE.  
 Query Match 4.9%; Score 48.2; DB 10; Length 2023;  
 Best Local Similarity 44.0%; Pred. No. 35;  
 RESULT 974  
 ID AAZ07514 standard; DNA; 2034 BP.  
 DE Human RIP-associated protein (RAP-2) clone #41072 nucleotide sequence.  
 PN WO9947672-A1.  
 PD 23-SEP-1999.  
 PA (YED) YEDA RES & DEV CO LTD.  
 PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.  
 Query Match 4.9%; Score 48.2; DB 2; Length 2034;  
 Best Local Similarity 47.8%; Pred. No. 35;  
 RESULT 975  
 ID ACD23012 standard; cDNA; 2035 BP.  
 DE Human NEMO cDNA.  
 PN US2003032055-A1.  
 PD 13-FEB-2003.  
 PA (KENW/) KENWRICK S J.  
 PA (WOF/) WOFENDIN H.  
 PA (MUNN/) MUNNICH A.  
 PA (SMAH/) SMAHI A.  
 PA (ISRA/) ISRAEL A.  
 PA (POUS/) POUSTKA A.  
 PA (HEIS/) HEISS N.  
 PA (DURS/) D'URSO M.  
 PA (LEWI/) LEWIS R A.  
 PA (NELS/) NELSON D L.  
 PA (ARAD/) ARADHYA S.  
 PA (LEVY/) LEVY M.  
 Query Match 4.9%; Score 48.2; DB 9; Length 2035;  
 Best Local Similarity 47.8%; Pred. No. 35;  
 RESULT 976  
 ID AAA35066 standard; DNA; 2171 BP.  
 DE Human adenosine receptor related polynucleotide SEQ ID NO:2755.  
 PN WO200009525-A2.  
 PD 24-FEB-2000.  
 PA (UYEC-) UNIV EAST CAROLINA.  
 Query Match 4.9%; Score 48.2; DB 3; Length 2171;  
 Best Local Similarity 47.2%; Pred. No. 35;  
 RESULT 977  
 ID AAF21188 standard; DNA; 2171 BP.  
 DE Human low adenosine antisense oligonucleotide related sequence #2755.  
 PN WO200062736-A2.  
 PD 26-OCT-2000.  
 PA (UYEC-) UNIV EAST CAROLINA.  
 PA (NYCE/) NYCE J W.

Query Match 4.9%; Score 48.2; DB 3; Length 2171;  
Best Local Similarity 47.2%; Pred. No. 35;  
RESULT 978  
ID ABZ96882 standard; DNA; 2171 BP.  
DE Human nucleic acid sequence.  
PN WO200285308-A2.  
PD 31-OCT-2002.  
PA (EPIG-) EPIGENESIS PHARM INC.  
Query Match 4.9%; Score 48.2; DB 10; Length 2171;  
Best Local Similarity 47.2%; Pred. No. 35;  
RESULT 979  
ID ABD20731 standard; DNA; 2171 BP.  
DE Human pulmonary and inflammatory target DNA #342.  
PN WO200285309-A2.  
PD 31-OCT-2002.  
PA (EPIG-) EPIGENESIS PHARM INC.  
Query Match 4.9%; Score 48.2; DB 11; Length 2171;  
Best Local Similarity 47.2%; Pred. No. 35;  
RESULT 980  
ID ACA27128 standard; DNA; 2595 BP.  
DE Prokaryotic essential gene #8785.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.9%; Score 48.2; DB 8; Length 2595;  
Best Local Similarity 46.3%; Pred. No. 35;  
RESULT 981  
ID AAD28564 standard; DNA; 3350 BP.  
DE Herpes simplex virus type 2 G10\_UL37consensus DNA.  
PN WO200202131-A2.  
PD 10-JAN-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 4.9%; Score 48.2; DB 6; Length 3350;  
Best Local Similarity 44.5%; Pred. No. 35;  
RESULT 982  
ID ADG74976 standard; DNA; 3350 BP.  
DE Human herpesvirus 2 isolated clone DNA - SEQ ID 48.  
PN WO2003086308-A2.  
PD 23-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 4.9%; Score 48.2; DB 10; Length 3350;  
Best Local Similarity 44.5%; Pred. No. 35;  
RESULT 983  
ID AAS77503 standard; cDNA; 3633 BP.  
DE DNA encoding novel human diagnostic protein #13307.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.9%; Score 48.2; DB 5; Length 3633;  
Best Local Similarity 44.0%; Pred. No. 35;  
RESULT 984  
ID ACC72669 standard; cDNA; 3636 BP.  
DE Human cancer related protein encoding cDNA SEQ ID NO:8.  
PN WO2003025138-A2.  
PD 27-MAR-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 4.9%; Score 48.2; DB 10; Length 3636;  
Best Local Similarity 44.0%; Pred. No. 35;  
RESULT 985  
ID ACA40841 standard; DNA; 4146 BP.  
DE Prokaryotic essential gene #22498.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.9%; Score 48.2; DB 8; Length 4146;  
Best Local Similarity 46.1%; Pred. No. 34;  
RESULT 986  
ID ACA40804 standard; DNA; 4542 BP.  
DE Prokaryotic essential gene #22461.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.9%; Score 48.2; DB 8; Length 4542;

Best Local Similarity 43.2%; Pred. No. 34;  
RESULT 987  
ID ACN37449 standard; cDNA; 4755 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA323899, SEQ ID NO:338.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 4.9%; Score 48.2; DB 13; Length 4755;  
Best Local Similarity 44.2%; Pred. No. 34;  
RESULT 988  
ID ADP09634 standard; DNA; 4941 BP.  
DE Rice cinnamic acid 5-hydroxylase genomic DNA without the T-DNA SeqID 25.  
PN WO2004046357-A1.  
PD 03-JUN-2004.  
PA (POSC-) POSCO.  
PA (POST-) POSTECH FOUND.  
Query Match 4.9%; Score 48.2; DB 12; Length 4941;  
Best Local Similarity 49.8%; Pred. No. 34;  
RESULT 989  
ID ADO10048 standard; cDNA; 5204 BP.  
DE Novel human protein Novid cDNA.  
PN US2004052806-A1.  
PD 18-MAR-2004.  
PA (KEKU) KEKUDA R.  
PA (ALSO) ALSOBOOK J P.  
PA (TCHE) TCHERNEV V T.  
PA (LIUX) LIU X.  
PA (SPYT) SPYTEK K A.  
PA (PATI) PATTURAJAN M.  
PA (GROS) GROSSE W M.  
PA (LEPL) LEFLEY D M.  
PA (BURG) BURGESS C E.  
PA (VERN) VERNET C A M.  
PA (LILL) LI L.  
PA (GORM) GORMAN L.  
PA (EDIN) EDINGER S R.  
PA (SCIO) SCIORE P.  
PA (ELLE) ELLERMAN K.  
PA (MALY) MALYANKAR U M.  
PA (ROTH) ROTHENBERG M E.  
PA (STON) STONE D J.  
PA (BOLD) BOLDOG F L.  
PA (GUOX) GUO X.  
PA (SHEN) SHENOY S G.  
PA (ANDE) ANDERSON D W.  
PA (PADI) PADIGARU M.  
PA (TAUP) TAUPIER R J.  
PA (MILL) MILLER C E.  
PA (EISE) EISEN A.  
Query Match 4.9%; Score 48.2; DB 12; Length 5204;  
Best Local Similarity 48.9%; Pred. No. 34;  
RESULT 990  
ID ADP75209 standard; cDNA; 6642 BP.  
DE Human ADAMTS2 cDNA splice variant 1.  
PN WO2003031594-A2.  
PD 17-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48.2; DB 11; Length 6642;  
Best Local Similarity 44.0%; Pred. No. 34;  
RESULT 991  
ID AAV06592 standard; cDNA; 6692 BP.  
DE Human N-proteinase (long form) cDNA.  
PN WO9800555-A1.  
PD 08-JAN-1998.  
PA (PROC) PROCKOP D J.  
PA (COLI) COLIGE A.  
PA (LAPI) LAPIERE C.  
Query Match 4.9%; Score 48.2; DB 2; Length 6692;  
Best Local Similarity 44.0%; Pred. No. 34;  
RESULT 992  
ID ABS57451 standard; cDNA; 6692 BP.  
DE Human long form N-proteinase cDNA.  
PN US6428998-B1.

PD 06-AUG-2002.  
 PA (UYLI-) UNIV LIEGE.  
 Query Match 4.9%; Score 48.2; DB 10; Length 6692;  
 Best Local Similarity 44.0%; Pred. No. 34;  
 RESULT 993  
 ID AAA35028 standard; DNA; 8631 BP.  
 DE Human adenosine receptor related polynucleotide SEQ ID NO:2717.  
 PN WO200009525-A2.  
 PD 24-FEB-2000.  
 PA (UYEC-) UNIV EAST CAROLINA.  
 Query Match 4.9%; Score 48.2; DB 3; Length 8631;  
 Best Local Similarity 47.8%; Pred. No. 34;  
 RESULT 994  
 ID AAF21150 standard; DNA; 8631 BP.  
 DE Human low adenosine antisense oligonucleotide related sequence #2717.  
 PN WO200062736-A2.  
 PD 26-OCT-2000.  
 PA (UYCE/) UNIV EAST CAROLINA.  
 Query Match 4.9%; Score 48.2; DB 3; Length 8631;  
 Best Local Similarity 47.8%; Pred. No. 34;  
 RESULT 995  
 ID ABZ96844 standard; DNA; 8631 BP.  
 DE Human nucleic acid sequence.  
 PN WO200285308-A2.  
 PD 31-OCT-2002.  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 Query Match 4.9%; Score 48.2; DB 10; Length 8631;  
 Best Local Similarity 47.8%; Pred. No. 34;  
 RESULT 996  
 ID ABD20693 standard; DNA; 8631 BP.  
 DE Human pulmonary and inflammatory target DNA #304.  
 PN WO200285309-A2.  
 PD 31-OCT-2002.  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 Query Match 4.9%; Score 48.2; DB 11; Length 8631;  
 Best Local Similarity 47.8%; Pred. No. 34;  
 RESULT 997  
 ID AAD54222 standard; DNA; 9579 BP.  
 DE Streptomyces platensis subspecies rosaceus dorrigocin ORF5 DNA.  
 PN WO200288176-A2.  
 PD 07-NOV-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 4.9%; Score 48.2; DB 10; Length 9579;  
 Best Local Similarity 47.2%; Pred. No. 34;  
 RESULT 998  
 ID ADC26981 standard; DNA; 20922 BP.  
 DE Sorangium cellulosum tmba gene cluster tmbB DNA.  
 PN US2003054547-A1.  
 PD 20-MAR-2003.  
 PA (JULI/) JULIEN B.  
 Query Match 4.9%; Score 48.2; DB 10; Length 20922;  
 Best Local Similarity 46.3%; Pred. No. 33;  
 RESULT 999  
 ID AAD17185 standard; DNA; 27541 BP.  
 DE Streptomyces noursei nys2 DNA of nystatin PKS gene cluster.  
 PN WO200159126-A2.  
 PD 16-AUG-2001.  
 PA (UYNO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.  
 PA (SNTF) SINTEF STIPELSEN IND TEK FORSK.  
 PA (ALPH-) ALPHARMA AS.  
 PA (SINV-) SINVENT AS.  
 PA (DZIE/) DZIEGLEWSKA H.  
 PA (ZOTC/) ZOTCHEV S B.  
 PA (SEKU/) SEKUROVA O N.  
 PA (FJAE/) FJAEVNIK E.  
 PA (BRAU/) BRAUTASET T.  
 PA (STRO/) STROM A R.  
 PA (VALL/) VALLA S.  
 Query Match 4.9%; Score 48.2; DB 4; Length 27541;  
 Best Local Similarity 47.0%; Pred. No. 33;  
 RESULT 1000  
 ID AAD54217 standard; DNA; 52101 BP.

DE Streptomyces platensis subspecies rosaceus dorrigocin DNA.  
 PN WO200288176-A2.  
 PD 07-NOV-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 4.9%; Score 48.2; DB 10; Length 52101;  
 Best Local Similarity 47.2%; Pred. No. 32;  
 RESULT 1001  
 ID ADC26995 standard; DNA; 67251 BP.  
 DE Sorangium cellulosum tmba gene cluster.  
 PN US2003054547-A1.  
 PD 20-MAR-2003.  
 PA (JULI/) JULIEN B.  
 Query Match 4.9%; Score 48.2; DB 10; Length 67251;  
 Best Local Similarity 46.4%; Pred. No. 32;  
 RESULT 1002  
 ID AAL60437 standard; DNA; 70383 BP.  
 DE Human kinase splice form 1 genomic DNA.  
 PN WO2003106653-A2.  
 PD 24-DEC-2003.  
 PA (KOSA-) KOSAN BIOSCIENCES INC.  
 Query Match 4.9%; Score 48.2; DB 9; Length 70383;  
 Best Local Similarity 45.5%; Pred. No. 32;  
 RESULT 1003  
 ID ADI39160 standard; DNA; 86941 BP.  
 DE Streptomyces hygroscopicus herbimycin gene cluster, SEQ ID NO:2.  
 PN WO2003106653-A2.  
 PD 24-DEC-2003.  
 PA (KOSA-) KOSAN BIOSCIENCES INC.  
 Query Match 4.9%; Score 48.2; DB 12; Length 86941;  
 Best Local Similarity 45.9%; Pred. No. 32;  
 RESULT 1004  
 Query Match 4.9%; Score 48.2; DB 4; Length 110000;  
 Best Local Similarity 43.2%; Pred. No. 31;  
 RESULT 1005  
 Query Match 4.9%; Score 48.2; DB 4; Length 110000;  
 Best Local Similarity 43.2%; Pred. No. 31;  
 RESULT 1006  
 ID ABD03629 standard; DNA; 465 BP.  
 DE Pseudomonas aeruginosa polynucleotide #2233.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.9%; Score 48; DB 11; Length 465;  
 Best Local Similarity 50.0%; Pred. No. 40;  
 RESULT 1007  
 ID ACF39326 standard; DNA; 660 BP.  
 DE Mycobacterium tuberculosis mycobacterial antigen DNA SEQ ID NO:28.  
 PN WO2003033530-A2.  
 PD 24-APR-2003.  
 PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.  
 Query Match 4.9%; Score 48; DB 8; Length 660;  
 Best Local Similarity 51.4%; Pred. No. 39;  
 RESULT 1008  
 ID ABQ40859 standard; DNA; 712 BP.  
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 27450.  
 PN WO200218632-A2.  
 PD 07-MAR-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.9%; Score 48; DB 6; Length 712;  
 Best Local Similarity 45.5%; Pred. No. 39;  
 RESULT 1009  
 ID ABQ40858 standard; DNA; 712 BP.  
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 27449.  
 PN WO200218632-A2.  
 PD 07-MAR-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.9%; Score 48; DB 6; Length 712;  
 Best Local Similarity 45.5%; Pred. No. 39;  
 RESULT 1010  
 ID ABZ66735 standard; DNA; 756 BP.  
 DE Orthosomycin biosynthetic polynucleotide SEQ ID NO 132.  
 PN WO200279505-A2.  
 PD 10-OCT-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 4.9%; Score 48; DB 10; Length 756;

Best Local Similarity 48.5%; Pred. No. 39;  
RESULT 1011  
ID ADS57559 standard; cDNA; 768 BP.  
DE Bacterial polynucleotide #9546.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 4.9%; Score 48; DB 13; Length 768;  
Best Local Similarity 46.2%; Pred. No. 39;  
RESULT 1012  
ID ABD08476 standard; DNA; 822 BP.  
DE Pseudomonas aeruginosa polynucleotide #7080.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48; DB 11; Length 822;  
Best Local Similarity 45.2%; Pred. No. 39;  
RESULT 1013  
ID ABD03843 standard; DNA; 852 BP.  
DE Pseudomonas aeruginosa polynucleotide #2447.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48; DB 11; Length 852;  
Best Local Similarity 50.0%; Pred. No. 39;  
RESULT 1014  
ID ABD03031 standard; DNA; 1071 BP.  
DE Pseudomonas aeruginosa polynucleotide #1635.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.9%; Score 48; DB 11; Length 1071;  
Best Local Similarity 50.0%; Pred. No. 39;  
RESULT 1015  
ID AAA02477 standard; cDNA; 1127 BP.  
DE Human colon cancer cell line polynucleotide sequence SEQ ID NO:2468.  
PN WO9958675-A2.  
PD 18-NOV-1999.  
PA (CHIR) CHIRON CORP.  
PA (HYSE-) HYSEQ INC.  
Query Match 4.9%; Score 48; DB 3; Length 1127;  
Best Local Similarity 34.2%; Pred. No. 39;  
RESULT 1016  
ID AAZ10560 standard; DNA; 1128 BP.  
DE DNA encoding G protein-coupled receptor protein designated SREB1.  
PN WO9946378-A1.  
PD 16-SEP-1999.  
PA (YANA) YANANOUCHI PHARM CO LTD.  
Query Match 4.9%; Score 48; DB 2; Length 1128;  
Best Local Similarity 45.1%; Pred. No. 39;  
RESULT 1017  
ID AAA46026 standard; cDNA; 1128 BP.  
DE Human G protein coupled receptor hGPCR27 encoding cDNA SEQ ID NO:17.  
PN WO200022131-A2.  
PD 20-APR-2000.  
PA (ARENA) ARENA PHARM INC.  
Query Match 4.9%; Score 48; DB 3; Length 1128;  
Best Local Similarity 45.1%; Pred. No. 39;  
RESULT 1018  
ID AAD01125 standard; cDNA; 1128 BP.  
DE Human orphan G protein-coupled receptor hGPCR27 cDNA.  
PN WO200031258-A2.  
PD 02-JUN-2000.  
PA (ARENA) ARENA PHARM INC.  
Query Match 4.9%; Score 48; DB 3; Length 1128;  
Best Local Similarity 45.1%; Pred. No. 39;  
RESULT 1019  
ID AAD27892 standard; DNA; 1128 BP.  
DE Human G-protein coupled receptor 14266 DNA.

PN WO200212344-A2.  
PD 14-FEB-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 4.9%; Score 48; DB 6; Length 1128;  
Best Local Similarity 45.1%; Pred. No. 39;  
RESULT 1020  
ID AAS98049 standard; DNA; 1128 BP.  
DE Human DNA for potential G protein-coupled receptor #7.  
PN WO200185791-A1.  
PD 15-NOV-2001.  
PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
Query Match 4.9%; Score 48; DB 6; Length 1128;  
Best Local Similarity 45.1%; Pred. No. 39;  
RESULT 1021  
ID ACA93263 standard; cDNA; 1128 BP.  
DE Human cDNA encoding GPCR hGPCR27.  
PN US2003017528-A1.  
PD 23-JAN-2003.  
PA (CHEN/) CHEN R.  
PA (DANG/) DANG H T.  
PA (LIAW/) LIAW C W.  
PA (LINI/) LIN I.  
Query Match 4.9%; Score 48; DB 8; Length 1128;  
Best Local Similarity 45.1%; Pred. No. 39;  
RESULT 1022  
ID ABZ42853 standard; DNA; 1128 BP.  
DE Human G protein-coupled receptor GPCR27 nucleotide SEQ ID NO:493.  
PN WO200261087-A2.  
PD 08-AUG-2002.  
PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
Query Match 4.9%; Score 48; DB 8; Length 1128;  
Best Local Similarity 45.1%; Pred. No. 39;  
RESULT 1023  
ID ADG98761 standard; cDNA; 1128 BP.  
DE Human orphan GPCR cDNA, GPCR27.  
PN US2003148450-A1.  
PD 07-AUG-2003.  
PA (CHEN/) CHEN R.  
PA (DANG/) DANG H T.  
PA (LIAW/) LIAW C W.  
PA (LINI/) LIN I.  
Query Match 4.9%; Score 48; DB 10; Length 1128;  
Best Local Similarity 45.1%; Pred. No. 39;  
RESULT 1024  
ID ADJ26924 standard; cDNA; 1128 BP.  
DE Human endogenous orphan G-protein coupled receptor (GPCR) 27 cDNA.  
PN US2003175891-A1.  
PD 18-SEP-2003.  
PA (CHEN/) CHEN R.  
PA (DANG/) DANG H T.  
PA (LIAW/) LIAW C W.  
PA (LINI/) LIN I.  
Query Match 4.9%; Score 48; DB 11; Length 1128;  
Best Local Similarity 45.1%; Pred. No. 39;  
RESULT 1025  
ID ADN39803 standard; cDNA; 1128 BP.  
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:C175.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 4.9%; Score 48; DB 11; Length 1128;  
Best Local Similarity 45.1%; Pred. No. 39;  
RESULT 1026  
ID ADG86378 standard; DNA; 1128 BP.  
DE Human endogenous orphan GPCR hGPCR27 DNA.  
PN US2003229216-A1.  
PD 11-DEC-2003.  
PA (CHEN/) CHEN R.  
PA (LIAW/) LIAW C W.  
PA (LOWI) LOWITZ K. T.  
PA (CHAL/) CHALMERS D T.  
PA (BEHA/) BEHAN D P.  
Query Match 4.9%; Score 48; DB 12; Length 1128;

```
Best Local Similarity 45.1%; Pred. No. 39;
RESULT 1027
ID ADO29912 standard; cDNA; 1128 BP.
DE Human GPCR GPR27 polynucleotide, SEQ ID NO:1014.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 4.9%; Score 48; DB 12; Length 1128;
Best Local Similarity 45.1%; Pred. No. 39;
RESULT 1028
ID ADP20171 standard; cDNA; 1128 BP.
DE Human G protein coupled receptor hGPCR27 cDNA.
PN US2004110238-A1.
PD 10-JUN-2004.
PA (CHEN/) CHEN R.
PA (LIAM/) LIAM C W.
PA (LOMI/) LOWITZ K.
PA (CHAL/) CHALMERS D T.
PA (BEHA/) BEHAN D P.
Query Match 4.9%; Score 48; DB 12; Length 1128;
Best Local Similarity 45.1%; Pred. No. 39;
RESULT 1029
ID ADO75075 standard; cDNA; 1128 BP.
DE Human cDNA encoding hGPCR27.
PN US2004137509-A1.
PD 15-JUL-2004.
PA (LIAM/) LIAM C W.
PA (LINI/) LIN I.
Query Match 4.9%; Score 48; DB 12; Length 1128;
Best Local Similarity 45.1%; Pred. No. 39;
RESULT 1030
ID ADRA6633 standard; DNA; 1128 BP.
DE Cancer-associated protein coding sequence, SEQ ID 46.
PN WO2004073657-A2.
PD 02-SEP-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 4.9%; Score 48; DB 13; Length 1128;
Best Local Similarity 45.1%; Pred. No. 39;
RESULT 1031
ID ADT44450 standard; cDNA; 1155 BP.
DE Bacterial polynucleotide #19201.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.9%; Score 48; DB 13; Length 1155;
Best Local Similarity 46.9%; Pred. No. 39;
RESULT 1032
ID ACC59401 standard; DNA; 1188 BP.
DE Microbial resistance gene PA1877 coding sequence.
PN WO2003041483-A2.
PD 22-MAY-2003.
PA (DART-) DARTMOUTH COLLEGE.
Query Match 4.9%; Score 48; DB 9; Length 1188;
Best Local Similarity 46.8%; Pred. No. 39;
RESULT 1033
ID ADC36366 standard; DNA; 1197 BP.
DE Weed controller metabolism associated gene SEQ ID NO:234.
PN WO2003040370-A1.
PD 15-MAY-2003.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 4.9%; Score 48; DB 10; Length 1197;
Best Local Similarity 44.1%; Pred. No. 39;
RESULT 1034
ID ACA37909 standard; DNA; 1275 BP.
DE Prokaryotic essential gene #19566.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.9%; Score 48; DB 8; Length 1275;
Best Local Similarity 50.0%; Pred. No. 38;
RESULT 1035
ID ABD03924 standard; DNA; 1359 BP.
DE Pseudomonas aeruginosa polynucleotide #2528.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.9%; Score 48; DB 11; Length 1359;
Best Local Similarity 50.0%; Pred. No. 38;
RESULT 1036
ID ADC36376 standard; DNA; 1411 BP.
DE Weed controller metabolism associated gene SEQ ID NO:244.
PN WO2003040370-A1.
PD 15-MAY-2003.
PA (SUMO) SUMITOMO CHEM CO LTD.
Query Match 4.9%; Score 48; DB 10; Length 1411;
Best Local Similarity 44.1%; Pred. No. 38;
RESULT 1037
ID ADT43932 standard; cDNA; 1437 BP.
DE Bacterial polynucleotide #18683.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.9%; Score 48; DB 13; Length 1437;
Best Local Similarity 49.2%; Pred. No. 38;
RESULT 1038
ID ABD03787 standard; DNA; 1473 BP.
DE Pseudomonas aeruginosa polynucleotide #2391.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.9%; Score 48; DB 11; Length 1473;
Best Local Similarity 50.0%; Pred. No. 38;
RESULT 1039
ID ADT44593 standard; cDNA; 1677 BP.
DE Bacterial polynucleotide #19344.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 4.9%; Score 48; DB 13; Length 1677;
Best Local Similarity 47.4%; Pred. No. 38;
RESULT 1040
ID ABD03082 standard; DNA; 1695 BP.
DE Pseudomonas aeruginosa polynucleotide #1686.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.9%; Score 48; DB 11; Length 1695;
Best Local Similarity 50.0%; Pred. No. 38;
RESULT 1041
ID ABD2888 standard; DNA; 1740 BP.
DE Pseudomonas aeruginosa polynucleotide #1492.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 4.9%; Score 48; DB 11; Length 1740;
Best Local Similarity 50.0%; Pred. No. 38;
RESULT 1042
ID ACA25954 standard; DNA; 1782 BP.
DE Prokaryotic essential gene #7611.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 4.9%; Score 48; DB 8; Length 1782;
Best Local Similarity 50.0%; Pred. No. 38;
```

RESULT 1043  
 ID ABD02930 standard; DNA; 1806 BP.  
 DE Pseudomonas aeruginosa polynucleotide #1534.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.9%; Score 48; DB 11; Length 1806;  
 Best Local Similarity 50.0%; Pred. No. 38;  
 RESULT 1044  
 ID ADF070581 standard; DNA; 1842 BP.  
 DE Orphan receptor ligand-related human protein gene SeqID204.  
 PN WO2003071272-A1.  
 PD 28-AUG-2003.  
 PA (TAKE ) TAKEDA CHEM IND LTD.  
 Query Match 4.9%; Score 48; DB 10; Length 1842;  
 Best Local Similarity 45.1%; Pred. No. 38;  
 RESULT 1045  
 ID AAX30924 standard; DNA; 1925 BP.  
 DE Epstein Barr Virus Nuclear Antigen 1 (EBNA 1) DNA.  
 PN WO9947647-A1.  
 PD 23-SEP-1999.  
 PA (PHAR-) PHARMACOPRIA INC.  
 Query Match 4.9%; Score 48; DB 2; Length 1925;  
 Best Local Similarity 51.4%; Pred. No. 38;  
 RESULT 1046  
 ID ABD08413 standard; DNA; 1929 BP.  
 DE Pseudomonas aeruginosa polynucleotide #7017.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.9%; Score 48; DB 11; Length 1929;  
 Best Local Similarity 45.2%; Pred. No. 38;  
 RESULT 1047  
 ID ABD08507 standard; DNA; 1947 BP.  
 DE Pseudomonas aeruginosa polynucleotide #7111.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.9%; Score 48; DB 11; Length 1947;  
 Best Local Similarity 45.2%; Pred. No. 38;  
 RESULT 1048  
 ID ABD08587 standard; DNA; 2253 BP.  
 DE Pseudomonas aeruginosa polynucleotide #7191.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.9%; Score 48; DB 11; Length 2253;  
 Best Local Similarity 45.5%; Pred. No. 38;  
 RESULT 1049  
 ID ABD08649 standard; DNA; 2409 BP.  
 DE Pseudomonas aeruginosa polynucleotide #7253.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.9%; Score 48; DB 11; Length 2409;  
 Best Local Similarity 45.5%; Pred. No. 38;  
 RESULT 1050  
 ID ADO24486 standard; cDNA; 2485 BP.  
 DE Human PRO87344 encoding cDNA SEQ ID NO:125.  
 PN WO2004043397-A2.  
 PD 27-MAY-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.9%; Score 48; DB 12; Length 2485;  
 Best Local Similarity 45.1%; Pred. No. 38;  
 RESULT 1051  
 ID ABD08843 standard; DNA; 2490 BP.  
 DE Pseudomonas aeruginosa polynucleotide #7447.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.9%; Score 48; DB 11; Length 2490;  
 Best Local Similarity 45.5%; Pred. No. 38;  
 RESULT 1052

ID AAS54094 standard; DNA; 3489 BP.  
 DE Pseudomonas aeruginosa DNA for cellular proliferation protein #225.  
 PN WO200170955-A2.  
 PD 27-SEP-2001.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.9%; Score 48; DB 4; Length 3489;  
 Best Local Similarity 45.1%; Pred. No. 37;  
 RESULT 1053  
 ID ACA42240 standard; DNA; 3489 BP.  
 DE Prokaryotic essential gene #23897.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.9%; Score 48; DB 8; Length 3489;  
 Best Local Similarity 45.1%; Pred. No. 37;  
 RESULT 1054  
 ID AAS08699 standard; DNA; 12152 BP.  
 DE M. carbonacea DNA encoding Everninomicin biosynthetic enzymes.  
 PN WO200151639-A2.  
 PD 19-JUL-2001.  
 PA (SCHE ) SCHERING CORP.  
 Query Match 4.9%; Score 48; DB 5; Length 12152;  
 Best Local Similarity 48.5%; Pred. No. 36;  
 RESULT 1055  
 ID AAS17367 standard; DNA; 33529 BP.  
 DE DNA sequence of S. cellulosum polyketide synthase cosmid, pKOS28-26.  
 PN US6280399-B1.  
 PD 28-AUG-2001.  
 PA (KOSA-) KOSAN BIOSCIENCE.  
 Query Match 4.9%; Score 48; DB 5; Length 33529;  
 Best Local Similarity 46.4%; Pred. No. 35;  
 RESULT 1056  
 ID ABZ66810 standard; DNA; 37116 BP.  
 DE Orthosomycin biosynthetic gene cluster SEQ ID NO 279.  
 PN WO200279505-A2.  
 PD 10-OCT-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 4.9%; Score 48; DB 10; Length 37116;  
 Best Local Similarity 48.5%; Pred. No. 35;  
 RESULT 1057  
 ID ADP64454 standard; DNA; 76994 BP.  
 DE Sorangium cellulosum disorazole polyketide synthase gene cluster DNA.  
 PN WO2004053065-A2.  
 PD 24-JUN-2004.  
 PA (KOSA-) KOSAN BIOSCIENCES INC.  
 Query Match 4.9%; Score 48; DB 12; Length 76994;  
 Best Local Similarity 44.4%; Pred. No. 34;  
 RESULT 1058  
 ID ABD08121 standard; DNA; 309 BP.  
 DE Pseudomonas aeruginosa polynucleotide #6725.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.8%; Score 47.8; DB 11; Length 309;  
 Best Local Similarity 49.4%; Pred. No. 43;  
 RESULT 1059  
 ID ADI42790 standard; DNA; 487 BP.  
 DE Plant transcription factor polynucleotide #800.  
 PN US2004019927-A1.  
 PD 29-JAN-2004.  
 PA (SHER/) SHERMAN B K.  
 PA (RIEC/) RIECHMANN J L.  
 PA (JIAN/) JIANG C.  
 PA (HEAR/) HEARD J E.  
 PA (HAAR/) HAAKE V.  
 PA (CREE/) CREELMAN R A.  
 PA (RATC/) RATCLIFFE O.  
 PA (ADAM/) ADAM L J.  
 PA (REUB/) REUBER T L.  
 PA (KEDD/) KEDDIE J.  
 PA (BROU/) BROUN P E.  
 PA (PILG/) PILGRIM M L.  
 PA (DUBE/) DUBELL A N.

PA (PINE/) PINEDA O.  
 PA (YUGG/) YU G.  
 Query Match 4.8%; Score 47.8; DB 12; Length 487;  
 Best Local Similarity 45.1%; Pred. No. 43;  
 RESULT 1060  
 ID ABK35609 standard; DNA; 777 BP.  
 DE Gene encoding novel human secreted or membrane-associated protein #28.  
 PN WO200204600-A2.  
 PD 17-JAN-2002.  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 PA (GLAX ) GLAXO GROUP LTD.  
 Query Match 4.8%; Score 47.8; DB 6; Length 777;  
 Best Local Similarity 51.8%; Pred. No. 42;  
 RESULT 1061  
 ID ADF58345 standard; cDNA; 777 BP.  
 DE Human polynucleotide sequence SEQ ID NO:712.  
 PN WO2003080795-A2.  
 PD 02-OCT-2003.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 4.8%; Score 47.8; DB 10; Length 777;  
 Best Local Similarity 51.8%; Pred. No. 42;  
 RESULT 1062  
 ID ABD17337 standard; DNA; 801 BP.  
 DE Pseudomonas aeruginosa polynucleotide #15941.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.8%; Score 47.8; DB 11; Length 801;  
 Best Local Similarity 47.5%; Pred. No. 42;  
 RESULT 1063  
 ID ABD15977 standard; DNA; 819 BP.  
 DE Pseudomonas aeruginosa polynucleotide #14581.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.8%; Score 47.8; DB 11; Length 819;  
 Best Local Similarity 47.1%; Pred. No. 42;  
 RESULT 1064  
 ID AAL61183 standard; DNA; 885 BP.  
 DE Actinosynnema pretiosum methyltransferase gene #2.  
 PN WO2003045312-A2.  
 PD 05-JUN-2003.  
 PA (UNIW ) UNIV WASHINGTON.  
 Query Match 4.8%; Score 47.8; DB 8; Length 885;  
 Best Local Similarity 44.9%; Pred. No. 42;  
 RESULT 1065  
 ID ABD08291 standard; DNA; 966 BP.  
 DE Pseudomonas aeruginosa polynucleotide #6895.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.8%; Score 47.8; DB 11; Length 966;  
 Best Local Similarity 49.4%; Pred. No. 42;  
 RESULT 1066  
 ID ACA37720 standard; DNA; 1029 BP.  
 DE Prokaryotic essential gene #19377.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.8%; Score 47.8; DB 8; Length 1029;  
 Best Local Similarity 45.6%; Pred. No. 42;  
 RESULT 1067  
 ID ADB80220 standard; DNA; 1173 BP.  
 DE Mycobacterium tuberculosis nutrient starvation-inducible gene #129.  
 PN WO2003004520-A2.  
 PD 16-JAN-2003.  
 PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.  
 Query Match 4.8%; Score 47.8; DB 10; Length 1173;  
 Best Local Similarity 47.0%; Pred. No. 42;  
 RESULT 1068  
 ID ABD17849 standard; DNA; 1218 BP.  
 DE Pseudomonas aeruginosa polynucleotide #16453.

PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.8%; Score 47.8; DB 11; Length 1218;  
 Best Local Similarity 47.5%; Pred. No. 42;  
 RESULT 1069  
 ID ACA6886 standard; DNA; 1287 BP.  
 DE Prokaryotic essential gene #8543.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.8%; Score 47.8; DB 8; Length 1287;  
 Best Local Similarity 45.4%; Pred. No. 41;  
 RESULT 1070  
 ID ABL15825 standard; cDNA; 1291 BP.  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 41957.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Query Match 4.8%; Score 47.8; DB 4; Length 1291;  
 Best Local Similarity 47.8%; Pred. No. 41;  
 RESULT 1071  
 ID ADS18615 standard; DNA; 1293 BP.  
 DE Barley Ror2 DNA.  
 PN WO2004081217-A2.  
 PD 23-SEP-2004.  
 PA (BADI ) BASF PLANT SCI GMBH.  
 Query Match 4.8%; Score 47.8; DB 13; Length 1293;  
 Best Local Similarity 46.7%; Pred. No. 41;  
 RESULT 1072  
 ID ABA16862 standard; DNA; 1343 BP.  
 DE Human nervous system related polynucleotide SEQ ID NO 9193.  
 PN WO200159063-A2.  
 PD 16-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 4.8%; Score 47.8; DB 5; Length 1343;  
 Best Local Similarity 51.8%; Pred. No. 41;  
 RESULT 1073  
 ID ABA19759 standard; DNA; 1343 BP.  
 DE Human nervous system related polynucleotide SEQ ID NO 12090.  
 PN WO200159063-A2.  
 PD 16-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 4.8%; Score 47.8; DB 5; Length 1343;  
 Best Local Similarity 51.8%; Pred. No. 41;  
 RESULT 1074  
 ID ACA37836 standard; DNA; 1404 BP.  
 DE Prokaryotic essential gene #19493.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.8%; Score 47.8; DB 8; Length 1404;  
 Best Local Similarity 46.8%; Pred. No. 41;  
 RESULT 1075  
 ID ABD08211 standard; DNA; 1485 BP.  
 DE Pseudomonas aeruginosa polynucleotide #6815.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.8%; Score 47.8; DB 11; Length 1485;  
 Best Local Similarity 49.4%; Pred. No. 41;  
 RESULT 1076  
 ID ABD08326 standard; DNA; 1509 BP.  
 DE Pseudomonas aeruginosa polynucleotide #6930.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.8%; Score 47.8; DB 11; Length 1509;  
 Best Local Similarity 49.4%; Pred. No. 41;  
 RESULT 1077  
 ID ACA37879 standard; DNA; 1527 BP.  
 DE Prokaryotic essential gene #19536.  
 PN WO200277183-A2.

PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.8%; Score 47.8; DB 8; Length 1527;  
Best Local Similarity 47.2%; Pred. No. 41;  
RESULT 1078  
ID AAD36877 standard; DNA; 1686 BP.  
DE S. clavuligerus clavulanic acid biosynthesis enzyme encoding DNA, ORF15.  
PN WO2003040372-A2.  
PD 15-MAY-2003.  
PA (SMIK) SMITHKLINE BEECHAM PLC.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 4.8%; Score 47.8; DB 8; Length 1686;  
Best Local Similarity 46.3%; Pred. No. 41;  
RESULT 1079  
ID AAT62138 standard; DNA; 1771 BP.  
DE Leishmania tropica Lt-210 antigen cDNA.  
PN WO9711180-A1.  
PD 27-MAR-1997.  
PA (CORI-) CORIXA CORP.  
Query Match 4.8%; Score 47.8; DB 2; Length 1771;  
Best Local Similarity 45.5%; Pred. No. 41;  
RESULT 1080  
ID AAV47558 standard; DNA; 1771 BP.  
DE Leishmania antigen Lt-210 coding sequence.  
PN WO9835045-A2.  
PD 13-AUG-1998.  
PA (CORI-) CORIXA CORP.  
Query Match 4.8%; Score 47.8; DB 2; Length 1771;  
Best Local Similarity 45.5%; Pred. No. 41;  
RESULT 1081  
ID AA225621 standard; DNA; 1771 BP.  
DE Leishmania tropica Lt-210 nucleotide sequence.  
PN US965142-A.  
PD 12-OCT-1999.  
PA (CORI-) CORIXA CORP.  
Query Match 4.8%; Score 47.8; DB 2; Length 1771;  
Best Local Similarity 45.5%; Pred. No. 41;  
RESULT 1082  
ID AAD40285 standard; DNA; 1771 BP.  
DE Leishmania tropica Lt-1 antigenic protein encoding DNA.  
PN US6375955-B1.  
PD 23-APR-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 4.8%; Score 47.8; DB 6; Length 1771;  
Best Local Similarity 45.5%; Pred. No. 41;  
RESULT 1083  
ID AAS96022 standard; cDNA; 1771 BP.  
DE Leishmania antigen Lt-1 DNA.  
PN WO200179276-A2.  
PD 25-OCT-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 4.8%; Score 47.8; DB 6; Length 1771;  
Best Local Similarity 45.5%; Pred. No. 41;  
RESULT 1084  
ID ABK81733 standard; DNA; 1771 BP.  
DE Leishmania antigenic polynucleotide #4.  
PN US635165-B1.  
PD 02-APR-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 4.8%; Score 47.8; DB 6; Length 1771;  
Best Local Similarity 45.5%; Pred. No. 41;  
RESULT 1085  
ID AAF88524 standard; DNA; 1771 BP.  
DE L. tropica Lt-210 antigen DNA SEQ ID 7.  
PN US2002081320-A1.  
PD 27-JUN-2002.  
PA (REED/) REED S G.  
PA (CAMP/) CAMPOS-NETO A.  
PA (WEBB/) WEBB J R.  
PA (DILL/) DILLON D C.  
PA (SKEI/) SKEIKY Y A W.  
PA (BHAT/) BHATIA A.  
PA (COL/) COLER R N.  
PA (PROB/) PROBST P.  
PA (BRAN/) BRANNON M.  
Query Match 4.8%; Score 47.8; DB 6; Length 1771;  
Best Local Similarity 45.5%; Pred. No. 41;  
RESULT 1086  
ID ADB78770 standard; DNA; 1771 BP.  
DE Leishmania DNA encoding antigen Lt-210.  
PN US2002169285-A1.  
PD 14-NOV-2002.  
PA (REED/) REED S G.  
PA (CAMP/) CAMPOS-NETO A.  
PA (WEBB/) WEBB J R.  
PA (DILL/) DILLON D C.  
Query Match 4.8%; Score 47.8; DB 9; Length 1771;  
Best Local Similarity 45.5%; Pred. No. 41;  
RESULT 1087  
ID ABD17433 standard; DNA; 1962 BP.  
DE Pseudomonas aeruginosa polynucleotide #16037.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.8; DB 11; Length 1962;  
Best Local Similarity 47.5%; Pred. No. 41;  
RESULT 1088  
ID ABD17959 standard; DNA; 2526 BP.  
DE Pseudomonas aeruginosa polynucleotide #16563.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.8; DB 11; Length 2526;  
Best Local Similarity 47.5%; Pred. No. 41;  
RESULT 1089  
ID AAL61203 standard; DNA; 3018 BP.  
DE Actinosynnema pretiosum cytochrome P450 gene.  
PN WO2003045312-A2.  
PD 05-JUN-2003.  
PA (UNIW) UNIV WASHINGTON.  
Query Match 4.8%; Score 47.8; DB 8; Length 3018;  
Best Local Similarity 47.9%; Pred. No. 41;  
RESULT 1090  
ID ABD10462 standard; DNA; 3126 BP.  
DE Pseudomonas aeruginosa polynucleotide #9066.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.8; DB 11; Length 3126;  
Best Local Similarity 51.1%; Pred. No. 40;  
RESULT 1091  
ID AAL61181 standard; DNA; 3354 BP.  
DE Actinosynnema pretiosum transcriptional regulator gene #1.  
PN WO2003045312-A2.  
PD 05-JUN-2003.  
PA (UNIW) UNIV WASHINGTON.  
Query Match 4.8%; Score 47.8; DB 8; Length 3354;  
Best Local Similarity 41.5%; Pred. No. 40;  
RESULT 1092  
ID ADQ19781 standard; DNA; 3824 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2600.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 4.8%; Score 47.8; DB 12; Length 3824;  
Best Local Similarity 47.3%; Pred. No. 40;  
RESULT 1093  
ID ADQ23914 standard; DNA; 3824 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6734.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 4.8%; Score 47.8; DB 12; Length 3824;  
Best Local Similarity 47.3%; Pred. No. 40;  
RESULT 1094  
ID ABD16585 standard; DNA; 5121 BP.



DE Pseudomonas aeruginosa polynucleotide #15189.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.8; DB 11; Length 5121;  
Best Local Similarity 47.1%; Pred. No. 40;  
RESULT 1095  
ID ADD16327 standard; DNA; 6327 BP.  
DE Pseudomonas aeruginosa polynucleotide #14931.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.8; DB 11; Length 6327;  
Best Local Similarity 47.1%; Pred. No. 40;  
RESULT 1096  
ID ACF05731 standard; DNA; 7201 BP.  
DE Plasmid pEAK128-IPAAA44548-6His.  
PN WO2003055913-A2.  
PD 10-JUL-2003.  
PA (ARES-) ARES TRADING SA.  
Query Match 4.8%; Score 47.8; DB 9; Length 7201;  
Best Local Similarity 48.7%; Pred. No. 40;  
RESULT 1097  
ID ACF06299 standard; DNA; 7231 BP.  
DE Plasmid pEAK128-IPAAA26841-6His nucleotide sequence.  
PN WO2003054012-A2.  
PD 03-JUL-2003.  
PA (ARES-) ARES TRADING SA.  
Query Match 4.8%; Score 47.8; DB 9; Length 7231;  
Best Local Similarity 48.7%; Pred. No. 40;  
RESULT 1098  
ID ACF06300 standard; DNA; 7297 BP.  
DE SigptdIPAAA26841s-6His nucleotide sequence.  
PN WO2003054012-A2.  
PD 03-JUL-2003.  
PA (ARES-) ARES TRADING SA.  
Query Match 4.8%; Score 47.8; DB 9; Length 7297;  
Best Local Similarity 48.7%; Pred. No. 40;  
RESULT 1099  
ID ACF05558 standard; DNA; 7429 BP.  
DE Plasmid pEAK128-IPAAA24020-6His.  
PN WO2003055912-A2.  
PD 10-JUL-2003.  
PA (ARES-) ARES TRADING SA.  
Query Match 4.8%; Score 47.8; DB 9; Length 7429;  
Best Local Similarity 48.7%; Pred. No. 40;  
RESULT 1100  
ID ACF06298 standard; DNA; 7456 BP.  
DE Plasmid pEAK128-IPAAA26841long-6His nucleotide sequence.  
PN WO2003054012-A2.  
PD 03-JUL-2003.  
PA (ARES-) ARES TRADING SA.  
Query Match 4.8%; Score 47.8; DB 9; Length 7456;  
Best Local Similarity 48.7%; Pred. No. 40;  
RESULT 1101  
ID ADP28653 standard; DNA; 8973 BP.  
DE Human secreted protein encoding sequence SEQ ID #651.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 4.8%; Score 47.8; DB 12; Length 8973;  
Best Local Similarity 44.6%; Pred. No. 39;  
RESULT 1102  
ID AAD36874 standard; DNA; 29870 BP.  
DE Streptomyces clavuligerus clavulanic acid biosynthesis gene cluster.  
PN WO2003040372-A2.  
PD 15-MAY-2003.  
PA (SMIK) SMITHKLINE BEECHAM PLC.  
PA (UYAL-) UNIV ALBERTA.  
Query Match 4.8%; Score 47.8; DB 8; Length 29870;  
Best Local Similarity 46.3%; Pred. No. 38;  
RESULT 1103  
ID AAA29349 standard; DNA; 71989 BP.

DE Sorangium cellulosum epothilone polyketide synthase operon genomic DNA.  
Query Match 4.8%; Score 47.8; DB 3; Length 71989;  
Best Local Similarity 48.2%; Pred. No. 37;  
RESULT 1104  
ID AAL61224 standard; DNA; 82746 BP.  
DE Actinosynnema pretiosum ansamitocin biosynthetic gene cluster I.  
PN WO2003045312-A2.  
PD 05-JUN-2003.  
PA (UNIW) UNIV WASHINGTON.  
Query Match 4.8%; Score 47.8; DB 8; Length 82746;  
Best Local Similarity 44.9%; Pred. No. 37;  
RESULT 1105  
Query Match 4.8%; Score 47.8; DB 4; Length 110000;  
Best Local Similarity 47.0%; Pred. No. 37;  
RESULT 1106  
Query Match 4.8%; Score 47.8; DB 4; Length 110000;  
Best Local Similarity 45.4%; Pred. No. 37;  
RESULT 1107  
Query Match 4.8%; Score 47.8; DB 4; Length 110000;  
Best Local Similarity 47.0%; Pred. No. 37;  
RESULT 1108  
ID ACL23251 standard; DNA; 422 BP.  
DE DNA clone originating in barley containing SNP encoding sequence #13242.  
PN WO2003057877-A1.  
PD 17-JUL-2003.  
PA (UYNI-) UNIV JAPAN OKAYAMA.  
Query Match 4.8%; Score 47.6; DB 9; Length 422;  
Best Local Similarity 59.7%; Pred. No. 46;  
RESULT 1109  
ID ADT43053 standard; cDNA; 633 BP.  
DE Bacterial polynucleotide #17804.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 4.8%; Score 47.6; DB 13; Length 633;  
Best Local Similarity 46.6%; Pred. No. 46;  
RESULT 1110  
ID ADR01252 standard; DNA; 825 BP.  
DE Farnesyl dibenzodiazepinone biosynthetic ORF21 protein ALDB DNA.  
PN WO2004065591-A1.  
PD 05-AUG-2004.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.  
Query Match 4.8%; Score 47.6; DB 13; Length 825;  
Best Local Similarity 44.5%; Pred. No. 45;  
RESULT 1111  
ID ACA19654 standard; DNA; 921 BP.  
DE Prokaryotic essential gene #1311.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.8%; Score 47.6; DB 8; Length 921;  
Best Local Similarity 47.8%; Pred. No. 45;  
RESULT 1112  
ID ABD17059 standard; DNA; 930 BP.  
DE Pseudomonas aeruginosa polynucleotide #15663.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.6; DB 11; Length 930;  
Best Local Similarity 47.8%; Pred. No. 45;  
RESULT 1113  
ID ADI45687 standard; cDNA; 1002 BP.  
DE Corn isoprenoid biosynthesis-associated cDNA #30.  
PN US2004010815-A1.  
PD 15-JAN-2004.  
PA (LANG/) LANGE B M.  
PA (GHAS/) GHASSEMIAN M.  
PA (BRIG/) BRIGGS S P.  
PA (COOP/) COOPER B.

```

PA (GLAZ/) GLAZEBROOK J.
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (MOUG/) MOUGHAMER T.
PA (PROV/) PROVANT N.
PA (RICK/) RICHKE D.
PA (ZHUT/) ZHU T.
  Query Match
    Best Local Similarity 4.8%; Score 47.6; DB 12; Length 1002;
    Best Local Similarity 47.0%; Pred. No. 45;
  RESULT 1114
  ID ADF31999 standard; DNA; 1170 BP.
  DE Transcriptional repressor of the ROK family.
  PN WO200309993-A2.
  PD 04-DEC-2003.
  PA (AVET ) AVENTIS PHARM INC.
    Query Match
      Best Local Similarity 4.8%; Score 47.6; DB 12; Length 1170;
      Best Local Similarity 43.8%; Pred. No. 45;
  RESULT 1115
  ID ADF32000 standard; DNA; 1170 BP.
  DE Transcriptional repressor of the ROK family complement.
  PN WO200309993-A2.
  PD 04-DEC-2003.
  PA (AVET ) AVENTIS PHARM INC.
    Query Match
      Best Local Similarity 4.8%; Score 47.6; DB 12; Length 1170;
      Best Local Similarity 43.8%; Pred. No. 45;
  RESULT 1116
  ID ADT42056 standard; cDNA; 1176 BP.
  DE Bacterial polynucleotide #16807.
  PN US2003233675-A1.
  PD 18-DEC-2003.
  PA (CAOY/) CAO Y.
  PA (HINK/) HINKLE G J.
  PA (SLAT/) SLATER S C.
  PA (CHEN/) CHEN X.
  PA (GOLD/) GOLDMAN B S.
    Query Match
      Best Local Similarity 4.8%; Score 47.6; DB 13; Length 1176;
      Best Local Similarity 45.3%; Pred. No. 45;
  RESULT 1117
  ID ACA37852 standard; DNA; 1203 BP.
  DE Prokaryotic essential gene #19509.
  PN WO200277183-A2.
  PD 03-OCT-2002.
  PA (ELIT-) ELITRA PHARM INC.
    Query Match
      Best Local Similarity 4.8%; Score 47.6; DB 8; Length 1203;
      Best Local Similarity 45.6%; Pred. No. 45;
  RESULT 1118
  ID ABD04031 standard; DNA; 1248 BP.
  DE Pseudomonas aeruginosa polynucleotide #2635.
  PN US6551795-B1.
  PD 22-APR-2003.
  PA (GENO-) GENOME THERAPEUTICS CORP.
    Query Match
      Best Local Similarity 4.8%; Score 47.6; DB 11; Length 1248;
      Best Local Similarity 46.4%; Pred. No. 45;
  RESULT 1119
  ID ABD05292 standard; DNA; 1278 BP.
  DE Pseudomonas aeruginosa polynucleotide #3896.
  PN US6551795-B1.
  PD 22-APR-2003.
  PA (GENO-) GENOME THERAPEUTICS CORP.
    Query Match
      Best Local Similarity 4.8%; Score 47.6; DB 11; Length 1278;
      Best Local Similarity 43.6%; Pred. No. 45;
  RESULT 1120
  ID ADT44381 standard; cDNA; 1410 BP.
  DE Bacterial polynucleotide #19132.
  PN US2003233675-A1.
  PD 18-DEC-2003.
  PA (CAOY/) CAO Y.
  PA (HINK/) HINKLE G J.
  PA (SLAT/) SLATER S C.
  PA (CHEN/) CHEN X.
  PA (GOLD/) GOLDMAN B S.
    Query Match
      Best Local Similarity 4.8%; Score 47.6; DB 13; Length 1410;
      Best Local Similarity 46.2%; Pred. No. 44;
  RESULT 1121
  ID ADS56254 standard; cDNA; 1572 BP.
  DE Bacterial polynucleotide #8241.
  PN US2003233675-A1.
  PD 18-DEC-2003.
  PA (CAOY/) CAO Y.
  PA (HINK/) HINKLE G J.
  PA (SLAT/) SLATER S C.
  PA (CHEN/) CHEN X.
  PA (GOLD/) GOLDMAN B S.
    Query Match
      Best Local Similarity 4.8%; Score 47.6; DB 13; Length 1572;
      Best Local Similarity 48.5%; Pred. No. 45;
  RESULT 1122
  ID ACA03563 standard; DNA; 1971 BP.
  DE Synthetic DNA encoding immunogenic HIV peptide #46.
  PN WO2003004657-A1.
  PD 16-JAN-2003.
  PA (CHIR ) CHIRON CORP.
    Query Match
      Best Local Similarity 4.8%; Score 47.6; DB 8; Length 1971;
      Best Local Similarity 46.8%; Pred. No. 44;
  RESULT 1123
  ID ACA03557 standard; DNA; 1971 BP.
  DE Synthetic DNA encoding immunogenic HIV peptide #40.
  PN WO2003004657-A1.
  PD 16-JAN-2003.
  PA (CHIR ) CHIRON CORP.
    Query Match
      Best Local Similarity 4.8%; Score 47.6; DB 8; Length 1971;
      Best Local Similarity 47.6%; Pred. No. 44;
  RESULT 1124
  ID ACC78513 standard; DNA; 1971 BP.
  DE HIV protInaRT YM.opt.SF2 nucleotide sequence.
  PN WO2003020876-A2.
  PD 13-MAR-2003.
  PA (CHIR ) CHIRON CORP.
    Query Match
      Best Local Similarity 4.8%; Score 47.6; DB 8; Length 1971;
      Best Local Similarity 47.6%; Pred. No. 44;
  RESULT 1125
  ID ADC13270 standard; DNA; 1971 BP.
  DE DNA of HIV construct protInaRT-YM-opt_C SEQ ID NO 49.
  PN WO2003004620-A2.
  PD 16-JAN-2003.
  PA (CHIR ) CHIRON CORP.
  PA (UYST-) UNIV STELLENBOSCH.
    Query Match
      Best Local Similarity 4.8%; Score 47.6; DB 10; Length 1971;
      Best Local Similarity 46.8%; Pred. No. 44;
  RESULT 1126
  ID ABD03593 standard; DNA; 1971 BP.
  DE Pseudomonas aeruginosa polynucleotide #2197.
  PN US6551795-B1.
  PD 22-APR-2003.
  PA (GENO-) GENOME THERAPEUTICS CORP.
    Query Match
      Best Local Similarity 4.8%; Score 47.6; DB 11; Length 1971;
      Best Local Similarity 46.4%; Pred. No. 44;
  RESULT 1127
  ID ABD05320 standard; DNA; 1977 BP.
  DE Pseudomonas aeruginosa polynucleotide #3924.
  PN US6551795-B1.
  PD 22-APR-2003.
  PA (GENO-) GENOME THERAPEUTICS CORP.
    Query Match
      Best Local Similarity 4.8%; Score 47.6; DB 11; Length 1977;
      Best Local Similarity 43.6%; Pred. No. 44;
  RESULT 1128
  ID AAD55732 standard; DNA; 2078 BP.
  DE Dolomedes tenebrosus fibroin 2 DNA.
  PN WO2003020916-A2.
  PD 13-MAR-2003.
  PA (UYWY-) UNIV WYOMING.
    Query Match
      Best Local Similarity 4.8%; Score 47.6; DB 8; Length 2078;
      Best Local Similarity 46.2%; Pred. No. 44;
  RESULT 1129
  ID ABD05412 standard; DNA; 2091 BP.
  DE Pseudomonas aeruginosa polynucleotide #4016.

```

PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.6; DB 11; Length 2091;  
Best Local Similarity 43.6%; Pred. No. 44;  
RESULT 1130  
ID ADT42133 standard; cDNA; 2175 BP.  
DE Bacterial polynucleotide #16884.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 4.8%; Score 47.6; DB 13; Length 2175;  
Best Local Similarity 48.8%; Pred. No. 44;  
RESULT 1131  
ID ABD03873 standard; DNA; 2211 BP.  
DE Pseudomonas aeruginosa polynucleotide #2477.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.8%; Score 47.6; DB 11; Length 2211;  
Best Local Similarity 46.4%; Pred. No. 44;  
RESULT 1132  
ID AAA70477 standard; DNA; 2305 BP.  
DE HIV FS(-) Protinact\_RTOpt\_YM coding sequence.  
PN WO200039302-A2.  
PD 06-JUL-2000.  
PA (CHIR ) CHIRON CORP.  
Query Match 4.8%; Score 47.6; DB 3; Length 2305;  
Best Local Similarity 47.6%; Pred. No. 44;  
RESULT 1133  
ID AAA70479 standard; DNA; 2306 BP.  
DE HIV FS(-) ProtMod\_RTOpt\_YM coding sequence.  
PN WO200039302-A2.  
PD 06-JUL-2000.  
PA (CHIR ) CHIRON CORP.  
Query Match 4.8%; Score 47.6; DB 3; Length 2306;  
Best Local Similarity 47.6%; Pred. No. 44;  
RESULT 1134  
ID ACA37615 standard; DNA; 2337 BP.  
DE Prokaryotic essential gene #19272.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.8%; Score 47.6; DB 8; Length 2337;  
Best Local Similarity 46.4%; Pred. No. 44;  
RESULT 1135  
ID ACA27167 standard; DNA; 2424 BP.  
DE Prokaryotic essential gene #8824.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.8%; Score 47.6; DB 8; Length 2424;  
Best Local Similarity 43.9%; Pred. No. 44;  
RESULT 1136  
ID ACA03547 standard; DNA; 2457 BP.  
DE Synthetic DNA encoding immunogenic HIV peptide #30.  
PN WO2003004657-A1.  
PD 16-JAN-2003.  
PA (CHIR ) CHIRON CORP.  
Query Match 4.8%; Score 47.6; DB 8; Length 2457;  
Best Local Similarity 46.8%; Pred. No. 44;  
RESULT 1137  
ID ADC13265 standard; DNA; 2457 BP.  
DE DNA of HIV construct p2Pol-opt\_YM\_C SEQ ID NO 44.  
PN WO2003004620-A2.  
PD 16-JAN-2003.  
PA (CHIR ) CHIRON CORP.  
Query Match 4.8%; Score 47.6; DB 13; Length 2457;  
Best Local Similarity 44.5%; Pred. No. 44;

Best Local Similarity 46.8%; Pred. No. 44;  
RESULT 1138  
ID ABL39960 standard; DNA; 2463 BP.  
DE Synthetic construct PR975YM SEQ ID NO:31.  
PN WO200204493-A2.  
PD 17-JAN-2002.  
PA (CHIR ) CHIRON CORP.  
PA (UYST-) UNIV STELLENBOSCH.  
Query Match 4.8%; Score 47.6; DB 6; Length 2463;  
Best Local Similarity 46.8%; Pred. No. 44;  
RESULT 1139  
ID ADM73765 standard; DNA; 2463 BP.  
DE HIV-1 polynucleotide #8.  
PN US2003223961-A1.  
PD 04-DEC-2003.  
PA (MEGE/) MEGEDE J Z.  
PA (BARN/) BARNETT S W.  
PA (ENGE/) ENGELBRECHT S.  
PA (RENS/) RENSBURG E J V.  
Query Match 4.8%; Score 47.6; DB 12; Length 2463;  
Best Local Similarity 46.8%; Pred. No. 44;  
RESULT 1140  
ID ACA03542 standard; DNA; 2466 BP.  
DE Synthetic DNA encoding immunogenic HIV peptide #25.  
PN WO2003004657-A1.  
PD 16-JAN-2003.  
PA (CHIR ) CHIRON CORP.  
Query Match 4.8%; Score 47.6; DB 8; Length 2466;  
Best Local Similarity 47.6%; Pred. No. 44;  
RESULT 1141  
ID ACC78506 standard; DNA; 2466 BP.  
DE HIV p2PolInaopt\_YM.SF2 nucleotide sequence.  
PN WO2003020876-A2.  
PD 13-MAR-2003.  
PA (CHIR ) CHIRON CORP.  
Query Match 4.8%; Score 47.6; DB 8; Length 2466;  
Best Local Similarity 47.6%; Pred. No. 44;  
RESULT 1142  
ID AAD28560 standard; DNA; 2481 BP.  
DE Herpes simplex virus type 2 full-length HSV-2 RL2 gene.  
PN WO200202131-A2.  
PD 10-JAN-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 4.8%; Score 47.6; DB 6; Length 2481;  
Best Local Similarity 51.4%; Pred. No. 44;  
RESULT 1143  
ID ADG74963 standard; DNA; 2481 BP.  
DE Human herpesvirus 2 RL2 DNA - SEQ ID 35.  
PN WO2003086308-A2.  
PD 23-OCT-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 4.8%; Score 47.6; DB 10; Length 2481;  
Best Local Similarity 51.4%; Pred. No. 44;  
RESULT 1144  
ID ACN40538 standard; cDNA; 2540 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA326641, SEQ ID NO:5378.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 4.8%; Score 47.6; DB 13; Length 2540;  
Best Local Similarity 42.3%; Pred. No. 44;  
RESULT 1145  
ID ADT44483 standard; cDNA; 2652 BP.  
DE Bacterial polynucleotide #19234.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 4.8%; Score 47.6; DB 13; Length 2652;  
Best Local Similarity 44.5%; Pred. No. 44;

RESULT 1146  
 ID ADG75080 standard; DNA; 3066 BP.  
 DE Human herpesvirus 2 RL2 DNA - SEQ ID 152.  
 PN WO2003086308-A2.  
 PD 23-OCT-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match 4.8%; Score 47.6; DB 10; Length 3066;  
 Best Local Similarity 51.4%; Pred. No. 44;  
 RESULT 1147  
 ID ADT42075 standard; cDNA; 3090 BP.  
 DE Bacterial polynucleotide #16826.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match 4.8%; Score 47.6; DB 13; Length 3090;  
 Best Local Similarity 49.1%; Pred. No. 44;  
 RESULT 1148  
 ID ADF30533 standard; cDNA; 3783 BP.  
 DE Rat angio genesis modulating protein cDNA #24.  
 PN US2003162706-A1.  
 PD 28-AUG-2003.  
 PA (PROC) PROCTER & GAMBLE CO.  
 Query Match 4.8%; Score 47.6; DB 10; Length 3783;  
 Best Local Similarity 43.6%; Pred. No. 43;  
 RESULT 1149  
 ID ADE71207 standard; DNA; 5369 BP.  
 DE Novel human protein coding sequence #23.  
 PN JP2002345493-A.  
 PD 03-DEC-2002.  
 PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.  
 Query Match 4.8%; Score 47.6; DB 10; Length 5369;  
 Best Local Similarity 45.6%; Pred. No. 43;  
 RESULT 1150  
 ID ADK18365 standard; DNA; 5780 BP.  
 DE Human NOVX protein encoding gene #10.  
 PN WO2003057854-A2.  
 PD 04-SEP-2002.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 4.8%; Score 47.6; DB 10; Length 5780;  
 Best Local Similarity 46.4%; Pred. No. 43;  
 RESULT 1151  
 ID ABS78696 standard; DNA; 5802 BP.  
 DE S. kaniharaisis DNA encoding PKSE.  
 PN CA2387401-A1.  
 PD 04-SEP-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 4.8%; Score 47.6; DB 6; Length 5802;  
 Best Local Similarity 46.0%; Pred. No. 43;  
 RESULT 1152  
 ID ADS97707 standard; DNA; 5886 BP.  
 DE Rabbit alpha-myosin heavy chain coding sequence.  
 PN WO2004082370-A2.  
 PD 30-SEP-2004.  
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 Query Match 4.8%; Score 47.6; DB 13; Length 5886;  
 Best Local Similarity 46.4%; Pred. No. 43;  
 RESULT 1153  
 ID ADK18367 standard; DNA; 6008 BP.  
 DE Human NOVX protein encoding gene #11.  
 PN WO2003057854-A2.  
 PD 17-JUL-2003.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 4.8%; Score 47.6; DB 10; Length 6008;  
 Best Local Similarity 46.4%; Pred. No. 43;  
 RESULT 1154  
 ID ADP13461 standard; DNA; 6008 BP.  
 DE Renal cell carcinoma differentially expressed gene #197.  
 PN WO2004048933-A2.  
 PD 10-JUN-2004.

PA (AMHP) WYETH.  
 PA (TWIN/) TWINE N C.  
 PA (BURC/) BURCZYNSKI M E.  
 PA (TREP/) TREPICCHIO W L.  
 PA (DORN/) DORNER A.  
 PA (STOV/) STOVER J A.  
 PA (SLON/) SLONI D K.  
 Query Match 4.8%; Score 47.6; DB 12; Length 6008;  
 Best Local Similarity 46.4%; Pred. No. 43;  
 RESULT 1155  
 ID AAV58939 standard; DNA; 9960 BP.  
 DE Mycobacterium smegmatis embCAB operon.  
 PN WO9841533-A1.  
 PD 24-SEP-1998.  
 PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.  
 Query Match 4.8%; Score 47.6; DB 2; Length 9960;  
 Best Local Similarity 45.1%; Pred. No. 42;  
 RESULT 1156  
 ID ADS97709 standard; DNA; 12801 BP.  
 DE Rabbit alpha-myosin heavy chain expression cassette.  
 PN WO2004082370-A2.  
 PD 30-SEP-2004.  
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 Query Match 4.8%; Score 47.6; DB 13; Length 12801;  
 Best Local Similarity 46.4%; Pred. No. 42;  
 RESULT 1157  
 ID AAD17185 standard; DNA; 27541 BP.  
 DE Streptomyces noursei nys2 DNA of nystatin PKS gene cluster.  
 PN WO200159126-A2.  
 PD 16-AUG-2001.  
 PA (UYNO-) UNIV NORGES TEKNISK NATURVITENSKAPELIGE.  
 PA (SNTF) STITEF STIFTELSEN IND TEK FORSK.  
 PA (ALPH-) ALPHARMA AS.  
 PA (SINV-) SINVENT AS.  
 PA (DZIE/) DZIEGLEWSKA H.  
 PA (ZOTC/) ZOTCHEV S B.  
 PA (SEKU/) SEKUROVA O N.  
 PA (FJAE/) FJAERVIK E.  
 PA (BRAU/) BRAUTASET T.  
 PA (STRO/) STROM A R.  
 PA (VALL/) VALLA S.  
 Query Match 4.8%; Score 47.6; DB 4; Length 27541;  
 Best Local Similarity 47.2%; Pred. No. 41;  
 RESULT 1158  
 ID AAS59516 standard; DNA; 29255 BP.  
 DE Propionibacterium acnes immunogenic protein encoding DNA #11.  
 PN WO200181581-A2.  
 PD 01-NOV-2001.  
 PA (CORI-) CORIXA CORP.  
 Query Match 4.8%; Score 47.6; DB 4; Length 29255;  
 Best Local Similarity 44.9%; Pred. No. 41;  
 RESULT 1159  
 ID ACF64445 standard; DNA; 29255 BP.  
 DE Propionibacterium acnes DNA contig sequence #11.  
 PN WO2003033515-A1.  
 PD 24-APR-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match 4.8%; Score 47.6; DB 8; Length 29255;  
 Best Local Similarity 44.9%; Pred. No. 41;  
 RESULT 1160  
 ID ADJ12143 standard; DNA; 414 BP.  
 DE Maize cDNA modulated by post-transcriptional gene silencing SeqID 779.  
 PN US200313588-A1.  
 PD 17-JUL-2003.  
 PA (ZHUT/) ZHU T.  
 PA (WANG/) WANG X.  
 PA (CHAN/) CHANG H.  
 PA (BRIG/) BRIGGS S P.  
 PA (COOP/) COOPER B.  
 PA (GLAZ/) GLAZERBROOK J.  
 PA (GOFF/) GOFF S A.  
 PA (KATA/) KATAGIRI F.  
 PA (KREP/) KREPS J.

PA (MOUG/) MOUGHAMER T.  
 PA (PROV/) PROVART N.  
 PA (RICK/) RIQUE D.  
 Query Match  
 Best Local Similarity 4.8%; Score 47.4; DB 11; Length 414;  
 Best Local Similarity 47.5%; Pred. No. 50;  
 RESULT 1161  
 ID ADJ44853 standard; cDNA; 504 BP.  
 DE Plant cDNA #5853.  
 PN US2004016025-A1.  
 PD 22-JAN-2004.  
 PA (BUDW/) BUDWORTH P.  
 PA (MOUG/) MOUGHAMER T.  
 PA (BRIG/) BRIGGS S P.  
 PA (COOP/) COOPER B.  
 PA (GLAZ/) GLAZEBROOK J.  
 PA (GOFF/) GOFF S A.  
 PA (KATA/) KATAGIRI F.  
 PA (KREP/) KREPS J.  
 PA (PROV/) PROVART N.  
 PA (RICK/) RIQUE D.  
 PA (ZHUT/) ZHU T.  
 Query Match  
 Best Local Similarity 4.8%; Score 47.4; DB 12; Length 504;  
 Best Local Similarity 45.2%; Pred. No. 50;  
 RESULT 1162  
 ID ADG3398 standard; DNA; 670 BP.  
 DE Maize lipoxygenase (LOX) DNA #15.  
 PN US2003166855-A1.  
 PD 04-SEP-2003.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Query Match  
 Best Local Similarity 4.8%; Score 47.4; DB 10; Length 670;  
 Best Local Similarity 49.0%; Pred. No. 49;  
 RESULT 1163  
 ID ADG33400 standard; DNA; 670 BP.  
 DE Maize lipoxygenase (LOX) DNA #16.  
 PN US2003166855-A1.  
 PD 04-SEP-2003.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Query Match  
 Best Local Similarity 4.8%; Score 47.4; DB 10; Length 670;  
 Best Local Similarity 49.0%; Pred. No. 49;  
 RESULT 1164  
 ID ABD10158 standard; DNA; 918 BP.  
 DE Pseudomonas aeruginosa polynucleotide #8762.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match  
 Best Local Similarity 4.8%; Score 47.4; DB 11; Length 918;  
 Best Local Similarity 46.3%; Pred. No. 49;  
 RESULT 1165  
 ID ABD10588 standard; DNA; 948 BP.  
 DE Pseudomonas aeruginosa polynucleotide #9192.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match  
 Best Local Similarity 4.8%; Score 47.4; DB 11; Length 948;  
 Best Local Similarity 46.3%; Pred. No. 49;  
 RESULT 1166  
 ID ABD07203 standard; DNA; 954 BP.  
 DE Pseudomonas aeruginosa polynucleotide #5807.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match  
 Best Local Similarity 4.8%; Score 47.4; DB 11; Length 948;  
 Best Local Similarity 46.3%; Pred. No. 49;  
 RESULT 1167  
 ID AAZ51701 standard; DNA; 1044 BP.  
 DE Burkholderia multivorans reca gene (1).  
 PN WO200014274-A1.  
 PD 16-MAR-2000.  
 PA (UYBR-) UNIV BRITISH COLUMBIA.  
 Query Match  
 Best Local Similarity 4.8%; Score 47.4; DB 3; Length 1044;  
 Best Local Similarity 43.6%; Pred. No. 49;  
 RESULT 1168  
 ID ABD12320 standard; DNA; 1116 BP.  
 DE Pseudomonas aeruginosa polynucleotide #10924.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match  
 Best Local Similarity 4.8%; Score 47.4; DB 11; Length 1116;  
 Best Local Similarity 48.0%; Pred. No. 49;  
 RESULT 1169  
 ID ABD10379 standard; DNA; 1149 BP.  
 DE Pseudomonas aeruginosa polynucleotide #8983.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match  
 Best Local Similarity 4.8%; Score 47.4; DB 11; Length 1149;  
 Best Local Similarity 46.3%; Pred. No. 49;  
 RESULT 1170  
 ID ABD12534 standard; DNA; 1209 BP.  
 DE Pseudomonas aeruginosa polynucleotide #11138.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match  
 Best Local Similarity 4.8%; Score 47.4; DB 11; Length 1209;  
 Best Local Similarity 48.0%; Pred. No. 48;  
 RESULT 1171  
 ID ABX56037 standard; DNA; 1248 BP.  
 DE M. echinospira calicheamicin biosynthesis gene calM.  
 PN WO200279465-A2.  
 PD 10-OCT-2002.  
 PA (SLOK) SLOAN KETTERING INST CANCER RES.  
 Query Match  
 Best Local Similarity 4.8%; Score 47.4; DB 8; Length 1248;  
 Best Local Similarity 49.3%; Pred. No. 48;  
 RESULT 1172  
 ID ABD07240 standard; DNA; 1251 BP.  
 DE Pseudomonas aeruginosa polynucleotide #5844.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match  
 Best Local Similarity 4.8%; Score 47.4; DB 11; Length 1251;  
 Best Local Similarity 44.2%; Pred. No. 48;  
 RESULT 1173  
 ID ACA27319 standard; DNA; 1404 BP.  
 DE Prokaryotic essential gene #8976.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match  
 Best Local Similarity 4.8%; Score 47.4; DB 8; Length 1404;  
 Best Local Similarity 44.6%; Pred. No. 48;  
 RESULT 1174  
 ID ABD04734 standard; DNA; 1650 BP.  
 DE Pseudomonas aeruginosa polynucleotide #3338.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match  
 Best Local Similarity 4.8%; Score 47.4; DB 11; Length 1650;  
 Best Local Similarity 43.9%; Pred. No. 48;  
 RESULT 1175  
 ID ACA37851 standard; DNA; 1734 BP.  
 DE Prokaryotic essential gene #19508.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match  
 Best Local Similarity 4.8%; Score 47.4; DB 8; Length 1734;  
 Best Local Similarity 52.8%; Pred. No. 48;  
 RESULT 1176  
 ID ABD04627 standard; DNA; 1869 BP.  
 DE Pseudomonas aeruginosa polynucleotide #3231.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match  
 Best Local Similarity 4.8%; Score 47.4; DB 11; Length 1869;  
 Best Local Similarity 43.9%; Pred. No. 48;  
 RESULT 1177  
 ID ABD12660 standard; DNA; 1881 BP.  
 DE Pseudomonas aeruginosa polynucleotide #11264.

PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.8%; Score 47.4; DB 11; Length 1881;  
 Best Local Similarity 48.0%; Pred. No. 48;  
 RESULT 1178  
 ID ABD07163 standard; DNA; 1986 BP.  
 DE Pseudomonas aeruginosa polynucleotide #5767.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.8%; Score 47.4; DB 11; Length 1986;  
 Best Local Similarity 44.2%; Pred. No. 48;  
 RESULT 1179  
 ID ABD04694 standard; DNA; 2283 BP.  
 DE Pseudomonas aeruginosa polynucleotide #3298.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.8%; Score 47.4; DB 11; Length 2283;  
 Best Local Similarity 43.9%; Pred. No. 48;  
 RESULT 1180  
 ID ADO26117 standard; DNA; 2354 BP.  
 DE Corn phenylalanine ammonia synthase (PAL) seqid 155.  
 PN WO2004046336-A2.  
 PD 03-JUN-2004.  
 PA (MONS) MONSANTO TECHNOLOGY LLC.  
 Query Match 4.8%; Score 47.4; DB 12; Length 2354;  
 Best Local Similarity 47.5%; Pred. No. 48;  
 RESULT 1181  
 ID ACA25940 standard; DNA; 2463 BP.  
 DE Prokaryotic essential gene #7597.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.8%; Score 47.4; DB 8; Length 2463;  
 Best Local Similarity 45.5%; Pred. No. 48;  
 RESULT 1182  
 ID ABD10506 standard; DNA; 2583 BP.  
 DE Pseudomonas aeruginosa polynucleotide #9110.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.8%; Score 47.4; DB 11; Length 2583;  
 Best Local Similarity 46.3%; Pred. No. 47;  
 RESULT 1183  
 ID AAQ39093 standard; DNA; 2634 BP.  
 DE Streptomyces nodosus 2634bp BamHI fragment.  
 PN WO9306219-A1.  
 PD 01-APR-1993.  
 PA (FAEH) HOECHST AG.  
 Query Match 4.8%; Score 47.4; DB 2; Length 2634;  
 Best Local Similarity 44.9%; Pred. No. 47;  
 RESULT 1184  
 ID ACA23465 standard; DNA; 2883 BP.  
 DE Prokaryotic essential gene #5122.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.8%; Score 47.4; DB 8; Length 2883;  
 Best Local Similarity 44.9%; Pred. No. 47;  
 RESULT 1185  
 ID ADA71066 standard; DNA; 3153 BP.  
 DE Rice gene, SEQ ID 4389.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Query Match 4.8%; Score 47.4; DB 8; Length 3153;  
 Best Local Similarity 46.3%; Pred. No. 47;  
 RESULT 1186  
 ID ADA69900 standard; DNA; 3252 BP.  
 DE Rice gene, SEQ ID 3223.  
 PN WO2003000898-A1.

PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Query Match 4.8%; Score 47.4; DB 8; Length 3252;  
 Best Local Similarity 45.4%; Pred. No. 47;  
 RESULT 1187  
 ID ADC68517 standard; cDNA; 3629 BP.  
 DE S. arundinaceus fructan biosynthesis protein cDNA SEQ ID NO:9.  
 PN WO2003040306-A2.  
 PD 15-MAY-2003.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (WRIG-) WRIGHTSON SEEDS LTD.  
 Query Match 4.8%; Score 47.4; DB 10; Length 3629;  
 Best Local Similarity 46.1%; Pred. No. 47;  
 RESULT 1188  
 ID ADC68420 standard; cDNA; 3633 BP.  
 DE S. arundinaceus fructan biosynthesis protein cDNA SEQ ID NO:130.  
 PN WO2003040306-A2.  
 PD 15-MAY-2003.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (WRIG-) WRIGHTSON SEEDS LTD.  
 Query Match 4.8%; Score 47.4; DB 10; Length 3633;  
 Best Local Similarity 46.1%; Pred. No. 47;  
 RESULT 1189  
 ID AAD47222 standard; DNA; 19016 BP.  
 DE Streptococcus sp. H021 DNA fragment for rabelomycin biosynthetic pathway.  
 PN WO200274800-A1.  
 PD 26-SEP-2002.  
 PA (GALI-) GALILAEUS OY.  
 Query Match 4.8%; Score 47.4; DB 8; Length 19016;  
 Best Local Similarity 43.3%; Pred. No. 45;  
 RESULT 1190  
 ID ADE86070 standard; DNA; 47988 BP.  
 DE Streptomyces hygroscopicus non-ribosomal peptide synthetase complex DNA.  
 PN WO2003082909-A1.  
 PD 09-OCT-2003.  
 PA (AMHP) WYETH.  
 Query Match 4.8%; Score 47.4; DB 10; Length 47988;  
 Best Local Similarity 44.2%; Pred. No. 44;  
 RESULT 1191  
 ID AAA09469 standard; DNA; 50937 BP.  
 DE Streptococcus oleandomycin gene cluster.  
 PN WO200026349-A2.  
 PD 11-MAY-2000.  
 PA (KOSA-) KOSAN BIOSCIENCES INC.  
 Query Match 4.8%; Score 47.4; DB 3; Length 50937;  
 Best Local Similarity 44.7%; Pred. No. 44;  
 RESULT 1192  
 ID AAA09469 standard; DNA; 50937 BP.  
 DE Streptococcus oleandomycin gene cluster.  
 PN WO200026349-A2.  
 PD 11-MAY-2000.  
 PA (KOSA-) KOSAN BIOSCIENCES INC.  
 Query Match 4.8%; Score 47.4; DB 3; Length 50937;  
 Best Local Similarity 45.7%; Pred. No. 44;  
 RESULT 1193  
 ID ADP74816 standard; DNA; 137560 BP.  
 DE Parapoxvirus ovis genome DNA sequence SeqID1.  
 Query Match 4.8%; Score 47.4; DB 12; Length 137560;  
 Best Local Similarity 47.9%; Pred. No. 42;  
 RESULT 1194  
 ID ADC76153 standard; DNA; 607 BP.  
 DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 1422.  
 PN WO2003020905-A2.  
 PD 13-MAR-2003.  
 PA (DOWC) DOW CHEM CO.  
 Query Match 4.8%; Score 47.2; DB 10; Length 607;  
 Best Local Similarity 47.8%; Pred. No. 53;  
 RESULT 1195  
 ID ADD17151 standard; DNA; 607 BP.  
 DE DNA (SeqID 1219) that confers an altered visual phenotype in plants.  
 PN WO2003020741-A1.  
 PD 13-MAR-2003.  
 PA (DOWC) DOW CHEM CO.

PA (DOWC ) DOW AGROSCIENCES LLC.  
 Query Match 4.8%; Score 47.2; DB 10; Length 607;  
 Best Local Similarity 47.8%; Pred. No. 53;  
 RESULT 1196  
 ID ADD17811 standard; DNA; 607 BP.  
 DE DNA (SeqID 1879) that confers an altered visual phenotype in plants.  
 PN WO2003020741-A1.  
 PD 13-MAR-2003.  
 PA (DOWC ) DOW CHEM CO.  
 Query Match 4.8%; Score 47.2; DB 10; Length 607;  
 Best Local Similarity 47.8%; Pred. No. 53;  
 RESULT 1197  
 ID ADK58311 standard; DNA; 607 BP.  
 DE Plant DNA sequence which confers altered metabolic characteristic #5694.  
 PN WO2003020936-A1.  
 PD 13-MAR-2003.  
 PA (DOWC ) DOW CHEM CO.  
 Query Match 4.8%; Score 47.2; DB 10; Length 607;  
 Best Local Similarity 47.8%; Pred. No. 53;  
 RESULT 1198  
 ID ABD17417 standard; DNA; 714 BP.  
 DE Pseudomonas aeruginosa polynucleotide #16021.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.8%; Score 47.2; DB 11; Length 714;  
 Best Local Similarity 48.8%; Pred. No. 53;  
 RESULT 1199  
 ID ACA23687 standard; DNA; 852 BP.  
 DE Prokaryotic essential gene #5344.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.8%; Score 47.2; DB 8; Length 852;  
 Best Local Similarity 47.9%; Pred. No. 53;  
 RESULT 1200  
 ID ADC76149 standard; DNA; 873 BP.  
 DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 1418.  
 PN WO2003020905-A2.  
 PD 13-MAR-2003.  
 PA (DOWC ) DOW CHEM CO.  
 Query Match 4.8%; Score 47.2; DB 10; Length 873;  
 Best Local Similarity 47.8%; Pred. No. 53;  
 RESULT 1201  
 ID ADD17156 standard; DNA; 873 BP.  
 DE DNA (SeqID 1224) that confers an altered visual phenotype in plants.  
 PN WO2003020741-A1.  
 PD 13-MAR-2003.  
 PA (DOWC ) DOW CHEM CO.  
 Query Match 4.8%; Score 47.2; DB 10; Length 873;  
 Best Local Similarity 47.8%; Pred. No. 53;  
 RESULT 1202  
 ID ADK58312 standard; DNA; 873 BP.  
 DE Plant DNA sequence which confers altered metabolic characteristic #5695.  
 PN WO2003020936-A1.  
 PD 13-MAR-2003.  
 PA (DOWC ) DOW CHEM CO.  
 Query Match 4.8%; Score 47.2; DB 10; Length 873;  
 Best Local Similarity 47.8%; Pred. No. 53;  
 RESULT 1203  
 ID RAT59269 standard; cDNA; 888 BP.  
 DE Streptomyces pristinaespiralis papC gene.  
 PN WO9601901-A1.  
 PD 25-JAN-1996.  
 PA (RHON ) RHONE-POULENC RORER SA.  
 Query Match 4.8%; Score 47.2; DB 2; Length 888;  
 Best Local Similarity 45.3%; Pred. No. 53;  
 RESULT 1204  
 ID ABD23366 standard; DNA; 999 BP.

DE Pseudomonas aeruginosa polynucleotide #970.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.8%; Score 47.2; DB 11; Length 999;  
 Best Local Similarity 46.4%; Pred. No. 53;  
 RESULT 1205  
 ID ADA48950 standard; DNA; 1044 BP.  
 DE Wheat gene conferring disease resistance in plants.  
 PN WO2003000906-A2.  
 PD 03-JAN-2003.  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 Query Match 4.8%; Score 47.2; DB 9; Length 1044;  
 Best Local Similarity 44.5%; Pred. No. 53;  
 RESULT 1206  
 ID ABD02410 standard; DNA; 1110 BP.  
 DE Pseudomonas aeruginosa polynucleotide #1014.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.8%; Score 47.2; DB 11; Length 1110;  
 Best Local Similarity 46.4%; Pred. No. 52;  
 RESULT 1207  
 ID ACA26954 standard; DNA; 1134 BP.  
 DE Prokaryotic essential gene #8611.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.8%; Score 47.2; DB 8; Length 1134;  
 Best Local Similarity 46.7%; Pred. No. 52;  
 RESULT 1208  
 ID ADQ83738 standard; cDNA; 1178 BP.  
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #552.  
 PN WO2004060270-A2.  
 PD 22-JUL-2004.  
 PA (GETH ) GENENTECH INC.  
 PA (WUTD/) WU T D.  
 PA (ZHOU/) ZHOU Y.  
 Query Match 4.8%; Score 47.2; DB 12; Length 1178;  
 Best Local Similarity 43.8%; Pred. No. 52;  
 RESULT 1209  
 ID ABX56038 standard; DNA; 1194 BP.  
 DE M. echinospira calicheamicin biosynthesis gene calN.  
 PN WO200279465-A2.  
 PD 10-OCT-2002.  
 PA (SLOK ) SLOAN KETTERING INST CANCER RES.  
 Query Match 4.8%; Score 47.2; DB 8; Length 1194;  
 Best Local Similarity 43.0%; Pred. No. 52;  
 RESULT 1210  
 ID ABD02476 standard; DNA; 1275 BP.  
 DE Pseudomonas aeruginosa polynucleotide #1080.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.8%; Score 47.2; DB 11; Length 1275;  
 Best Local Similarity 46.4%; Pred. No. 52;  
 RESULT 1211  
 ID ABX56047 standard; DNA; 1347 BP.  
 DE M. echinospira calicheamicin biosynthesis gene calW.  
 PN WO200279465-A2.  
 PD 10-OCT-2002.  
 PA (SLOK ) SLOAN KETTERING INST CANCER RES.  
 Query Match 4.8%; Score 47.2; DB 8; Length 1347;  
 Best Local Similarity 47.0%; Pred. No. 52;  
 RESULT 1212  
 ID ACA23577 standard; DNA; 1374 BP.  
 DE Prokaryotic essential gene #5234.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.8%; Score 47.2; DB 8; Length 1374;  
 Best Local Similarity 47.3%; Pred. No. 52;  
 RESULT 1213

```
ID ADT43862 standard; cDNA; 1386 BP.
DE Bacterial polynucleotide #18613.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 4.8%; Score 47.2; DB 13; Length 1386;
Best Local Similarity 47.1%; Pred. No. 52;
RESULT 1214
ID ACA26528 standard; DNA; 1395 BP.
DE Prokaryotic essential gene #8185.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 4.8%; Score 47.2; DB 8; Length 1395;
Best Local Similarity 46.6%; Pred. No. 52;
RESULT 1215
ID ACA37685 standard; DNA; 1410 BP.
DE Prokaryotic essential gene #19342.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 4.8%; Score 47.2; DB 8; Length 1410;
Best Local Similarity 45.8%; Pred. No. 52;
RESULT 1216
ID ABQ55009 standard; cDNA; 1616 BP.
DE Human ovarian antigen HUKJ46 cDNA, SEQ ID NO:889.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 4.8%; Score 47.2; DB 6; Length 1616;
Best Local Similarity 45.3%; Pred. No. 52;
RESULT 1217
ID ABL39997 standard; DNA; 1680 BP.
DE Synthetic RT polynucleotide sequence SEQ ID NO:76.
PN WO200204493-A2.
PD 17-JAN-2002.
PA (CHIR) CHIRON CORP.
PA (UYST-) UNIV STELLENBOSCH.
Query Match
Best Local Similarity 4.8%; Score 47.2; DB 6; Length 1680;
Best Local Similarity 47.6%; Pred. No. 52;
RESULT 1218
ID ADM73810 standard; DNA; 1680 BP.
DE HIV-1 polynucleotide #45.
PN US2003233961-A1.
PD 04-DEC-2003.
PA (MEGE/) MEGEDE J Z.
PA (BARN/) BARNETT S W.
PA (ENGE/) ENGELBRECHT S.
PA (RENS/) RENSBURG E J V.
Query Match
Best Local Similarity 4.8%; Score 47.2; DB 12; Length 1680;
Best Local Similarity 47.6%; Pred. No. 52;
RESULT 1219
ID ACH91868 standard; DNA; 1737 BP.
DE Human genome derived single exon probe #25063.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match
Best Local Similarity 4.8%; Score 47.2; DB 12; Length 1737;
Best Local Similarity 49.2%; Pred. No. 52;
RESULT 1220
ID ACH92275 standard; DNA; 1738 BP.
DE Human genome derived single exon probe #25470.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match
Best Local Similarity 4.8%; Score 47.2; DB 12; Length 1738;
Best Local Similarity 49.2%; Pred. No. 52;
RESULT 1221
ID AAL40132 standard; DNA; 1896 BP.
DE Isoprenoid related nucleic acid sequence SEQ ID NO 16.
PN WO200226933-A2.
PD 04-APR-2002.
PA (CRGI) CARGILL INC.
Query Match
Best Local Similarity 4.8%; Score 47.2; DB 6; Length 1896;
Best Local Similarity 45.3%; Pred. No. 52;
RESULT 1222
ID ABD17641 standard; DNA; 1944 BP.
DE Pseudomonas aeruginosa polynucleotide #16245.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 4.8%; Score 47.2; DB 11; Length 1944;
Best Local Similarity 48.8%; Pred. No. 52;
RESULT 1223
ID ACA03560 standard; DNA; 1977 BP.
DE Synthetic DNA encoding immunogenic HIV peptide #43.
PN WO2003004657-A1.
PD 16-JAN-2003.
PA (CHIR) CHIRON CORP.
Query Match
Best Local Similarity 4.8%; Score 47.2; DB 8; Length 1977;
Best Local Similarity 47.6%; Pred. No. 52;
RESULT 1224
ID ACC78516 standard; DNA; 1977 BP.
DE HIV protRT.opt.SF2 nucleotide sequence.
PN WO2003020876-A2.
PD 13-MAR-2003.
PA (CHIR) CHIRON CORP.
Query Match
Best Local Similarity 4.8%; Score 47.2; DB 8; Length 1977;
Best Local Similarity 47.6%; Pred. No. 52;
RESULT 1225
ID ADM73804 standard; DNA; 1977 BP.
DE HIV-1 polynucleotide #39.
PN US2003233961-A1.
PD 04-DEC-2003.
PA (MEGE/) MEGEDE J Z.
PA (BARN/) BARNETT S W.
PA (ENGE/) ENGELBRECHT S.
PA (RENS/) RENSBURG E J V.
Query Match
Best Local Similarity 4.8%; Score 47.2; DB 12; Length 1977;
Best Local Similarity 47.6%; Pred. No. 52;
RESULT 1226
ID ABL39991 standard; DNA; 1978 BP.
DE Synthetic protease and RT polynucleotide sequence SEQ ID NO:70.
PN WO200204493-A2.
PD 17-JAN-2002.
PA (CHIR) CHIRON CORP.
PA (UYST-) UNIV STELLENBOSCH.
Query Match
Best Local Similarity 4.8%; Score 47.2; DB 6; Length 1978;
Best Local Similarity 47.6%; Pred. No. 52;
RESULT 1227
ID ACA03571 standard; DNA; 1989 BP.
DE Synthetic DNA encoding immunogenic HIV peptide #54.
PN WO2003004657-A1.
PD 16-JAN-2003.
PA (CHIR) CHIRON CORP.
Query Match
Best Local Similarity 4.8%; Score 47.2; DB 8; Length 1989;
Best Local Similarity 47.6%; Pred. No. 52;
RESULT 1228
ID ACC78522 standard; DNA; 1989 BP.
DE HIV RT.opt.SF2 (native) nucleotide sequence.
PN WO2003020876-A2.
PD 13-MAR-2003.
PA (CHIR) CHIRON CORP.
Query Match
Best Local Similarity 4.8%; Score 47.2; DB 8; Length 1989;
Best Local Similarity 47.6%; Pred. No. 52;
RESULT 1229
ID ABD07303 standard; DNA; 2133 BP.
DE Pseudomonas aeruginosa polynucleotide #5907.
```



PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.8%; Score 47.2; DB 11; Length 2133;  
 Best Local Similarity 44.1%; Pred. No. 52;  
 RESULT 1230  
 ID ACA03552 standard; DNA; 2145 BP.  
 DE Synthetic DNA encoding immunogenic HIV peptide #35.  
 PN WO2003004657-A1.  
 PD 16-JAN-2003.  
 PA (CHIR ) CHIRON CORP.  
 Query Match 4.8%; Score 47.2; DB 8; Length 2145;  
 Best Local Similarity 47.8%; Pred. No. 52;  
 RESULT 1231  
 ID ACC78510 standard; DNA; 2145 BP.  
 DE HIV pol.opt.SF2 nucleotide sequence.  
 PN WO2003020876-A2.  
 PD 13-MAR-2003.  
 PA (CHIR ) CHIRON CORP.  
 Query Match 4.8%; Score 47.2; DB 8; Length 2145;  
 Best Local Similarity 47.6%; Pred. No. 52;  
 RESULT 1232  
 ID AAA70481 standard; DNA; 2312 BP.  
 DE HIV FS(-) ProMod\_RTopt(-) coding sequence.  
 PN WO200033302-A2.  
 PD 06-JUL-2000.  
 PA (CHIR ) CHIRON CORP.  
 Query Match 4.8%; Score 47.2; DB 3; Length 2312;  
 Best Local Similarity 47.6%; Pred. No. 51;  
 RESULT 1233  
 ID ACA03543 standard; DNA; 2472 BP.  
 DE Synthetic DNA encoding immunogenic HIV peptide #26.  
 PN WO2003004657-A1.  
 PD 16-JAN-2003.  
 PA (CHIR ) CHIRON CORP.  
 Query Match 4.8%; Score 47.2; DB 8; Length 2472;  
 Best Local Similarity 47.8%; Pred. No. 51;  
 RESULT 1234  
 ID ACC78507 standard; DNA; 2472 BP.  
 DE HIV p2Polopt.SF2 nucleotide sequence.  
 PN WO2003020876-A2.  
 PD 13-MAR-2003.  
 PA (CHIR ) CHIRON CORP.  
 Query Match 4.8%; Score 47.2; DB 8; Length 2472;  
 Best Local Similarity 47.6%; Pred. No. 51;  
 RESULT 1235  
 ID ADA69874 standard; DNA; 2529 BP.  
 DE Rice gene, SEQ ID 3197.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 Query Match 4.8%; Score 47.2; DB 8; Length 2529;  
 Best Local Similarity 44.5%; Pred. No. 51;  
 RESULT 1236  
 ID ADC72236 standard; DNA; 2691 BP.  
 DE Human NR3B gene SEQ ID NO:9.  
 PN WO2003016479-A2.  
 PD 27-FEB-2003.  
 PA (BURN-) BURNHAM INST.  
 PA (UYTA ) UNIV YALE.  
 PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.  
 Query Match 4.8%; Score 47.2; DB 10; Length 2691;  
 Best Local Similarity 43.7%; Pred. No. 51;  
 RESULT 1237  
 ID ADN49187 standard; cDNA; 2691 BP.  
 DE Human N-methyl-D-aspartate (NMDA) type 3B (NR3B) EST cDNA.  
 PN US2004033500-A1.  
 PD 19-FEB-2004.  
 PA (BURN-) BURNHAM INST.  
 PA (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.  
 Query Match 4.8%; Score 47.2; DB 12; Length 2691;  
 Best Local Similarity 43.7%; Pred. No. 51;  
 RESULT 1238

ID AAL47419 standard; cDNA; 2706 BP.  
 DE Human N-methyl-D-aspartate receptor coding sequence.  
 PN WO200240538-A2.  
 PD 23-MAY-2002.  
 PA (FARB ) BAYER AG.  
 Query Match 4.8%; Score 47.2; DB 6; Length 2706;  
 Best Local Similarity 43.7%; Pred. No. 51;  
 RESULT 1239  
 ID ACC47899 standard; cDNA; 2706 BP.  
 DE Human NR3B subunit receptor polypeptide coding sequence.  
 PN WO2003033672-A2.  
 PD 24-APR-2003.  
 PA (RIKE ) RIKEN KK.  
 Query Match 4.8%; Score 47.2; DB 8; Length 2706;  
 Best Local Similarity 43.7%; Pred. No. 51;  
 RESULT 1240  
 ID ACA38169 standard; DNA; 2751 BP.  
 DE Prokaryotic essential gene #19826.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.8%; Score 47.2; DB 8; Length 2751;  
 Best Local Similarity 47.1%; Pred. No. 51;  
 RESULT 1241  
 ID ADA69752 standard; DNA; 2763 BP.  
 DE Rice gene, SEQ ID 3075.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 Query Match 4.8%; Score 47.2; DB 8; Length 2763;  
 Best Local Similarity 48.2%; Pred. No. 51;  
 RESULT 1242  
 ID ABD17862 standard; DNA; 2808 BP.  
 DE Pseudomonas aeruginosa polynucleotide #16466.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.8%; Score 47.2; DB 11; Length 2808;  
 Best Local Similarity 48.8%; Pred. No. 51;  
 RESULT 1243  
 ID ABD12055 standard; DNA; 2862 BP.  
 DE Pseudomonas aeruginosa polynucleotide #10659.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.8%; Score 47.2; DB 11; Length 2862;  
 Best Local Similarity 43.1%; Pred. No. 51;  
 RESULT 1244  
 ID AAT59268 standard; cDNA; 2888 BP.  
 DE Streptomyces pristinaespiralis papA and papM intergenic region.  
 PN WO9601901-A1.  
 PD 25-JAN-1996.  
 PA (RHON ) RHONE-POULENC RORER SA.  
 Query Match 4.8%; Score 47.2; DB 2; Length 2888;  
 Best Local Similarity 45.3%; Pred. No. 51;  
 RESULT 1245  
 ID ADN49407 standard; DNA; 2898 BP.  
 DE Human glutamate receptor (MEM2) DNA.  
 PN US2004086931-A1.  
 PD 06-MAY-2004.  
 PA (SPAD/) SPADERNA S K.  
 PA (QUIN/) QUINN K E.  
 PA (SHIM/) SHIMKETS R A.  
 PA (PADI/) PADIGARU M.  
 PA (SPYT/) SPYTEK K A.  
 Query Match 4.8%; Score 47.2; DB 12; Length 2898;  
 Best Local Similarity 43.7%; Pred. No. 51;  
 RESULT 1246  
 ID ABD11810 standard; DNA; 2910 BP.  
 DE Pseudomonas aeruginosa polynucleotide #10414.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.

Query Match  
 Best Local Similarity 4.8%; Score 47.2; DB 11; Length 2910;  
 RESULT 1247  
 ID AAS06334 standard; cDNA; 2916 BP.  
 DE DNA encoding human glutamate receptor-like protein, MEM3.  
 PN WO200144473-A2.  
 PD 21-JUN-2001.  
 PA (CURA-) CURAGEN CORP.  
 Query Match  
 Best Local Similarity 4.8%; Score 47.2; DB 4; Length 2916;  
 RESULT 1248  
 ID ADN49409 standard; DNA; 2916 BP.  
 DE Human glutamate receptor (MEM3) DNA.  
 PN US2004086931-A1.  
 PD 06-MAY-2004.  
 PA (SPAD/) SPADERNA S K.  
 PA (QUIN/) QUINN K E.  
 PA (SHIM/) SHIMKETS R A.  
 PA (PADI/) PADIGARU M.  
 PA (SPYT/) SPYTEK K A.  
 Query Match  
 Best Local Similarity 4.8%; Score 47.2; DB 12; Length 2916;  
 RESULT 1249  
 ID AA252054 standard; DNA; 3012 BP.  
 DE Codon optimised Human immunodeficiency virus pol coding region.  
 PN WO200015819-A1.  
 PD 23-MAR-2000.  
 PA (CHIL-) CHILDRENS MEDICAL CENT.  
 Query Match  
 Best Local Similarity 4.8%; Score 47.2; DB 3; Length 3012;  
 RESULT 1250  
 ID ABL39983 standard; DNA; 3015 BP.  
 DE Synthetic Pol polynucleotide sequence SEQ ID NO:62.  
 PN WO200204493-A2.  
 PD 17-JAN-2002.  
 PA (CHIR-) CHIRON CORP.  
 PA (UYST-) UNIV STELLENBOSCH.  
 Query Match  
 Best Local Similarity 4.8%; Score 47.2; DB 6; Length 3015;  
 RESULT 1251  
 ID ACA03553 standard; DNA; 3015 BP.  
 DE Synthetic DNA encoding immunogenic HIV peptide #36.  
 PN WO2003004657-A1.  
 PD 16-JAN-2003.  
 PA (CHIR-) CHIRON CORP.  
 Query Match  
 Best Local Similarity 4.8%; Score 47.2; DB 8; Length 3015;  
 RESULT 1252  
 ID ADM73796 standard; DNA; 3015 BP.  
 DE HIV-1 polynucleotide #31.  
 PN US2003223961-A1.  
 PD 04-DEC-2003.  
 PA (MEGE/) MEGEDE J Z.  
 PA (BARN/) BARNETT S W.  
 PA (ENGE/) ENGELBRECHT S.  
 PA (RENS/) RENSBURG E J V.  
 Query Match  
 Best Local Similarity 4.8%; Score 47.2; DB 12; Length 3015;  
 RESULT 1253  
 ID ADC72232 standard; DNA; 3096 BP.  
 DE Human NR3B gene SEQ ID NO:5.  
 PN WO2003016479-A2.  
 PD 27-FEB-2003.  
 PA (BURN-) BURNHAM INST.  
 PA (UYVA) UNIV YALE.  
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.  
 Query Match  
 Best Local Similarity 4.8%; Score 47.2; DB 10; Length 3096;  
 RESULT 1254  
 ID ADN49183 standard; cDNA; 3096 BP.  
 DE Human N-methyl-D-aspartate (NMDA) type 3B (NR3B) cDNA #1.  
 PN US2004033500-A1.  
 PD 19-FEB-2004.

PA (BURN-) BURNHAM INST.  
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.  
 Query Match  
 Best Local Similarity 4.8%; Score 47.2; DB 12; Length 3096;  
 RESULT 1255  
 ID ADC72287 standard; DNA; 3097 BP.  
 DE Human NR3B gene SEQ ID NO:61.  
 PN WO2003016479-A2.  
 PD 27-FEB-2003.  
 PA (BURN-) BURNHAM INST.  
 PA (UYVA) UNIV YALE.  
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.  
 Query Match  
 Best Local Similarity 4.8%; Score 47.2; DB 10; Length 3097;  
 RESULT 1256  
 ID ADN49238 standard; cDNA; 3097 BP.  
 DE Human N-methyl-D-aspartate (NMDA) type 3B (NR3B) cDNA #2.  
 PN US2004033500-A1.  
 PD 19-FEB-2004.  
 PA (BURN-) BURNHAM INST.  
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.  
 Query Match  
 Best Local Similarity 4.8%; Score 47.2; DB 12; Length 3097;  
 RESULT 1257  
 ID ABD11900 standard; DNA; 3111 BP.  
 DE Pseudomonas aeruginosa polynucleotide #10504.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match  
 Best Local Similarity 4.8%; Score 47.2; DB 11; Length 3111;  
 RESULT 1258  
 ID AAS06335 standard; cDNA; 3132 BP.  
 DE DNA encoding human glutamate receptor-like protein, MEM4.  
 PN WO200144473-A2.  
 PD 21-JUN-2001.  
 PA (CURA-) CURAGEN CORP.  
 Query Match  
 Best Local Similarity 4.8%; Score 47.2; DB 4; Length 3132;  
 RESULT 1259  
 ID ABZ33750 standard; cDNA; 3132 BP.  
 DE Human TRICH encoding cDNA SEQ ID NO 56.  
 PN WO200246415-A2.  
 PD 13-JUN-2002.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Query Match  
 Best Local Similarity 4.8%; Score 47.2; DB 6; Length 3132;  
 RESULT 1260  
 ID ADN49411 standard; DNA; 3132 BP.  
 DE Human glutamate receptor (MEM4) DNA.  
 PN US2004086931-A1.  
 PD 06-MAY-2004.  
 PA (SPAD/) SPADERNA S K.  
 PA (QUIN/) QUINN K E.  
 PA (SHIM/) SHIMKETS R A.  
 PA (PADI/) PADIGARU M.  
 PA (SPYT/) SPYTEK K A.  
 Query Match  
 Best Local Similarity 4.8%; Score 47.2; DB 12; Length 3132;  
 RESULT 1261  
 ID ABD07318 standard; DNA; 3135 BP.  
 DE Pseudomonas aeruginosa polynucleotide #5922.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match  
 Best Local Similarity 4.8%; Score 47.2; DB 11; Length 3135;  
 RESULT 1262  
 ID AAC76703 standard; cDNA; 3207 BP.  
 DE Human ORFX ORF2258 polynucleotide sequence SEQ ID NO:4515.  
 PN WO200058473-A2.  
 PD 05-OCT-2000.  
 PA (CURA-) CURAGEN CORP.

Query Match 4.8%; Score 47.2; DB 3; Length 3207;  
 Best Local Similarity 43.7%; Pred. No. 51;  
 RESULT 1263  
 ID ACA03544 standard; DNA; 3639 BP.  
 DE Synthetic DNA encoding immunogenic HIV peptide #27.  
 PN WO2003004657-A1.  
 PD 16-JAN-2003.  
 PA (CHIR ) CHIRON CORP.  
 Query Match 4.8%; Score 47.2; DB 8; Length 3639;  
 Best Local Similarity 47.6%; Pred. No. 51;  
 RESULT 1264  
 ID ACC78508 standard; DNA; 3639 BP.  
 DE HIV p2PolTatRevNef.opt.native\_B nucleotide sequence.  
 PN WO2003020876-A2.  
 PD 13-MAR-2003.  
 PA (CHIR ) CHIRON CORP.  
 Query Match 4.8%; Score 47.2; DB 8; Length 3639;  
 Best Local Similarity 47.6%; Pred. No. 51;  
 RESULT 1265  
 ID ADM02119 standard; cDNA; 3955 BP.  
 DE Human cDNA of the invention SEQ ID NO:804.  
 PN EP1347046-A1.  
 PD 24-SEP-2003.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 Query Match 4.8%; Score 47.2; DB 11; Length 3955;  
 Best Local Similarity 49.2%; Pred. No. 51;  
 RESULT 1266  
 ID AAA70414 standard; DNA; 4319 BP.  
 DE HIV Gag-polymerase expression cassette coding sequence GagPol.ModSf.  
 PN WO200039302-A2.  
 PD 06-JUL-2000.  
 PA (CHIR ) CHIRON CORP.  
 Query Match 4.8%; Score 47.2; DB 3; Length 4319;  
 Best Local Similarity 47.6%; Pred. No. 51;  
 RESULT 1267  
 ID ADI60576 standard; DNA; 4532 BP.  
 DE Secreted polypeptide encoding gene #115.  
 PN WO2003025142-A2.  
 PD 27-MAR-2003.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 4.8%; Score 47.2; DB 10; Length 4532;  
 Best Local Similarity 49.2%; Pred. No. 50;  
 RESULT 1268  
 ID ADO24366 standard; cDNA; 4973 BP.  
 DE Human PRO87327 encoding cDNA SEQ ID NO:5.  
 PN WO2004043397-A2.  
 PD 27-MAY-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 4.8%; Score 47.2; DB 12; Length 4973;  
 Best Local Similarity 49.2%; Pred. No. 50;  
 RESULT 1269  
 ID AAV21186 standard; DNA; 5676 BP.  
 DE Mycolatopsis mediterranei strain wt3136 5.7 kb KpnI DNA fragment.  
 PN WO9807868-A1.  
 PD 26-FEB-1998.  
 PA (NOVS ) NOVARTIS AG.  
 Query Match 4.8%; Score 47.2; DB 2; Length 5676;  
 Best Local Similarity 44.9%; Pred. No. 50;  
 RESULT 1270  
 ID ADB53354 standard; DNA; 6402 BP.  
 DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3896.  
 PN WO2003065993-A2.  
 PD 14-AUG-2003.  
 PA (GENE-) GENE LOGIC INC.  
 Query Match 4.8%; Score 47.2; DB 10; Length 6402;  
 Best Local Similarity 43.0%; Pred. No. 50;  
 RESULT 1271  
 ID AAZ52055 standard; DNA; 8908 BP.  
 DE Packaging construct pHDHgm2 DNA.  
 PN WO200015819-A1.  
 PD 23-MAR-2000.  
 PA (CHIL-) CHILDRENS MEDICAL CENT.  
 Query Match 4.8%; Score 47.2; DB 3; Length 8908;

Best Local Similarity 47.6%; Pred. No. 50;  
 RESULT 1272  
 ID AAZ87298 standard; DNA; 11220 BP.  
 DE S. venezuelae macrolide biosynthetic gene pikAII, SEQ ID NO:32.  
 PN WO200000620-A2.  
 PD 06-JAN-2000.  
 PA (MINU ) UNIV MINNESOTA.  
 Query Match 4.8%; Score 47.2; DB 3; Length 11220;  
 Best Local Similarity 47.3%; Pred. No. 49;  
 RESULT 1273  
 ID ADL91917 standard; DNA; 11220 BP.  
 DE Streptomycetes macrolide biosynthetic protein (PikAII) coding sequence.  
 PN US2003194784-A1.  
 PD 16-OCT-2003.  
 PA (SHER/) SHERMAN D H.  
 PA (LIUH/) LIU H.  
 PA (XUEY/) XUE Y.  
 PA (ZHAO/) ZHAO L.  
 Query Match 4.8%; Score 47.2; DB 12; Length 11220;  
 Best Local Similarity 47.3%; Pred. No. 49;  
 RESULT 1274  
 ID ADJ72366 standard; DNA; 23949 BP.  
 DE Streptomycetes roseosporus daptomycin biosynthesis gene fragment.  
 PN WO2003014237-A2.  
 PD 20-FEB-2003.  
 PA (CUBI-) CUBIST PHARM INC.  
 Query Match 4.8%; Score 47.2; DB 10; Length 23949;  
 Best Local Similarity 44.7%; Pred. No. 48;  
 RESULT 1275  
 ID ADC69979 standard; DNA; 27705 BP.  
 DE Sorangium cellulosum tmba gene cluster tmba DNA.  
 PN US2003054547-A1.  
 PD 20-MAR-2003.  
 PA (JULI/) JULIEN B.  
 Query Match 4.8%; Score 47.2; DB 10; Length 27705;  
 Best Local Similarity 46.1%; Pred. No. 48;  
 RESULT 1276  
 ID AAV21187 standard; DNA; 53789 BP.  
 DE Amycolatopsis mediterranei rifamycin synthesis gene cluster fragment.  
 PN WO9807868-A1.  
 PD 26-FEB-1998.  
 PA (NOVS ) NOVARTIS AG.  
 Query Match 4.8%; Score 47.2; DB 2; Length 53789;  
 Best Local Similarity 44.9%; Pred. No. 47;  
 RESULT 1277  
 ID ABD16054 standard; DNA; 441 BP.  
 DE Pseudomonas aeruginosa polynucleotide #14658.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.8%; Score 47; DB 11; Length 441;  
 Best Local Similarity 46.1%; Pred. No. 58;  
 RESULT 1278  
 ID ADB68842 standard; DNA; 536 BP.  
 DE Minority luxI consensus sequence DNA 14.  
 PN WO2003057902-A2.  
 PD 17-JUL-2003.  
 PA (FRAU ) FRAUNHOFER USA INC.  
 Query Match 4.8%; Score 47; DB 10; Length 536;  
 Best Local Similarity 12.9%; Pred. No. 58;  
 RESULT 1279  
 ID ADC08861 standard; DNA; 597 BP.  
 DE Corn DNA sequence Seq ID1166 related to grain filling.  
 PN WO2003000905-A2.  
 PD 03-JAN-2003.  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 Query Match 4.8%; Score 47; DB 10; Length 597;  
 Best Local Similarity 49.8%; Pred. No. 58;  
 RESULT 1280  
 ID ACA26778 standard; DNA; 675 BP.  
 DE Prokaryotic essential gene #8435.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.

PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.8%; Score 47; DB 8; Length 675;  
 Best Local Similarity 47.0%; Pred. No. 57;  
 RESULT 1281  
 ID ADO63457 standard; DNA; 715 BP.  
 DE Transcription factor G3083 orthologous sequence, SEQ ID 1924.  
 PN WO2004031349-A2.  
 PD 15-APR-2004.  
 PA (MEND-) MENDEL BIOTECHNOLOGY INC.  
 Query Match 4.8%; Score 47; DB 12; Length 715;  
 Best Local Similarity 48.1%; Pred. No. 57;  
 RESULT 1282  
 ID ABQ78042 standard; cDNA; 758 BP.  
 DE Maize SCIP-1 orthologue encoding cDNA SEQ ID NO 5.  
 PN US2002069428-A1.  
 PD 06-JUN-2002.  
 PA (PION-) PIONEER HI-BRED INT INC.  
 Query Match 4.8%; Score 47; DB 6; Length 758;  
 Best Local Similarity 46.9%; Pred. No. 57;  
 RESULT 1283  
 ID ABX12766 standard; DNA; 930 BP.  
 DE DNA encoding murine ischaemia activated protein (IAP).  
 PN US2002160495-A1.  
 PD 31-OCT-2002.  
 PA (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.  
 Query Match 4.8%; Score 47; DB 8; Length 930;  
 Best Local Similarity 50.7%; Pred. No. 57;  
 RESULT 1284  
 ID ADL17042 standard; cDNA; 1120 BP.  
 DE Streptomyces coelicolor Bcl-2 domain cDNA #1.  
 PN US2004023866-A1.  
 PD 05-FEB-2004.  
 PA (GODZ/) GODZIK A.  
 PA (REED/) REED J C.  
 Query Match 4.8%; Score 47; DB 12; Length 1120;  
 Best Local Similarity 48.7%; Pred. No. 57;  
 RESULT 1285  
 ID ABD15922 standard; DNA; 1260 BP.  
 DE Pseudomonas aeruginosa polynucleotide #14526.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.8%; Score 47; DB 11; Length 1260;  
 Best Local Similarity 46.1%; Pred. No. 56;  
 RESULT 1286  
 ID ABD16234 standard; DNA; 1260 BP.  
 DE Pseudomonas aeruginosa polynucleotide #14838.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.8%; Score 47; DB 11; Length 1260;  
 Best Local Similarity 46.1%; Pred. No. 56;  
 RESULT 1287  
 ID ABZ66692 standard; DNA; 1293 BP.  
 DE Orthostomycin biosynthetic polynucleotide SEQ ID NO 46.  
 PN WO200279505-A2.  
 PD 10-OCT-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 4.8%; Score 47; DB 10; Length 1293;  
 Best Local Similarity 44.1%; Pred. No. 56;  
 RESULT 1288  
 ID AAO22481 standard; DNA; 1320 BP.  
 DE groEL-1 gene partial sequence.  
 PN WO9204452-A.  
 PD 19-MAR-1992.  
 PA (INSP-) INST PASTEUR.  
 Query Match 4.8%; Score 47; DB 8; Length 1707;  
 Best Local Similarity 48.0%; Pred. No. 56;  
 RESULT 1296  
 ID AAA64515 standard; cDNA; 1722 BP.  
 DE Nucleotide sequence of truncated FEZ1 transcript G3612.  
 PN WO200050565-A2.  
 PD 31-AUG-2000.  
 PA (UVJE-) UNIV JEFFERSON THOMAS.  
 Query Match 4.8%; Score 47; DB 3; Length 1722;  
 Best Local Similarity 45.9%; Pred. No. 56;  
 RESULT 1297  
 ID ADA71120 standard; DNA; 1790 BP.  
 DE Rice gene, SEQ ID 4443.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN-) SYNGENTA PARTICIPATIONS AG.  
 Query Match 4.8%; Score 47; DB 8; Length 1790;  
 Best Local Similarity 50.2%; Pred. No. 56;  
 RESULT 1298  
 ID ACA23626 standard; DNA; 1968 BP.  
 DE Prokaryotic essential gene #5283.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.

PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 4.8%; Score 47; DB 6; Length 1354;  
 Best Local Similarity 44.6%; Pred. No. 56;  
 RESULT 1290  
 ID AAV20099 standard; DNA; 1416 BP.  
 DE Pseudomonas LipR kinase coding sequence.  
 PN WO9806836-A2.  
 PD 19-FEB-1998.  
 PA (GENV-) GENENCOR INT INC.  
 Query Match 4.8%; Score 47; DB 2; Length 1416;  
 Best Local Similarity 45.7%; Pred. No. 56;  
 RESULT 1291  
 ID AAA13891 standard; DNA; 1416 BP.  
 DE Pseudomonas alcaligenes LipR nucleotide sequence SEQ ID NO:3.  
 PN US6048710-A.  
 PD 11-APR-2000.  
 PA (GENV-) GENENCOR INT INC.  
 Query Match 4.8%; Score 47; DB 3; Length 1416;  
 Best Local Similarity 45.7%; Pred. No. 56;  
 RESULT 1292  
 ID AAD22868 standard; DNA; 1416 BP.  
 DE Pseudomonas alcaligenes LipR DNA.  
 PN US6313283-B1.  
 PD 06-NOV-2001.  
 PA (GENV-) GENENCOR INT INC.  
 Query Match 4.8%; Score 47; DB 6; Length 1416;  
 Best Local Similarity 45.7%; Pred. No. 56;  
 RESULT 1293  
 ID ACA27226 standard; DNA; 1536 BP.  
 DE Prokaryotic essential gene #8883.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.8%; Score 47; DB 8; Length 1536;  
 Best Local Similarity 51.1%; Pred. No. 56;  
 RESULT 1294  
 ID AAQ22482 standard; DNA; 1620 BP.  
 DE groEL-1 gene coding region.  
 PN WO9204452-A.  
 PD 19-MAR-1992.  
 PA (INSP-) INST PASTEUR.  
 Query Match 4.8%; Score 47; DB 2; Length 1620;  
 Best Local Similarity 44.2%; Pred. No. 56;  
 RESULT 1295  
 ID ABX56033 standard; DNA; 1707 BP.  
 DE M. echinospira calicheamicin biosynthesis gene call.  
 PN WO200279465-A2.  
 PD 10-OCT-2002.  
 PA (SLOK-) SLOAN KETTERING INST CANCER RES.  
 Query Match 4.8%; Score 47; DB 8; Length 1707;  
 Best Local Similarity 48.0%; Pred. No. 56;  
 RESULT 1296  
 ID AAA64515 standard; cDNA; 1722 BP.  
 DE Nucleotide sequence of truncated FEZ1 transcript G3612.  
 PN WO200050565-A2.  
 PD 31-AUG-2000.  
 PA (UVJE-) UNIV JEFFERSON THOMAS.  
 Query Match 4.8%; Score 47; DB 3; Length 1722;  
 Best Local Similarity 45.9%; Pred. No. 56;  
 RESULT 1297  
 ID ADA71120 standard; DNA; 1790 BP.  
 DE Rice gene, SEQ ID 4443.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN-) SYNGENTA PARTICIPATIONS AG.  
 Query Match 4.8%; Score 47; DB 8; Length 1790;  
 Best Local Similarity 50.2%; Pred. No. 56;  
 RESULT 1298  
 ID ACA23626 standard; DNA; 1968 BP.  
 DE Prokaryotic essential gene #5283.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.

Query Match 4.8%; Score 47; DB 8; Length 1968;  
 Best Local Similarity 45.2%; Pred. No. 56;  
 RESULT 1299  
 ID AAN92408 standard; DNA; 2061 BP.  
 DE Sequence encoding pseudorabies virus (PRV) glycoprotein gH.  
 PN WC8910965-A.  
 PD 16-NOV-1989.  
 PA (UPJO) UPOJOH CO.  
 Query Match 4.8%; Score 47; DB 1; Length 2061;  
 Best Local Similarity 44.7%; Pred. No. 56;  
 RESULT 1300  
 ID AAO22484 standard; DNA; 2167 BP.  
 DE gro es el operon with promoter sequence.  
 PN WO9204452-A.  
 PD 19-MAR-1992.  
 PA (INSP) INST PASTEUR.  
 Query Match 4.8%; Score 47; DB 2; Length 2167;  
 Best Local Similarity 44.2%; Pred. No. 56;  
 RESULT 1301  
 ID ADD22490 standard; DNA; 2335 BP.  
 DE HLA-B46 T cell recognised tumour antigenic polypeptide, SEQ NO 140.  
 PN JP2003111595-A.  
 PD 15-APR-2003.  
 PA (ITOY/) ITO Y.  
 Query Match 4.8%; Score 47; DB 10; Length 2335;  
 Best Local Similarity 46.9%; Pred. No. 55;  
 RESULT 1302  
 ID ADI15967 standard; cDNA; 2335 BP.  
 DE Human PP 100 cDNA.  
 PN WO2003008450-A1.  
 PD 30-JAN-2003.  
 PA (ITOY/) ITOH K.  
 Query Match 4.8%; Score 47; DB 10; Length 2335;  
 Best Local Similarity 46.9%; Pred. No. 55;  
 RESULT 1303  
 ID ADS34440 standard; DNA; 2335 BP.  
 DE FOSH protein associated DNA #194.  
 PN WO2004078130-A2.  
 PD 16-SEP-2004.  
 PA (PROT-) PROTEOLOGICS INC.  
 Query Match 4.8%; Score 47; DB 13; Length 2335;  
 Best Local Similarity 46.9%; Pred. No. 55;  
 RESULT 1304  
 ID AAO22485 standard; DNA; 2668 BP.  
 DE GROEL-1 gene.  
 PN WO9204452-A.  
 PD 19-MAR-1992.  
 PA (INSP) INST PASTEUR.  
 Query Match 4.8%; Score 47; DB 2; Length 2668;  
 Best Local Similarity 44.2%; Pred. No. 55;  
 RESULT 1305  
 ID AAV23493 standard; DNA; 4377 BP.  
 DE Pseudomonas LipQ, LipR, OrfV operon.  
 PN WO9806836-A2.  
 PD 19-FEB-1998.  
 PA (GEMV) GENENCOR INT INC.  
 Query Match 4.8%; Score 47; DB 2; Length 4377;  
 Best Local Similarity 45.7%; Pred. No. 55;  
 RESULT 1306  
 ID AAA13904 standard; DNA; 4377 BP.  
 DE Pseudomonas alcaligenes nucleotide sequence SEQ ID NO:28.  
 PN US6048710-A.  
 PD 11-APR-2000.  
 PA (GEMV) GENENCOR INT INC.  
 Query Match 4.8%; Score 47; DB 3; Length 4377;  
 Best Local Similarity 45.7%; Pred. No. 55;  
 RESULT 1307  
 ID AAF30869 standard; DNA; 4377 BP.  
 DE Pseudomonas alcaligenes LipQ, LipR and OrfZ gene region.  
 PN US6225106-B1.  
 PD 01-MAY-2001.  
 PA (GEMV) GENENCOR INT INC.  
 Query Match 4.8%; Score 47; DB 4; Length 4377;  
 Best Local Similarity 45.7%; Pred. No. 55;  
 RESULT 1308  
 ID RAD22881 standard; DNA; 4377 BP.  
 DE P. alcaligenes DNA comprising cosmids #71, #201, #505 and #726.  
 PN US6313283-B1.  
 PD 06-NOV-2001.  
 PA (GEMV) GENENCOR INT INC.  
 Query Match 4.8%; Score 47; DB 6; Length 4377;  
 Best Local Similarity 45.7%; Pred. No. 55;  
 RESULT 1309  
 ID AAF88336 standard; DNA; 6459 BP.  
 DE S. spinosa DNA fragment encoding ORF19, SEQ ID 43.  
 PN DE19957268-A1.  
 PD 08-MAR-2001.  
 PA (FARB) BAYER AG.  
 Query Match 4.8%; Score 47; DB 4; Length 6459;  
 Best Local Similarity 46.9%; Pred. No. 54;  
 RESULT 1310  
 ID ARK52418 standard; DNA; 6868 BP.  
 DE DNA encoding propionibacterium associated proteins.  
 PN JP2002112790-A.  
 PD 16-APR-2002.  
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
 Query Match 4.8%; Score 47; DB 6; Length 6868;  
 Best Local Similarity 51.7%; Pred. No. 54;  
 RESULT 1311  
 ID AAF88313 standard; DNA; 50000 BP.  
 DE S. spinosa DNA fragment SEQ ID 2.  
 PN DE19957268-A1.  
 PD 08-MAR-2001.  
 PA (FARB) BAYER AG.  
 Query Match 4.8%; Score 47; DB 4; Length 50000;  
 Best Local Similarity 46.9%; Pred. No. 51;  
 RESULT 1312  
 ID AAF88316 standard; DNA; 50000 BP.  
 DE S. spinosa DNA fragment SEQ ID 5.  
 PN DE19957268-A1.  
 PD 08-MAR-2001.  
 PA (FARB) BAYER AG.  
 Query Match 4.8%; Score 47; DB 4; Length 50000;  
 Best Local Similarity 46.9%; Pred. No. 51;  
 RESULT 1313  
 ID AAZ21501 standard; DNA; 80161 BP.  
 DE DNA fragment of Saccharopolyspora spinosa containing biosynthetic genes.  
 Query Match 4.8%; Score 47; DB 2; Length 80161;  
 Best Local Similarity 46.9%; Pred. No. 50;  
 RESULT 1314  
 ID ADI39159 standard; DNA; 85692 BP.  
 DE Streptomyces hygroscopicus geldanamycin gene cluster, SEQ ID NO:1.  
 PN WO2003106653-A2.  
 PD 24-DEC-2003.  
 PA (KOSA-) KOSAN BIOSCIENCES INC.  
 PA (REID/) REID R C.  
 Query Match 4.8%; Score 47; DB 12; Length 85692;  
 Best Local Similarity 43.9%; Pred. No. 50;  
 RESULT 1315  
 Query Match 4.8%; Score 47; DB 4; Length 110000;  
 Best Local Similarity 45.1%; Pred. No. 50;  
 RESULT 1316  
 Query Match 4.8%; Score 47; DB 4; Length 110000;  
 Best Local Similarity 45.1%; Pred. No. 50;  
 RESULT 1317  
 ID AAA68102 standard; DNA; 296 BP.  
 DE E. grandis caffeoyl CoA methyl transferase DNA sequence SEQ ID NO:195.  
 PN WO200022099-A1.  
 PD 20-APR-2000.  
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 Query Match 4.7%; Score 46.8; DB 3; Length 296;  
 Best Local Similarity 54.7%; Pred. No. 63;  
 RESULT 1318  
 ID ADD41852 standard; DNA; 296 BP.  
 DE Caffeoyl CoA methyl transferase DNA #3.

PN US2003131373-A1.  
PD 10-JUL-2003.  
PA (BLOK/) BLOKSBERG L N.  
PA (HAVU/) HAVUKKALA I.  
Query Match 4.7%; Score 46.8; DB 10; Length 296;  
Best Local Similarity 54.7%; Pred. No. 63;  
RESULT 1319  
ID ADS14636 standard; DNA; 663 BP.  
DE Pseudomonas aeruginosa quorum sensing controlled gene PA3181, SEQ ID 191.  
PN WO2004083385-A2.  
PD 30-SEP-2004.  
PA (IOWA) UNIV IOWA RES FOUND.  
Query Match 4.7%; Score 46.8; DB 13; Length 663;  
Best Local Similarity 50.4%; Pred. No. 62;  
RESULT 1320  
ID AB213007 standard; DNA; 768 BP.  
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 812.  
PN WO200216655-A2.  
PD 28-FEB-2002.  
PA (SCRI) SCRIPPS RES INST.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 4.7%; Score 46.8; DB 6; Length 768;  
Best Local Similarity 46.0%; Pred. No. 62;  
RESULT 1321  
ID ABD06367 standard; DNA; 792 BP.  
DE Pseudomonas aeruginosa polynucleotide #4971.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.7%; Score 46.8; DB 11; Length 792;  
Best Local Similarity 50.4%; Pred. No. 62;  
RESULT 1322  
ID AAV73801 standard; DNA; 801 BP.  
DE KSHV LUR terminal repeat unit DNA.  
PN US5849564-A.  
PD 15-DEC-1998.  
PA (UYCO) UNIV COLUMBIA NEW YORK.  
Query Match 4.7%; Score 46.8; DB 2; Length 801;  
Best Local Similarity 45.3%; Pred. No. 62;  
RESULT 1323  
ID AAA30291 standard; DNA; 801 BP.  
DE Rhadino virus cis-acting element, RVCAE.  
PN WO200029626-A1.  
PD 25-MAY-2000.  
PA (KIEF/) KIEFF E D.  
PA (BALL/) BALLESTAS M E.  
PA (KAYE/) KAYE K M.  
Query Match 4.7%; Score 46.8; DB 3; Length 801;  
Best Local Similarity 45.3%; Pred. No. 62;  
RESULT 1324  
ID ABA93488 standard; DNA; 801 BP.  
DE Kaposi's sarcoma-associated herpesvirus terminal repeat unit.  
PN US6322792-B1.  
PD 27-NOV-2001.  
PA (KIEF/) KIEFF E D.  
Query Match 4.7%; Score 46.8; DB 6; Length 801;  
Best Local Similarity 45.3%; Pred. No. 62;  
RESULT 1325  
ID ADJ65097 standard; DNA; 801 BP.  
DE HHV8 terminal repeat region, TR.  
PN US2004037847-A1.  
PD 26-FEB-2004.  
PA (KIEF/) KIEFF E D.  
PA (BALL/) BALLESTAS M E.  
PA (KAYE/) KAYE K M.  
Query Match 4.7%; Score 46.8; DB 12; Length 801;  
Best Local Similarity 45.3%; Pred. No. 62;  
RESULT 1326  
ID ADD17814 standard; DNA; 872 BP.  
DE DNA (SeqID 1882) that confers an altered visual phenotype in plants.  
PN WO2003020741-A1.  
PD 13-NAR-2003.  
PA (DOWC) DOW CHEM CO.

PA (DOWC) DOW AGROSCIENCES LLC.  
Query Match 4.7%; Score 46.8; DB 10; Length 872;  
Best Local Similarity 48.8%; Pred. No. 62;  
RESULT 1327  
ID ACA37750 standard; DNA; 984 BP.  
DE Prokaryotic essential gene #19407.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.7%; Score 46.8; DB 8; Length 984;  
Best Local Similarity 50.4%; Pred. No. 61;  
RESULT 1328  
ID ABD06351 standard; DNA; 1071 BP.  
DE Pseudomonas aeruginosa polynucleotide #4955.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.7%; Score 46.8; DB 11; Length 1071;  
Best Local Similarity 50.4%; Pred. No. 61;  
RESULT 1329  
ID ABD06390 standard; DNA; 1131 BP.  
DE Pseudomonas aeruginosa polynucleotide #4994.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.7%; Score 46.8; DB 11; Length 1131;  
Best Local Similarity 50.4%; Pred. No. 61;  
RESULT 1330  
ID ABD06380 standard; DNA; 1215 BP.  
DE Pseudomonas aeruginosa polynucleotide #4984.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.7%; Score 46.8; DB 11; Length 1215;  
Best Local Similarity 50.4%; Pred. No. 61;  
RESULT 1331  
ID ADA45210 standard; cDNA; 1358 BP.  
DE Recombinant Max & JLP N-terminal region protein, M2LZII coding sequence.  
PN WO2003066652-A2.  
PD 14-AUG-2003.  
PA (UTEM) UNIV TEMPLE.  
Query Match 4.7%; Score 46.8; DB 9; Length 1358;  
Best Local Similarity 54.1%; Pred. No. 61;  
RESULT 1332  
ID ADA45206 standard; cDNA; 1358 BP.  
DE Recombinant Max and JLP N-terminal region protein, M2, coding sequence.  
PN WO2003066652-A2.  
PD 14-AUG-2003.  
PA (UTEM) UNIV TEMPLE.  
Query Match 4.7%; Score 46.8; DB 9; Length 1358;  
Best Local Similarity 54.1%; Pred. No. 61;  
RESULT 1333  
ID ADA45208 standard; cDNA; 1358 BP.  
DE Recombinant Max and JLP N-terminal region protein, M2LZI coding sequence.  
PN WO2003066652-A2.  
PD 14-AUG-2003.  
PA (UTEM) UNIV TEMPLE.  
Query Match 4.7%; Score 46.8; DB 9; Length 1358;  
Best Local Similarity 54.1%; Pred. No. 61;  
RESULT 1334  
ID ACA40293 standard; DNA; 1464 BP.  
DE Prokaryotic essential gene #21950.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.7%; Score 46.8; DB 8; Length 1464;  
Best Local Similarity 42.2%; Pred. No. 61;  
RESULT 1335  
ID ADR01290 standard; DNA; 1722 BP.  
DE Farnesyl dibenzodiazepinone biosynthetic ORF39 protein ABCA DNA.  
PN WO2004065591-A1.  
PD 05-AUG-2004.  
PA (ECOP-) ECOPIA BIOSCIENCES INC.

Query Match 4.7%; Score 46.8; DB 13; Length 1722;  
 Best Local Similarity 46.3%; Pred. No. 60;  
 RESULT 1336  
 ID ADS55765 standard; cDNA; 2013 BP.  
 DE Bacterial polynucleotide #7752.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match 4.7%; Score 46.8; DB 13; Length 2013;  
 Best Local Similarity 49.2%; Pred. No. 60;  
 RESULT 1337  
 ID ADT48680 standard; cDNA; 2226 BP.  
 DE Bacterial polynucleotide #23431.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Query Match 4.7%; Score 46.8; DB 13; Length 2226;  
 Best Local Similarity 44.3%; Pred. No. 60;  
 RESULT 1338  
 ID ACA37666 standard; DNA; 2739 BP.  
 DE Prokaryotic essential gene #19323.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.7%; Score 46.8; DB 8; Length 2739;  
 Best Local Similarity 45.1%; Pred. No. 60;  
 RESULT 1339  
 ID ABD08987 standard; DNA; 3171 BP.  
 DE Pseudomonas aeruginosa polynucleotide #7591.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.7%; Score 46.8; DB 11; Length 3171;  
 Best Local Similarity 43.4%; Pred. No. 59;  
 RESULT 1340  
 ID ABD09358 standard; DNA; 3210 BP.  
 DE Pseudomonas aeruginosa polynucleotide #7962.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.7%; Score 46.8; DB 11; Length 3210;  
 Best Local Similarity 43.4%; Pred. No. 59;  
 RESULT 1341  
 ID AAH47802 standard; DNA; 3535 BP.  
 DE Chimeric CBP-fused FR301379 acylase DNA.  
 PN WO200131038-A1.  
 PD 03-MAY-2001.  
 PA (FUJI) FUJISAWA PHARM CO LTD.  
 Query Match 4.7%; Score 46.8; DB 4; Length 3535;  
 Best Local Similarity 49.3%; Pred. No. 59;  
 RESULT 1342  
 ID AAI57831 standard; cDNA; 4176 BP.  
 DE Human polynucleotide SEQ ID NO 34.  
 PN WO200153312-A1.  
 PD 26-JUL-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 4.7%; Score 46.8; DB 4; Length 4176;  
 Best Local Similarity 49.4%; Pred. No. 59;  
 RESULT 1343  
 ID AAO95540 standard; DNA; 4356 BP.  
 DE Cardiac adenylyl cyclase gene.  
 PN TW243453-A.  
 PD 21-MAR-1995.  
 PA (AMCY) AMERICAN CYANAMID CO.  
 Query Match 4.7%; Score 46.8; DB 2; Length 4356;

Best Local Similarity 45.9%; Pred. No. 59;  
 RESULT 1344  
 ID ADA45191 standard; cDNA; 4667 BP.  
 DE Murine JLP coding sequence.  
 PN WO2003066652-A2.  
 PD 14-AUG-2003.  
 PA (UTEM) UNIV TEMPLE.  
 Query Match 4.7%; Score 46.8; DB 9; Length 4667;  
 Best Local Similarity 54.1%; Pred. No. 59;  
 RESULT 1345  
 ID ADC10001 standard; DNA; 5220 BP.  
 DE Human NOVX polypeptide coding sequence SEQ ID NO: 21.  
 PN WO2003000842-A2.  
 PD 03-JAN-2003.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 4.7%; Score 46.8; DB 10; Length 5220;  
 Best Local Similarity 42.6%; Pred. No. 59;  
 RESULT 1346  
 ID AAF32248 standard; DNA; 5692 BP.  
 DE Streptomyces sp. cyclic lipopeptide acylase encoding DNA SEQ ID NO:1.  
 PN WO200102585-A1.  
 PD 11-JAN-2001.  
 PA (FUJI) FUJISAWA PHARM CO LTD.  
 Query Match 4.7%; Score 46.8; DB 4; Length 5692;  
 Best Local Similarity 49.3%; Pred. No. 58;  
 RESULT 1347  
 ID AAD54224 standard; DNA; 5862 BP.  
 DE Streptomyces platensis subspecies rosaceus dorrigocin ORF7 DNA.  
 PN WO200288176-A2.  
 PD 07-NOV-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 4.7%; Score 46.8; DB 10; Length 5862;  
 Best Local Similarity 46.8%; Pred. No. 58;  
 RESULT 1348  
 ID ACA37617 standard; DNA; 10232 BP.  
 DE Prokaryotic essential gene #19274.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.7%; Score 46.8; DB 8; Length 10232;  
 Best Local Similarity 44.0%; Pred. No. 58;  
 RESULT 1349  
 ID AAA58472 standard; DNA; 18660 BP.  
 DE Nucleotide sequence of the bleomycin (BLM) gene cluster ORFs 31-40.  
 PN WO200040704-A1.  
 PD 13-JUL-2000.  
 PA (REGC) UNIV CALIFORNIA.  
 Query Match 4.7%; Score 46.8; DB 3; Length 18660;  
 Best Local Similarity 47.5%; Pred. No. 57;  
 RESULT 1350  
 ID ABL68348 standard; DNA; 25000 BP.  
 DE Kidney cancer related gene sequence SEQ ID NO:6685.  
 PN WO200194629-A2.  
 PD 13-DEC-2001.  
 PA (AVAL-) AVALON PHARM.  
 Query Match 4.7%; Score 46.8; DB 6; Length 25000;  
 Best Local Similarity 47.3%; Pred. No. 56;  
 RESULT 1351  
 ID AAA11992 standard; DNA; 37856 BP.  
 DE S. cellulosum DNA encoding polyketide and hereropolyketide enzymes.  
 PN DE19846493-A1.  
 PD 13-APR-2000.  
 PA (GBPB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.  
 Query Match 4.7%; Score 46.8; DB 3; Length 37856;  
 Best Local Similarity 48.2%; Pred. No. 55;  
 RESULT 1352  
 ID ADQ74672 standard; DNA; 74787 BP.  
 DE Streptomyces parvulus borrelidin polyketide synthase gene cluster.  
 Query Match 4.7%; Score 46.8; DB 12; Length 74787;  
 Best Local Similarity 44.3%; Pred. No. 54;  
 RESULT 1353  
 Query Match 4.7%; Score 46.8; DB 4; Length 110000;  
 Best Local Similarity 42.2%; Pred. No. 54;

RESULT 1354  
ID ABD15774 standard; DNA; 270 BP.  
DE Pseudomonas aeruginosa polynucleotide #14378.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.7%; Score 46.6; DB 11; Length 270;  
Best Local Similarity 50.2%; Pred. No. 69;  
RESULT 1355  
ID ABD01848 standard; DNA; 489 BP.  
DE Pseudomonas aeruginosa polynucleotide #452.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.7%; Score 46.6; DB 11; Length 489;  
Best Local Similarity 47.9%; Pred. No. 68;  
RESULT 1356  
ID ACA38033 standard; DNA; 723 BP.  
DE Prokaryotic essential gene #19690.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.7%; Score 46.6; DB 8; Length 723;  
Best Local Similarity 45.3%; Pred. No. 67;  
RESULT 1357  
ID ADT44804 standard; cDNA; 762 BP.  
DE Bacterial polynucleotide #19555.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 4.7%; Score 46.6; DB 13; Length 762;  
Best Local Similarity 47.9%; Pred. No. 67;  
RESULT 1358  
ID ABD13964 standard; DNA; 777 BP.  
DE Pseudomonas aeruginosa polynucleotide #12568.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.7%; Score 46.6; DB 11; Length 777;  
Best Local Similarity 53.6%; Pred. No. 67;  
RESULT 1359  
ID ABD14635 standard; DNA; 786 BP.  
DE Pseudomonas aeruginosa polynucleotide #13239.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.7%; Score 46.6; DB 11; Length 786;  
Best Local Similarity 53.6%; Pred. No. 67;  
RESULT 1360  
ID ACC59353 standard; DNA; 948 BP.  
DE R ruber esterase estA coding sequence #1.  
PN WO2003031625-A1.  
PD 17-APR-2003.  
PA (DEGS/) DEGUSSA AG.  
PA (SCHW/) SCHWAB H.  
Query Match 4.7%; Score 46.6; DB 10; Length 948;  
Best Local Similarity 46.0%; Pred. No. 66;  
RESULT 1361  
ID ACC59354 standard; DNA; 948 BP.  
DE R ruber esterase estA coding sequence #2.  
PN WO2003031625-A1.  
PD 17-APR-2003.  
PA (DEGS/) DEGUSSA AG.  
PA (SCHW/) SCHWAB H.  
Query Match 4.7%; Score 46.6; DB 10; Length 948;  
Best Local Similarity 46.0%; Pred. No. 66;  
RESULT 1362  
ID ABD01827 standard; DNA; 981 BP.  
DE Pseudomonas aeruginosa polynucleotide #431.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.7%; Score 46.6; DB 11; Length 981;  
Best Local Similarity 47.9%; Pred. No. 66;  
RESULT 1363  
ID ABD11883 standard; DNA; 981 BP.  
DE Pseudomonas aeruginosa polynucleotide #10487.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.7%; Score 46.6; DB 11; Length 981;  
Best Local Similarity 47.7%; Pred. No. 66;  
RESULT 1364  
ID ADR13680 standard; DNA; 1032 BP.  
DE Amidase coding sequence, SEQ ID 17.  
PN WO2004069848-A2.  
PD 19-AUG-2004.  
PA (DIVE-) DIVERSA CORP.  
Query Match 4.7%; Score 46.6; DB 13; Length 1032;  
Best Local Similarity 44.3%; Pred. No. 66;  
RESULT 1365  
ID ABD08147 standard; DNA; 1062 BP.  
DE Pseudomonas aeruginosa polynucleotide #6751.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.7%; Score 46.6; DB 11; Length 1062;  
Best Local Similarity 47.2%; Pred. No. 66;  
RESULT 1366  
ID ACA38086 standard; DNA; 1224 BP.  
DE Prokaryotic essential gene #19743.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 4.7%; Score 46.6; DB 8; Length 1224;  
Best Local Similarity 52.3%; Pred. No. 66;  
RESULT 1367  
ID AAD33021 standard; DNA; 1299 BP.  
DE Streptomyces species ema5 gene.  
PN WO200292801-A2.  
PD 21-NOV-2002.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 4.7%; Score 46.6; DB 10; Length 1299;  
Best Local Similarity 48.0%; Pred. No. 66;  
RESULT 1368  
ID ABD04946 standard; DNA; 1380 BP.  
DE Pseudomonas aeruginosa polynucleotide #3550.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 4.7%; Score 46.6; DB 11; Length 1380;  
Best Local Similarity 45.1%; Pred. No. 66;  
RESULT 1369  
ID ABZ71149 standard; DNA; 1473 BP.  
DE S. murayamaensis ATCC 21414 kinamycin encoding DNA SEQ ID NO:36.  
PN WO2003002066-A2.  
PD 09-JAN-2003.  
PA (DIVE-) DIVERSA CORP.  
Query Match 4.7%; Score 46.6; DB 8; Length 1473;  
Best Local Similarity 46.4%; Pred. No. 66;  
RESULT 1370  
ID ACC59357 standard; DNA; 1494 BP.  
DE R ruber vector pMSS12 coding sequence insert #4.  
PN WO2003031625-A1.  
PD 17-APR-2003.  
PA (DEGS) DEGUSSA AG.  
PA (SCHW/) SCHWAB H.  
Query Match 4.7%; Score 46.6; DB 10; Length 1494;  
Best Local Similarity 46.0%; Pred. No. 65;  
RESULT 1371  
ID ACC59352 standard; DNA; 1494 BP.  
DE R ruber vector pMSS12 coding sequence insert #2.



PN WO2003031625-A1.  
 PD 17-APR-2003.  
 PA (DEGS ) DEGUSSA AG.  
 PA (SCHW/) SCHWAB H.  
 Query Match 4.7%; Score 46.6; DB 10; Length 1494;  
 Best Local Similarity 46.0%; Pred. No. 65;  
 RESULT 1372  
 ID ABD08270 standard; DNA; 1530 BP.  
 DE Pseudomonas aeruginosa polynucleotide #6874.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.7%; Score 46.6; DB 11; Length 1530;  
 Best Local Similarity 47.2%; Pred. No. 65;  
 RESULT 1373  
 ID AAL61148 standard; DNA; 1710 BP.  
 DE Human mutant ARX gene #1.  
 PN WO2003045989-A1.  
 PD 05-JUN-2003.  
 PA (WOMB-) WOMEN'S & CHILDREN'S HOSPITAL.  
 Query Match 4.7%; Score 46.6; DB 9; Length 1710;  
 Best Local Similarity 46.3%; Pred. No. 65;  
 RESULT 1374  
 ID ABD04953 standard; DNA; 1947 BP.  
 DE Pseudomonas aeruginosa polynucleotide #3557.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.7%; Score 46.6; DB 11; Length 1947;  
 Best Local Similarity 45.1%; Pred. No. 65;  
 RESULT 1375  
 ID ABD14312 standard; DNA; 2325 BP.  
 DE Pseudomonas aeruginosa polynucleotide #12916.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.7%; Score 46.6; DB 11; Length 2325;  
 Best Local Similarity 53.6%; Pred. No. 65;  
 RESULT 1376  
 ID ADB87421 standard; DNA; 2500 BP.  
 DE Transgene expression regulatory element, STAR66F.  
 PN WO2003004704-A2.  
 PD 16-JAN-2003.  
 PA (CHRO-) CHROMAGENICS BV.  
 Query Match 4.7%; Score 46.6; DB 10; Length 2500;  
 Best Local Similarity 46.1%; Pred. No. 65;  
 RESULT 1377  
 ID ADJ35230 standard; DNA; 2500 BP.  
 DE Human stabilising anti-repression, STAR, element #66.  
 PN WO2003106674-A2.  
 PD 24-DEC-2003.  
 PA (CHRO-) CHROMAGENICS BV.  
 Query Match 4.7%; Score 46.6; DB 12; Length 2500;  
 Best Local Similarity 46.1%; Pred. No. 65;  
 RESULT 1378  
 ID ADL96848 standard; DNA; 2500 BP.  
 DE Stabilizing Anti-Repressor DNA sequence, T2F STAR 66F.  
 PN WO2003106684-A2.  
 PD 24-DEC-2003.  
 PA (CHRO-) CHROMAGENICS BV.  
 Query Match 4.7%; Score 46.6; DB 12; Length 2500;  
 Best Local Similarity 46.1%; Pred. No. 65;  
 RESULT 1379  
 ID ACC44572 standard; cDNA; 3285 BP.  
 DE Alpha-amylase/glucosylase fusion nucleotide sequence SEQ ID NO:46.  
 PN WO2003018766-A2.  
 PD 06-MAR-2003.  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 Query Match 4.7%; Score 46.6; DB 8; Length 3285;  
 Best Local Similarity 48.7%; Pred. No. 64;  
 RESULT 1380  
 ID ABL15824 standard; cDNA; 3790 BP.  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO:41954.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Query Match 4.7%; Score 46.6; DB 4; Length 3790;  
 Best Local Similarity 47.2%; Pred. No. 64;  
 RESULT 1381  
 ID ACA26449 standard; DNA; 3963 BP.  
 DE Prokaryotic essential gene #8106.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.7%; Score 46.6; DB 8; Length 3963;  
 Best Local Similarity 43.1%; Pred. No. 64;  
 RESULT 1382  
 ID AAL61172 standard; DNA; 4770 BP.  
 DE Actinosynnema pretiosum polyketide synthase (PKS) gene #3.  
 PN WO2003045312-A2.  
 PD 05-JUN-2003.  
 PA (UNIW ) UNIV WASHINGTON.  
 Query Match 4.7%; Score 46.6; DB 8; Length 4770;  
 Best Local Similarity 44.8%; Pred. No. 63;  
 RESULT 1383  
 ID ADC10001 standard; DNA; 5220 BP.  
 DE Human NOVX polypeptide coding sequence SEQ ID NO: 21.  
 PN WO2003000842-A2.  
 PD 03-JAN-2003.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 4.7%; Score 46.6; DB 10; Length 5220;  
 Best Local Similarity 44.2%; Pred. No. 63;  
 RESULT 1384  
 ID ABS78655 standard; DNA; 5811 BP.  
 DE S. macromyceticus DNA encoding PKSE protein macromomycin.  
 PN CA2387401-A1.  
 PD 04-SEP-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 4.7%; Score 46.6; DB 6; Length 5811;  
 Best Local Similarity 47.6%; Pred. No. 63;  
 RESULT 1385  
 ID ABD01877 standard; DNA; 7419 BP.  
 DE Pseudomonas aeruginosa polynucleotide #481.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.7%; Score 46.6; DB 11; Length 7419;  
 Best Local Similarity 47.9%; Pred. No. 63;  
 RESULT 1386  
 ID ABD01792 standard; DNA; 7449 BP.  
 DE Pseudomonas aeruginosa polynucleotide #396.  
 PN US6551795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.7%; Score 46.6; DB 11; Length 7449;  
 Best Local Similarity 47.9%; Pred. No. 63;  
 RESULT 1387  
 ID ABL66291 standard; DNA; 14800 BP.  
 DE Lung cancer related gene sequence SEQ ID NO:4628.  
 PN WO200194629-A2.  
 PD 13-DEC-2001.  
 PA (AVAL-) AVALON PHARM.  
 Query Match 4.7%; Score 46.6; DB 6; Length 14800;  
 Best Local Similarity 44.8%; Pred. No. 61;  
 RESULT 1388  
 ID ADP13447 standard; DNA; 14800 BP.  
 DE Renal cell carcinoma differentially expressed gene #183.  
 PN WO2004048933-A2.  
 PD 10-JUN-2004.  
 PA (AMHP ) WYETH.  
 PA (TWIN/) TWINE N C.  
 PA (BURC/) BURCZYNSKI M E.  
 PA (TREE/) TREPICCHIO W L.  
 PA (DORN/) DORNER A.  
 PA (STOV/) STOVER J A.  
 PA (SLON/) SLONI D K.

Query Match 4.7%; Score 46.6; DB 12; Length 14800;  
 Best Local Similarity 44.8%; Pred. No. 61;  
 RESULT 1389  
 ID AAS94858 standard; DNA; 14835 BP.  
 DE Human DNA sequence #113 expressed during foam cell differentiation.  
 PN WO200177389-A2.  
 PD 18-OCT-2001.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Query Match 4.7%; Score 46.6; DB 6; Length 14835;  
 Best Local Similarity 44.8%; Pred. No. 61;  
 RESULT 1390  
 ID AAD54223 standard; DNA; 24081 BP.  
 DE Streptomyces platensis subspecies rosaceus dorrigocin ORF6 DNA.  
 PN WO200288176-A2.  
 PD 07-NOV-2002.  
 PA (ECOP-) ECOPIA BIOSCIENCES INC.  
 Query Match 4.7%; Score 46.6; DB 10; Length 24081;  
 Best Local Similarity 46.7%; Pred. No. 61;  
 RESULT 1391  
 ID ADQ07566 standard; DNA; 25467 BP.  
 DE Streptomyces kanamyceticus kanamycin biosynthesis genes SEQ ID NO:1.  
 PN JP2004173537-A.  
 PD 24-JUN-2004.  
 PA (MEIJ) MEIJI SEIKA KAISHA LTD.  
 Query Match 4.7%; Score 46.6; DB 12; Length 25467;  
 Best Local Similarity 46.9%; Pred. No. 61;  
 RESULT 1392  
 ID ABZ71131 standard; DNA; 36321 BP.  
 DE Streptomyces murayamaensis ATCC 21414 kinamycin related DNA SEQ ID NO:1.  
 PN WO2003002066-A2.  
 PD 09-JAN-2003.  
 PA (DIVE-) DIVERSA CORP.  
 Query Match 4.7%; Score 46.6; DB 8; Length 36321;  
 Best Local Similarity 46.4%; Pred. No. 60;  
 RESULT 1393  
 ID ACF30939 standard; DNA; 53905 BP.  
 DE Rice cultivar Asominori fertility restorer gene Rf-1, SEQ ID NO:28.  
 PN WO2003027290-A1.  
 PD 03-APR-2003.  
 PA (NISE) JAPAN TOBACCO INC.  
 PA (SYGN) SYNGENTA LTD.  
 Query Match 4.7%; Score 46.6; DB 8; Length 53905;  
 Best Local Similarity 46.2%; Pred. No. 59;  
 RESULT 1394  
 ID ADI09998 standard; DNA; 53905 BP.  
 DE Rice cultivar Asominori fertility restorer gene Rf-1, SEQ ID NO:28.  
 PN WO2004005515-A1.  
 PD 15-JAN-2004.  
 PA (NISE) JAPAN TOBACCO INC.  
 PA (SYGN) SYNGENTA LTD.  
 Query Match 4.7%; Score 46.6; DB 12; Length 53905;  
 Best Local Similarity 46.2%; Pred. No. 59;  
 RESULT 1395  
 ID ABQ81849 standard; DNA; 349980 BP.  
 DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1105.  
 PN EP1227152-A1.  
 PD 31-JUL-2002.  
 PA (NEST) SOC PROD NESTLE SA.  
 Query Match 4.7%; Score 46.6; DB 6; Length 349980;  
 Best Local Similarity 48.7%; Pred. No. 56;  
 RESULT 1397  
 ID AAU51695 standard; cDNA; 314 BP.  
 DE Kukulcania hibernalis spider silk protein coding sequence #3.  
 PN WO200299082-A2.  
 PD 12-DEC-2002.  
 PA (UYWY-) UNIV WYOMING.  
 Query Match 4.7%; Score 46.4; DB 8; Length 314;  
 Best Local Similarity 51.4%; Pred. No. 74;  
 RESULT 1398  
 ID ACH87193 standard; DNA; 461 BP.

DE Human genome derived single exon probe #20388.  
 PN US2003194704-A1.  
 PD 16-OCT-2003.  
 PA (PENN/) PENN S G.  
 PA (RANK/) RANK D R.  
 PA (HANZ/) HANZEL D K.  
 Query Match 4.7%; Score 46.4; DB 12; Length 461;  
 Best Local Similarity 50.7%; Pred. No. 73;  
 RESULT 1399  
 ID ACH73807 standard; DNA; 529 BP.  
 DE Human genome derived single exon probe #7002.  
 PN US2003194704-A1.  
 PD 16-OCT-2003.  
 PA (PENN/) PENN S G.  
 PA (RANK/) RANK D R.  
 PA (HANZ/) HANZEL D K.  
 Query Match 4.7%; Score 46.4; DB 12; Length 529;  
 Best Local Similarity 49.6%; Pred. No. 73;  
 RESULT 1400  
 ID AAH06810 standard; cDNA; 872 BP.  
 DE Human cDNA clone (5'-primer) SEQ ID NO:3645.  
 PN EP1074617-A2.  
 PD 07-FEB-2001.  
 PA (HELI-) HELIX RES INST.  
 Query Match 4.7%; Score 46.4; DB 4; Length 872;  
 Best Local Similarity 50.0%; Pred. No. 72;  
 RESULT 1401  
 ID ABD15695 standard; DNA; 981 BP.  
 DE Pseudomonas aeruginosa polynucleotide #14299.  
 PN US651795-B1.  
 PD 22-APR-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Query Match 4.7%; Score 46.4; DB 11; Length 981;  
 Best Local Similarity 44.2%; Pred. No. 72;  
 RESULT 1402  
 ID ACA37963 standard; DNA; 1065 BP.  
 DE Prokaryotic essential gene #19620.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Query Match 4.7%; Score 46.4; DB 8; Length 1065;  
 Best Local Similarity 47.3%; Pred. No. 71;  
 RESULT 1403  
 ID AAH46980 standard; cDNA; 1072 BP.  
 DE Human glutathione peroxidase (GPx6) encoding cDNA.  
 PN US6231853-B1.  
 PD 15-MAY-2001.  
 PA (INCY-) INCYTE PHARM INC.  
 Query Match 4.7%; Score 46.4; DB 4; Length 1072;  
 Best Local Similarity 50.0%; Pred. No. 71;  
 RESULT 1404  
 ID ABU59157 standard; cDNA; 1072 BP.  
 DE Nucleotide sequence of human glutathione peroxidase-6 (GPx6).  
 PN US2002031506-A1.  
 PD 14-MAR-2002.  
 PA (INCY-) INCYTE PHARM INC.  
 Query Match 4.7%; Score 46.4; DB 6; Length 1072;  
 Best Local Similarity 50.0%; Pred. No. 71;  
 RESULT 1405  
 ID AA158027 standard; cDNA; 1100 BP.  
 DE Human polynucleotide SEQ ID NO 230.  
 PN WO200153312-A1.  
 PD 26-JUL-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 4.7%; Score 46.4; DB 4; Length 1100;  
 Best Local Similarity 50.0%; Pred. No. 71;  
 RESULT 1406  
 ID AA159813 standard; cDNA; 1205 BP.  
 DE Human polynucleotide SEQ ID NO 3802.  
 PN WO200153312-A1.  
 PD 26-JUL-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 4.7%; Score 46.4; DB 4; Length 1205;

Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1407  
ID AD142681 standard; DNA; 1219 BP.  
DE Plant transcription factor polynucleotide #735.  
PN US2004019927-A1.  
PD 29-JAN-2004.  
PA (SHER/) SHERMAN B K.  
PA (RIEC/) RIECHMANN J L.  
PA (JIAN/) JIANG C.  
PA (HEAR/) HEARD J E.  
PA (HAAK/) HAAKE V.  
PA (CREE/) CREELMAN R A.  
PA (RATC/) RATCLIFFE O.  
PA (ADAM/) ADAM L J.  
PA (REUB/) REUBER T L.  
PA (KEDD/) KEDDIE J.  
PA (BROU/) BROUN P E.  
PA (PILG/) PILGRIM M L.  
PA (DUBE/) DUBELL A N.  
PA (PINE/) PINEDA O.  
PA (YUGG/) YU G.  
Query Match 4.7%; Score 46.4; DB 12; Length 1219;  
Best Local Similarity 44.2%; Pred. No. 71;  
RESULT 1408  
ID ADO02930 standard; cDNA; 1219 BP.  
DE Corn orthologue of Thalecress transcription factor, cDNA #98.  
PN US2004045049-A1.  
PD 04-MAR-2004.  
PA (ZHAN/) ZHANG J.  
PA (FROM/) FROMM M E.  
PA (HEAR/) HEARD J E.  
PA (RIEC/) RIECHMANN J L.  
PA (ADAM/) ADAM L J.  
PA (BROU/) BROUN P E.  
PA (PINE/) PINEDA O.  
PA (REUB/) REUBER T L.  
PA (KEDD/) KEDDIE J S.  
PA (YUGG/) YU G.  
PA (JIAN/) JIANG C.  
PA (SAMA/) SAMAHA R S.  
PA (PILG/) PILGRIM M L.  
PA (CREE/) CREELMAN R A.  
PA (DUBE/) DUBELL A N.  
PA (RATC/) RATCLIFFE O.  
PA (KUMI/) KUMIMOTO R.  
PA (SHER/) SHERMAN B K.  
Query Match 4.7%; Score 46.4; DB 12; Length 1219;  
Best Local Similarity 44.2%; Pred. No. 71;  
RESULT 1409  
ID AAZ65013 standard; cDNA; 1227 BP.  
DE Membrane-bound protein PRO828 encoding cDNA.  
PN WO9963088-A2.  
PD 09-DEC-1999.  
PA (GETH/) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 12; Length 1219;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1410  
ID AAS46137 standard; cDNA; 1227 BP.  
DE Human DNA encoding PRO polypeptide sequence #213.  
PN WO200168848-A2.  
PD 20-SEP-2001.  
PA (GETH/) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 4; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1411  
ID AAF44159 standard; cDNA; 1227 BP.  
DE Human PRO828 (UNQ469) nucleotide sequence SEQ ID NO:188.  
PN WO200073454-A1.  
PD 07-DEC-2000.  
PA (GETH/) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 5; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1412  
ID ABL86133 standard; cDNA; 1227 BP.  
DE Human PRO828 cDNA sequence SEQ ID NO:123.  
PN WO200200690-A2.  
PD 03-JAN-2002.  
PA (GETH/) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 6; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1413  
ID ABK28599 standard; cDNA; 1227 BP.  
DE Human DNA57037-1444 encoding PRO828.  
PN WO200109327-A2.  
PD 08-FEB-2001.  
PA (GETH/) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 6; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1414  
ID ABL95622 standard; cDNA; 1227 BP.  
DE Human angiogenesis related cDNA PRO828 SEQ ID NO: 123.  
PN WO200208284-A2.  
PD 31-JAN-2002.  
PA (GETH/) GENENTECH INC.  
PA (BAKE/) BAKER K P.  
PA (FERR/) FERRARA N.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODG/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (MARS/) MARSTERS S A.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (STEP/) STEPHAN J F.  
PA (WATA/) WATANABE C K.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 4.7%; Score 46.4; DB 6; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1415  
ID ACA89587 standard; cDNA; 1227 BP.  
DE cDNA encoding human PRO polypeptide #213.  
PN US2003036141-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1416  
ID ACA73597 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003036146-A1.  
PD 20-FEB-2003.  
PA (GETH/) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1417  
ID ACA05912 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GETH/) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1418  
ID ACA66746 standard; cDNA; 1227 BP.  
DE cDNA encoding human PRO protein #213.  
PN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH/) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1419  
ID ACA64292 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003003531-A1.

PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC. 4.7%; Score 46.4; DB 8; Length 1227;  
Query Match 50.0%; Pred. No. 71;  
Best Local Similarity 50.0%; Pred. No. 71;  
ID AC88795 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1431  
ID AC970237 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1432  
ID AC12459 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1433  
ID AC74374 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1434  
ID AC16002 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003027324-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1435  
ID AC25570 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003036118-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC. 4.7%; Score 46.4; DB 8; Length 1227;  
Query Match 50.0%; Pred. No. 71;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1436  
ID AC18047 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003036123-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1437  
ID ACC88334 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003036148-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1438  
ID AC21688 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003040060-A1.  
PD 27-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1439  
ID AC18755 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003044916-A1.  
PD 06-MAR-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
PD 27-FEB-2003.

PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC. 4.7%; Score 46.4; DB 8; Length 1227;  
Query Match 50.0%; Pred. No. 71;  
Best Local Similarity 50.0%; Pred. No. 71;  
ID ACF20321 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003040063-A1.  
PD 27-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1421  
ID ACF19707 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1422  
ID ACD1995 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003027267-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1423  
ID ACF13160 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003036160-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1424  
ID ACD25263 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1425  
ID ACF00312 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC. 4.7%; Score 46.4; DB 8; Length 1227;  
Query Match 50.0%; Pred. No. 71;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1426  
ID AC972369 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1427  
ID ACD04893 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1428  
ID ACD18354 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003036124-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1429  
ID ACD08361 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003040054-A1.  
PD 27-FEB-2003.

RESULT 1440  
ID ABX98365 standard; cDNA; 1227 BP.  
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 425.  
PN US2003036156-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1441  
ID ACD14116 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003032117-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1442  
ID ACD09896 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003036128-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1443  
ID ACC8641 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003027286-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1444  
ID ACD21381 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1445  
ID ABX75753 standard; cDNA; 1227 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO828.  
PN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1446  
ID ABX97956 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003032102-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1447  
ID ACA97432 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1448  
ID ACA57895 standard; cDNA; 1227 BP.  
DE Human PRO828 cDNA.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1449  
ID ACD14423 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1450  
ID ACC91206 standard; cDNA; 1227 BP.

DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1451  
ID ACC88948 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1452  
ID ACD07145 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1453  
ID ACA67596 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1454  
ID ACC81651 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1455  
ID ACC89255 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1456  
ID ACC86611 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1457  
ID ACC9869 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1458  
ID ACC93048 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1459  
ID ABX80751 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein cDNA, #73.  
PN US2003027162-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1460  
ID ACA72676 standard; cDNA; 1227 BP.

DE Human PRO polynucleotide #213.  
PN US2003022255-A1.  
PD 30-JAN-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1461  
ID ACA9194 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003022237-A1.  
PD 30-JAN-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1462  
ID ACA6930 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1463  
ID ACA97073 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1464  
ID ACA91069 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1465  
ID ACA70851 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1466  
ID ACA95361 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1467  
ID ACDA4260 standard; cDNA; 1227 BP.  
DE cDNA encoding human PRO828 polypeptide.  
PN US2002127576-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1468  
ID ACC86304 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1469  
ID ACC90176 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1470  
ID ACD12784 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1471  
ID ACF20014 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1472  
ID ABX76958 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1473  
ID ACA73290 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1474  
ID ACA68833 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003036136-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1475  
ID ACA74677 standard; cDNA; 1227 BP.  
DE cDNA encoding human PRO polypeptide #213.  
PN US2003036138-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1476  
ID ACA70544 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003032109-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1477  
ID ACD14730 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003040066-A1.  
PD 27-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1478  
ID ACA68402 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003032104-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1479  
ID ABX98867 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003036157-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1480  
ID ACC81344 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003032120-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;

Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1481  
ID ACA95668 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003036155-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1482  
ID ACDO4586 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003022296-A1.  
PD 30-JAN-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1483  
ID ACC8027 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003027281-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1484  
ID ACF12689 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003040058-A1.  
PD 27-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1485  
ID ABX79431 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein cDNA, #73.  
PN US2002142961-A1.  
PD 03-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1486  
ID ACA96404 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003017540-A1.  
PD 23-JAN-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1487  
ID ACA65178 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003032106-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1488  
ID ACA73904 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003032129-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1489  
ID ACA74316 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003032131-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1490  
ID ACA96711 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003032103-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;

RESULT 1491  
ID ACD10817 standard; cDNA; 1227 BP.  
DE cDNA encoding human PRO polypeptide #213.  
PN US2003032107-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1492  
ID ACC91513 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003032139-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1493  
ID ACA93452 standard; cDNA; 1227 BP.  
DE Novel human secreted and transmembrane protein PRO828 cDNA.  
PN US2003022187-A1.  
PD 30-JAN-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1494  
ID ACD02848 standard; cDNA; 1227 BP.  
DE cDNA encoding human PRO polypeptide #213.  
PN US2003022301-A1.  
PD 30-JAN-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1495  
ID ACC87413 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003036165-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1496  
ID ACC85997 standard; cDNA; 1227 BP.  
DE Human secreted polypeptide PRO828-encoding cDNA, SEQ ID NO:425.  
PN US2003027262-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1497  
ID ABX81134 standard; DNA; 1227 BP.  
DE Human secreted or transmembrane protein related PCR primer #48.  
PN US2003027985-A1.  
PD 06-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1498  
ID ACA65485 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003032110-A1.  
PD 13-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1499  
ID ACA94302 standard; cDNA; 1227 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #213.  
PN US2003036142-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;  
RESULT 1500  
ID ACA98046 standard; cDNA; 1227 BP.  
DE Human PRO polynucleotide #213.  
PN US2003036145-A1.  
PD 20-FEB-2003.  
Query Match 4.7%; Score 46.4; DB 8; Length 1227;  
Best Local Similarity 50.0%; Pred. No. 71;

**THIS PAGE BLANK (USPTO)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 19, 2005, 16:05:28 ; Search time 7487 Seconds  
(without alignments)  
6400.722 Million cell updates/sec

Title: US-10-017-407A-305

Perfect score: 989  
Sequence: 1 gggggccgcggtccgaga.....Caataaaaaaaaaaaaaa 989

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 1500 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_hgt.\*

3: gb\_in.\*

4: gb\_cm.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sta.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	989	100.0	989	6	AX201342
2	989	100.0	989	6	AX697237 Sequence
3	989	100.0	989	9	AY358476 Homo sapi
4	985.8	99.7	1037	6	AX338454 Sequence
5	985.8	99.7	1041	9	BC047774 Homo sapi
6	981.8	99.3	985	6	BD222712 Human sig
7	938.2	94.9	988	9	AK074421 Homo sapi
8	907.8	91.8	913	9	BC023663 Homo sapi
9	789	79.8	789	6	CQ721501 Sequence
10	789	79.8	789	6	AX338456 Sequence
11	625	63.2	946	10	BC049670 Mus muscu
12	312	31.5	326	6	AX407985 Sequence
13	309.2	31.3	237829	2	AC120475 Rattus no
14	256.8	26.0	38679	9	AL390034 Human DNA
15	256.8	26.0	169612	2	AC027393 Homo sapi
16	224.6	22.7	157428	10	AL606832 Mouse DNA
17	224.6	22.7	209643	10	AC080018 Mus muscu
18	200	20.2	14100	1	MXU24657 Myxococcu
19	194.8	19.7	11171	6	CQ801141 Sequence

20	193.8	19.6	675	6	CQ801150 Sequence
21	188.8	19.1	10840	1	AE004550 Pseudomon
22	185.8	18.8	2381	1	STMWDMBC
23	185.8	18.8	2381	6	E06690 DNA encodin
24	185.4	18.7	304282	1	AE016910 Chromobac
25	185	18.7	663	12	AV657514 Synthetic
26	182.4	18.4	69644	1	AY179507 Streptomy
27	161.8	16.4	953	6	AR236716 Sequence
28	161.8	16.4	953	8	BT009394 Triticum
29	159.6	16.1	976	8	AB110168 Oryza sat
30	159.6	16.1	996	8	AK104326 Oryza sat
31	159.6	16.1	1096	8	AK104801 Oryza sat
32	159.6	16.1	1098	8	AK071482 Oryza sat
33	159.2	16.0	1049	6	AR236715 Sequence
34	158.6	16.0	997	6	AR236700 Sequence
35	158.6	16.0	1338	6	AX654529 Sequence
36	157.2	15.9	1078	6	AR236714 Sequence
37	157.2	15.9	1078	8	BT009389 Triticum
38	155.6	15.7	1018	6	AR236711 Sequence
39	154	15.6	891	6	AR236694 Sequence
40	154	15.6	1167	8	ZMA2422981
41	153	15.5	77534	1	AF235504 Streptomy
42	153	15.5	77536	6	BD235937 Polyketid
43	153	15.5	77536	6	AR271638 Sequence
44	153	15.5	77536	6	AR564393 Sequence
45	152.8	15.4	1112	6	AX660732 Sequence
46	152.4	15.4	1218	6	AX146637 Sequence
47	151.4	15.3	82746	1	AF453501 Actinosyn
48	150.2	15.2	1158	8	AY644637 Oryza sat
49	150.2	15.2	1895	8	AK106735 Oryza sat
50	150.2	15.2	137354	8	AP000364 Oryza sat
51	148	15.0	798	6	AX660925 Sequence
52	148	15.0	1118	6	AR236712 Sequence
53	148	15.0	1118	8	BT009186 Triticum
54	148	15.0	1136	8	ZMA242980 Zea mays
55	148	15.0	1146	6	AR236695 Sequence
56	147.6	14.9	1252	6	CQ857676 Sequence
57	146.8	14.8	10882	1	AE002493 Neisseria
58	146.8	14.8	349980	6	AX044032 Sequence
59	146.2	14.8	875	8	AB158406 Triticum
60	146.2	14.8	1018	8	BT009093 Triticum
61	145	14.7	959	8	AK108479 Oryza sat
62	144.6	14.6	329861	1	NMA522491
63	144.4	14.6	1057	6	AR236696 Sequence
64	143.6	14.5	1052	8	AK065744 Oryza sat
65	141.8	14.3	783	6	AX654528 Sequence
66	141.8	14.3	1149	8	AK061757 Oryza sat
67	140.6	14.2	1058	6	AR236699 Sequence
68	140	14.2	783	6	AX654276 Sequence
69	137	13.9	1116	8	AY644638 Oryza sat
70	129.6	13.1	1466	8	AK065515 Oryza sat
71	128.2	13.0	237221	1	AP003599 Nostoc sp
72	127.4	12.9	651	6	AX196012 Sequence
73	127.4	12.9	109519	6	AX195929 Sequence
74	126	12.7	923	6	AR236697 Sequence
75	125.4	12.7	835	6	AX660084 Sequence
76	123.2	12.5	300465	1	AE016962 Coxella
77	122.8	12.4	1810	6	E09625 Streptomyce
78	122.8	12.4	3267	1	STMACYA
79	118.6	12.0	2001	11	BV202015 sgm20798
80	118.6	12.0	89888	2	AY294423.3
81	118.6	12.0	161371	10	AC132590 Mus muscu
82	116.8	11.8	188267	2	AC137230 Rattus no
83	116.8	11.8	228354	2	AC137429 Rattus no
84	116.8	11.8	266834	2	AC123487 Rattus no
85	110	11.1	1013	8	AF168780 Rucalyptu
86	110	11.1	1944	1	AF145250 Rhodother
87	109.8	11.1	1006	8	AF046122 Eucalyptu
88	109.8	11.1	1068	8	EG122228 E.gunnii nr
89	109.6	11.1	110000	2	AC105718.3
90	107.8	10.9	486	8	AY651026 Boehmeria
91	107.4	10.9	304282	1	AE016910 Chromobac
92	106.2	10.7	976	8	VVCCOAMT

c	93	103.6	10.5	343	6	AX400599	Sequence	166	84	8.5	1026	8	AY057554	AY057554 Arabidops
	94	102	10.3	134199	1	SYCSLRF	D64004	167	84	8.5	110000	1	CRG28336_25	Continuation (26 o
c	95	101.4	10.3	300425	1	AP005044	Streptomy	168	83.6	8.5	1033	8	AY088577	Arabidops
	96	99.4	10.1	300800	1	SC0393112	AL939112	169	83.2	8.4	110000	1	AP006618_26	Continuation (27 o
	97	98.4	9.9	772	6	FVAJ1447	BD001447	170	82.8	8.4	1258	6	ARI22016	Sequence 1
	98	96.8	9.8	1012	6	BD224370	BD224370	171	82.8	8.4	1258	6	I92681	M69184 Petroselinu
	99	96.8	9.8	1012	6	AR216420	AD216420	172	82.8	8.4	1258	8	PUMCCOAMT	AF429315 Homo sapi
	100	96.8	9.8	1012	6	AR432822	AR432822	173	82.6	8.4	125020	9	AR429315	AF429315 Homo sapi
	101	96.8	9.8	1026	6	AR066484	AR066484	174	82.2	8.3	1272	8	AY644636	Oryza sat
	102	96.8	9.8	1026	6	AR074097	AR074097	175	82.2	8.3	105815	8	AP002536	AP002536 Oryza sat
	103	96.8	9.8	1026	6	AR143609	AR143609	176	82.2	8.3	156054	8	AB023482	AB023482 Oryza sat
	104	96.8	9.8	1026	6	BD224282	BD224282	177	81	8.2	622	8	AB076979	AB076979 Avena sat
	105	96.8	9.8	1026	6	AR216332	AR216332	178	79.6	8.0	1258	6	A22706	A22706 Caffeyol-Co
	106	96.8	9.8	1026	6	AR432734	AR432734	179	79.2	8.0	980	6	AR236704	AR236704 Sequence
	107	96.8	9.8	1026	6	BD005645	BD005645	180	78	7.9	1098	8	AY128822	AY128822 Arabidops
	108	96.8	9.8	1172	8	AY279007	AY279007	181	78	7.9	1185	8	AY087981	AY087981 Arabidops
	109	96.4	9.7	1136	8	AY279011	AY279011	182	78	7.9	1201	8	AY093172	AY093172 Arabidops
	110	96.4	9.7	1145	8	AY279031	AY279031	183	77.4	7.8	837	8	AY094008	AY094008 Arabidops
	111	96.4	9.7	1150	8	AY279012	AY279012	184	77.4	7.8	1107	8	AY070483	AY070483 Arabidops
	112	96.4	9.7	1150	8	AY279013	AY279013	185	76.6	7.7	110000	1	AP006618_48	Continuation (49 o
	113	96.4	9.7	1150	8	AY279030	AY279030	186	76.2	7.7	760	6	AR074116	Continuation (49 o
	114	96.4	9.7	1150	8	AY279033	AY279033	187	76.2	7.7	760	6	BD224301	BD224301 Materials
	115	96.4	9.7	1150	8	AY279035	AY279035	188	76.2	7.7	760	6	BD272991	BD272991 Materials
	116	95.2	9.6	1172	8	AY279006	AY279006	189	76.2	7.7	760	6	AR216351	AR216351 Sequence
	117	95.2	9.6	1172	8	AY279025	AY279025	190	76.2	7.7	760	6	AR432753	AR432753 Sequence
	118	95.2	9.6	1172	8	AY279027	AY279027	191	76.2	7.7	760	6	BD005664	BD005664 Materials
	119	95.2	9.6	1180	6	AY798857	AY798857	192	75.8	7.7	1046	8	PTU27116	U27116 Populus tre
	120	95.2	9.6	1182	8	AY279009	AY279009	193	74.8	7.6	816	8	AF022775	AF022775 Nicotiana
	121	95.2	9.6	1438	8	AY279021	AY279021	194	74.4	7.5	929	6	AR236703	AR236703 Sequence
	122	95.2	9.6	1442	8	AY279019	AY279019	195	74.4	7.5	1104	8	AF053553	AF053553 Mesembrya
	123	95.2	9.6	1445	8	AY279017	AY279017	196	74.2	7.5	726	8	AF240466	AF240466 Populus t
	124	95.2	9.6	1445	8	AY279018	AY279018	197	73.8	7.5	920	4	AX340812	AX340812 Canis fam
	125	95.2	9.6	1445	8	AY279022	AY279022	198	73.8	7.5	1834	8	AK105550	AK105550 Oryza sat
	126	95.2	9.6	1451	8	AY279004	AY279004	199	73.8	7.5	2768	8	AK109619	AK109619 Oryza sat
	127	95.2	9.6	1451	8	AY279020	AY279020	200	73.8	7.5	170021	8	AP003256	AP003256 Oryza sat
	128	95.2	9.6	1463	8	AY279016	AY279016	201	73.8	7.5	176261	8	AP003274	AP003274 Oryza sat
	129	95.2	9.6	1464	8	AY279015	AY279015	202	73.4	7.4	145828	8	AP005392	AP005392 Oryza sat
	130	94.8	9.6	110000	1	BX571966_17	Continuation (18 o	203	73.4	7.4	154188	8	AP005633	AP005633 Oryza sat
	131	94.8	9.6	110000	1	CP000011_09	Continuation (10 o	204	73.2	7.4	870	6	AP025246	AP025246 Sequence
	132	94.8	9.6	110000	1	CP000011_10	Continuation (11 o	205	72.8	7.4	706	8	PBA130841	PBA130841 Populus b
	133	94.6	9.6	1152	8	AY279023	AY279023	206	72.6	7.3	1213	9	BC011935	BC011935 Homo sapi
	134	94.6	9.6	1152	8	AY279032	AY279032	207	71.8	7.3	280558	1	AE017301	AE017301 Thermsu t
	135	93.6	9.5	110000	1	CRG28337_25	Continuation (26 o	208	71.6	7.2	744	8	AF327458	AF327458 Populus a
	136	93.4	9.4	675	6	AR3930021	AR3930021	209	71.2	7.2	601	11	BV167609	BV167609 sqm6022
	137	93	9.4	1136	8	AY279034	AY279034	210	71.2	7.2	2084	11	BV177509	BV177509 sqm95100
	138	93	9.4	1153	8	AY279010	AY279010	211	71.2	7.2	2084	11	BV179316	BV179316 sqm10484
	139	93	9.4	1181	6	AY798855	AY798855	212	71	7.2	816	9	CR456997	CR456997 Homo sapi
	140	93	9.4	1181	8	AY279005	AY279005	213	71	7.2	1025	8	PBTJ4894	AY224894 Populus b
	141	93	9.4	1181	8	AY279024	AY279024	214	71	7.2	1107	6	CQ812330	CQ812330 Sequence
	142	93	9.4	1181	8	AY279026	AY279026	215	71	7.2	1107	9	HUMCOMTA	M65212 Homo sapien
	143	93	9.4	1206	8	AY279008	AY279008	216	71	7.2	1291	6	CQ716680	CQ716680 Sequence
	144	93	9.4	1209	8	AY279028	AY279028	217	70.6	7.1	918	8	ZEU13151	U13151 Zimnia eleg
	145	93	9.4	1232	8	AF036095	AF036095	218	70.6	7.1	2084	11	BV177077	BV177077 sqm92606
	146	93	9.4	1232	8	AF036095	AF036095	219	70.4	7.1	189038	2	AC120323	AC120323 Rattus no
	147	93	9.4	1434	8	AY279014	AY279014	220	70	7.1	811	6	AR225247	AR225247 Sequence
	148	88	8.9	931	6	AR236702	AR236702	221	69.8	7.1	5222	1	DRU52145	DRU52145 Deinococcus
	149	87.8	8.9	534	6	AR236717	AR236717	222	69.6	7.0	591	8	AY607699	AY607699 Apium gra
	150	87.4	8.8	1210	8	AK063541	AK063541	223	69.6	7.0	6090	1	U30252	U30252 Synchococ
	151	87.2	8.8	2955	1	AF075724	AF075724	224	69.4	7.0	873	9	AX456422	AX456422 Homo sapi
	152	87.2	8.8	110000	1	AE017354_25	Continuation (26 o	225	69.4	7.0	1206	6	AY774876	AY774876 Sequence
	153	86.2	8.7	347660	1	AP002994	AP002994	226	69.4	7.0	1206	9	HUMCOMTC	HUMCOMTC Homo sapien
	154	85.6	8.7	962	6	AR236705	AR236705	227	69.2	7.0	297850	1	AP006577	AP006577 Gloeobact
	155	85.6	8.7	1023	6	AR236706	AR236706	228	68	6.9	976	11	PM12D6G	PM12D6G Penicilli
	156	85.4	8.6	607	8	AY098515	AY098515	229	67.8	6.9	1217	9	BC000419	BC000419 Homo sapi
	157	85.4	8.6	125020	9	AF429315	AF429315	230	67.8	6.9	1217	9	BC005867	BC005867 Mus muscu
	158	84.4	8.5	939	8	PBTJ4896	AY224896	231	67.8	6.9	239130	2	AC079420	AC079420 Populus k
	159	84.4	8.5	963	8	AY620245	AY620245	232	67.6	6.8	930	8	AB000408	AB000408 Populus k
	160	84.4	8.5	1049	8	PBTJ4895	AY224895	233	67.4	6.8	890	8	AY145521	AY145521 Mesembrya
	161	84	8.5	780	6	CQ804646	CQ804646	234	67.4	6.8	12454	1	AE002019	AE002019 Deinococ
	162	84	8.5	780	6	CQ805684	CQ805684	235	67.2	6.8	132151	8	AC144491	AC144491 Oryza sat
	163	84	8.5	780	6	AY143979	AY143979	236	67.2	6.8	160738	8	AC073556	AC073556 Oryza sat
	164	84	8.5	815	8	AY081457	AY081457	237	67	6.8	323	8	AF534905	AF534905 Coffea ca
	165	84	8.5	999	8	AY062630	AY062630	238	67	6.8	110000	2	LMFLCHR32_06	Continuation (7 of

c 239	67	6.8	110000	2	LMFLCHR36_31	Continuation (32 o	312	62.4	6.3	219952	2	AC084804	AC084804 Mus muscu
240	67	6.8	175837	2	AC022045	Homo sapi	313	62.4	6.3	341957	1	EX842572	EX842572 Mycobacte
241	67	6.8	215235	9	AP001972	Homo sapi	314	62.4	6.3	343050	1	EX248334	EX248334 Mycobacte
242	66.8	6.8	1023	8	AB0611268	Sequence	c 315	62.2	6.3	300029	1	AE0117178	AE0117178 Porphyrom
243	66.8	6.8	1074	6	AR074145	Sequence	c 316	62.2	6.3	301332	1	AE017237	AE017237 Mycobacte
244	66.8	6.8	1074	6	BD224330	Materials	c 317	62	6.3	175963	2	AC148913	AC148913 Sus scrofa
245	66.8	6.8	1074	6	AR216380	Sequence	c 318	62	6.3	295150	1	SC0939126	SC0939126 Streptomy
246	66.8	6.8	1074	6	AR432782	Sequence	c 319	61.8	6.2	186752	9	AC111200	AC111200 Homo sapi
247	66.8	6.8	1074	6	BD005693	Materials	c 320	61.6	6.2	281450	1	AP005032	AP005032 Streptomy
248	66.8	6.8	1075	6	AR074146	Sequence	c 321	61.6	6.2	845	6	AR225248	AR225248 Sequence
249	66.8	6.8	1075	6	BD224331	Materials	c 322	61.6	6.2	110000	1	AP006840_30	Continuation (31 o
250	66.8	6.8	1075	6	AR216381	Sequence	c 323	61.6	6.2	276289	1	AE017306	AE017306 Thermus t
251	66.8	6.8	1075	6	AR432783	Sequence	c 324	61.4	6.2	146111	10	AC132340	AC132340 Mus muscu
252	66.8	6.8	1075	6	BD005694	Materials	c 325	61.4	6.2	215342	4	AC149292	AC149292 Sus scrofa
253	66.8	6.8	339650	1	SC0939108	Streptomy	c 326	61.2	6.2	302325	1	AE017236	AE017236 Mycobacte
c 254	66.6	6.7	13533	1	AF257324	Streptomy	c 327	61	6.2	976	11	PM12D6G	PM12D6G Mycobacte
255	66.4	6.7	744	6	CQ760958	Sequence	c 328	61	6.2	110000	8	AP006618_49	Continuation (50 o
256	66.4	6.7	744	6	AX259371	Sequence	c 329	61	6.2	151085	8	AP003239	AP003239 Oryza sat
257	66.4	6.7	966	8	MSU20736	Medicago sa	c 330	61	6.2	292100	1	SC0939121	SC0939121 Streptomy
258	66.4	6.7	1906	6	CQ760964	Sequence	c 331	60.8	6.1	1578	6	A38265	A38265 Sequence 1
259	66.4	6.7	86000	2	AC136951	Leishmani	c 332	60.8	6.1	1578	6	AR001081	AR001081 Sequence
c 260	66.4	6.7	346301	1	EX640432	Bordetell	c 333	60.8	6.1	2357	14	AY363172	AY363172 Pseudorab
c 261	66.4	6.7	348642	1	EX640446	Bordetell	c 334	60.8	6.1	2510	14	SH1UL2XA	SH1UL2XA
c 262	66.2	6.7	312	6	AR236707	Sequence	c 335	60.8	6.1	9382	14	SH1ULGNS	SH1ULGNS
c 263	66	6.7	30425	1	AP005041	Streptomy	c 336	60.8	6.1	110000	8	AE016818_02	Continuation (3 of
c 264	66	6.7	300800	1	SC0939112	Streptomy	c 337	60.6	6.1	917	8	AY087244	AY087244 Arabidops
265	65.8	6.7	6375	1	AY632768	Myobacte	c 338	60.6	6.1	7413	1	PAAPRAG	PAAPRAG Arabidops
266	65.4	6.6	101	11	BV185588	sqmm14856	c 339	60.6	6.1	11588	1	AE004554	AE004554 Pseudom
267	65.4	6.6	110000	1	AP006840_15	Continuation (16 o	c 340	60.6	6.1	201050	1	AL646064	AL646064 Ralstonia
268	64.8	6.6	908	8	AY500159	Corchorus	c 341	60.6	6.1	298550	1	AP005029	AP005029 Streptomy
269	64.8	6.6	967	6	AR225249	Sequence	c 342	60.6	6.1	301068	1	AE017231	AE017231 Mycobacte
270	64.8	6.6	283100	1	SC0939110	Streptomy	c 343	60.4	6.1	1094	11	PM7G11B	PM7G11B
271	64.6	6.5	2832	8	AY452532	Chlamydom	c 344	60.4	6.1	10445	1	AB008466	AB008466 Streptomy
272	64.6	6.5	110000	2	LMFLCHR36_07	Continuation (8 of	c 345	60.4	6.1	25883	1	AE004716	AE004716 Bifidobac
273	64.6	6.5	311000	1	SC0939122	Streptomy	c 346	60.4	6.1	136753	2	AC149968	AC149968 Strongylo
274	64.4	6.5	143	6	AX899439	Sequence	c 347	60.4	6.1	349980	6	AX492784	AX492784 Sequence
275	64.4	6.5	143	6	BD035032	Sequence	c 348	60.4	6.1	349980	6	AX553951	AX553951 Sequence
276	64.2	6.5	600	6	AR236713	Sequence	c 349	60.2	6.1	1007	11	PM3H11G	PM3H11G
277	64.2	6.5	346362	1	EX640439	Bordetell	c 350	60.2	6.1	1062	6	BD180422	BD180422 Highly th
c 278	64.2	6.5	346362	1	EX640439	Bordetell	c 351	60.2	6.1	3797	14	PVULSGENE	PVULSGENE
c 279	64	6.5	31000	1	SC0939122	Streptomy	c 352	60.2	6.1	6653	1	AY162971	AY162971 Micromono
280	64	6.5	954	8	AK073585	Oryza sat	c 353	60.2	6.1	211161	2	AC098271	AC098271 Rattus no
c 281	64	6.5	1543	8	AK058441	Oryza sat	c 354	60	6.1	729	6	AX507705	AX507705 Sequence
c 282	64	6.5	85130	2	AC074054	Oryza sat	c 355	60	6.1	730	8	AY056313	AY056313 Arabidops
c 283	64	6.5	135876	8	AC113337	Genomic s	c 356	60	6.1	956	8	AF360317	AF360317 Arabidops
c 284	64	6.5	145510	8	AC074355	Oryza sat	c 357	60	6.1	982	6	AR236709	AR236709 Sequence
c 285	64	6.5	172407	2	AC148515	Sus scrofa	c 358	60	6.1	1065	11	PM2B12B	PM2B12B
c 286	64	6.5	299886	1	AE017240	Myobacte	c 359	60	6.1	1227	8	NT282982	NT282982 Penicilli
c 287	63.8	6.5	306096	8	AE017062	Oryza sat	c 360	60	6.1	123019	9	AC111006	AC111006 Homo sapi
288	63.6	6.4	510	6	AR236698	Deinococc	c 361	60	6.1	277000	1	SC0939109	SC0939109 Streptomy
289	63.6	6.4	1279	11	PM2H12G	Sequence	c 362	60	6.1	1242	6	BD180349	BD180349 Highly th
c 290	63.6	6.4	2039	9	AK1330031	Homo sapi	c 363	59.8	6.0	399	6	BD224470	BD224470 Materials
c 291	63.4	6.4	296300	1	AP005035	Streptomy	c 364	59.6	6.0	399	6	AR216520	AR216520 Sequence
292	63.2	6.4	1016	8	NTCCOAROMT	N. tabacum m	c 365	59.6	6.0	956	11	PM2D12B	PM2D12B
c 293	63.2	6.4	1065	11	PM2B12B	Penicilli	c 366	59.6	6.0	1980	14	AC2NK24	AC2NK24
c 294	63.2	6.4	110000	1	AP006618_31	Continuation (32 o	c 367	59.6	6.0	2253	5	GHKCP0SA	GHKCP0SA
c 295	63.2	6.4	110000	1	AP006618_32	Continuation (33 o	c 368	59.6	6.0	2253	5	GHKCP0SA	GHKCP0SA
c 296	63.2	6.4	136753	2	AC149968	Strongylo	c 369	59.6	6.0	7185	6	AX803764	AX803764 Sequence
c 297	63.2	6.4	176704	2	CR628364	Danio rer	c 370	59.6	6.0	48177	7	AY369485	AY369485 Burkholde
c 298	63.2	6.4	299425	1	AP005037	Streptomy	c 371	59.6	6.0	61944	6	AX803750	AX803750 Sequence
c 299	63.2	6.4	301068	1	AE017231	Myobacte	c 372	59.6	6.0	110000	1	AE016822_23	AE016822_23
c 300	63.2	6.4	349672	1	EX640419	Bordetell	c 373	59.6	6.0	110000	1	AE016822_24	Continuation (25 o
c 301	63	6.4	135005	9	HS860F19	Human DNA	c 374	59.6	6.0	110000	1	AP006618_55	Continuation (56 o
c 302	62.8	6.3	2595	10	RATREBA	M60647 Rat tropel	c 375	59.6	6.0	110000	1	SC0939110	SC0939110 Streptomy
c 303	62.8	6.3	75216	6	AX704275	Sequence	c 376	59.6	6.0	283100	1	SC0939125	SC0939125 Streptomy
c 304	62.8	6.3	110000	1	AE000516_13	Continuation (14 o	c 377	59.6	6.0	295150	1	SC0939125	SC0939125 Streptomy
c 305	62.8	6.3	299450	1	EX248338	Myobacte	c 378	59.6	6.0	308015	1	AE016783	AE016783 Pseudom
c 306	62.8	6.3	349306	1	EX842575	Myobacte	c 379	59.4	6.0	110000	1	AP006618_09	Continuation (10 o
c 307	62.6	6.3	1014	8	UT62734	Nicotiana t	c 380	59.4	6.0	110000	8	AP003992_10	Continuation (11 o
c 308	62.6	6.3	216050	1	AL646076	Ralstonia	c 381	59.4	6.0	116305	8	AP003992	AP003992 Oryza sat
c 309	62.6	6.3	348257	1	EX640425	Bordetell	c 382	59.4	6.0	141477	8	AP005456	AP005456 Oryza sat
c 310	62.4	6.3	110000	1	AE000516_02	Continuation (3 of	c 383	59.4	6.0	170051	2	AC148233	AC148233 Oryctolag
c 311	62.4	6.3	110000	1	AP006618_52	Continuation (53 o	c 384	59.4	6.0	189910	2	AC148233	AC148233 Oryctolag

385	59.4	6.0	196834	8	AP005458	Oryza sat	AP005458	458	57.4	5.8	1298	8	AY323261	Zea mays
386	59.4	6.0	197050	1	AL646081	Ralstonia	AL646081	459	57.4	5.8	1298	8	AY323263	Zea mays
c 387	59.4	6.0	296500	1	SC0939128	Streptomy	AL939128	460	57.4	5.8	1298	8	AY323265	Zea mays
388	59.2	6.0	1791	6	BD179866	Highly th	BD179866	461	57.4	5.8	1311	8	AY323267	Zea mays
389	59.2	6.0	196950	2	CR589874	Danio rer	CR589874	462	57.4	5.8	1311	8	AY323269	Zea mays
390	59.2	6.0	273285	1	AE017304	Thermus t	AE017304	463	57.4	5.8	1311	8	AY323270	Zea mays
391	59.2	6.0	298450	1	SC0939107	Streptomy	AL939107	464	57.4	5.8	1536	8	AY323271	Zea mays
392	59	6.0	2531	8	AY341851	Oryza sat	AY341851	465	57.4	5.8	1536	8	AY323272	Zea mays
393	59	6.0	3152	8	AY341843	Oryza sat	AY341843	466	57.4	5.8	1536	8	AY323273	Zea mays
394	59	6.0	10800	6	AX512249	Sequence	AX512249	467	57.4	5.8	1536	8	AY323274	Zea mays
395	59	6.0	10809	6	AX512245	Sequence	AX512245	468	57.4	5.8	1536	8	AY323275	Zea mays
396	59	6.0	110000	2	LMFLCHR36_03	Continuation (4 of	Continuation (4 of	469	57.4	5.8	1536	8	AY323276	Zea mays
c 397	59	6.0	139298	8	OSJN00012	Oryza sat	AL606441	470	57.4	5.8	1537	8	AY323277	Zea mays
398	59	6.0	277000	1	SC0939109	Streptomy	AL939109	471	57.4	5.8	1537	8	AY323278	Zea mays
399	58.8	5.9	1393	11	PM11H12G	Penicilli	AL684264	472	57.4	5.8	1549	8	AY323279	Zea mays
c 400	58.8	5.9	2320	8	AK069799	Oryza sat	AK069799	473	57.4	5.8	1597	1	AF306513	Pseudomon
c 401	58.8	5.9	2793	8	AK067140	Oryza sat	AK067140	474	57.4	5.8	23451	1	AB070952	Streptomy
402	58.8	5.9	3849	6	AX058889	Sequence	AX058889	475	57.4	5.8	66637	3	AC090053	Leishmani
403	58.8	5.9	5858	3	AF350276	Nephila m	AF350276	c 476	57.4	5.8	131563	9	HS212310	Hom sapi
404	58.8	5.9	12744	1	AF204401	Streptomy	AF204401	c 477	57.4	5.8	195859	14	AF281817	Tupaia he
405	58.8	5.9	187517	5	AY519500	Gallus ga	AY519500	c 478	57.4	5.8	223201	9	HS531110	Hom sapi
c 406	58.8	5.9	247910	1	AE017307	Thermus t	AE017307	c 479	57.4	5.8	276289	1	AE017306	Thermus t
c 407	58.8	5.9	299800	1	AP005040	Streptomy	AP005040	c 480	57.4	5.8	302300	1	AP005034	Streptomy
c 408	58.8	5.9	311000	1	SC0939122	Streptomy	AL939122	c 481	57.4	5.8	319550	1	SC0939113	Streptomy
c 409	58.6	5.9	48024	7	AY368235	Burkholde	AY368235	c 482	57.4	5.8	340000	9	HS21C102	Hom sapi
410	58.6	5.9	110000	1	AP006840_11	Continuation (12 o	Continuation (12 o	c 483	57.2	5.8	584	6	AX660579	Sequence
c 411	58.6	5.9	274676	1	AE017305	Thermus t	AE017305	c 484	57.2	5.8	987	6	BD180315	Highly th
c 412	58.6	5.9	289308	1	AE017242	Mycobacte	AE017242	485	57.2	5.8	1143	11	PM12A11G	Penicilli
c 413	58.6	5.9	293050	1	SC0939116	Streptomy	AL939116	486	57.2	5.8	1506	10	MUSHSP68A	Mouse heat
c 414	58.6	5.9	299925	1	AP005045	Streptomy	AP005045	487	57.2	5.8	73882	6	CQ870950	Sequence
415	58.6	5.9	300327	1	AE017228	Mycobacte	AE017228	488	57.2	5.8	89713	1	AJ605139	Actinopla
416	58.4	5.9	1288	6	AR007563	Sequence	AR007563	489	57.2	5.8	110000	1	AP006840_06	Continuation (7 of
c 417	58.4	5.9	3858	5	CHKCFOS	Chicken c-f	M18043	c 490	57.2	5.8	110000	1	AP006840_07	Continuation (8 of
c 418	58.4	5.9	7413	14	PVUL50S	Suid herpes	X87246	c 491	57.2	5.8	110000	2	LMFLCHR28_1	Continuation (2 of
419	58.4	5.9	127304	2	AC119051	Gallus ga	AL119051	c 492	57.2	5.8	272101	1	AE017302	Thermus t
c 420	58.4	5.9	309050	1	SC0939117	Streptomy	AL939117	493	57	5.8	10136	6	CQ879023	Sequence
c 421	58.2	5.9	1970	5	SGY17794	Gallus gall	Y17794	494	57	5.8	1113	6	CQ879023	Sequence
422	58.2	5.9	4237	8	D84400	Oryza sativ	D84400	495	57	5.8	11219	1	SERERYAA	Microomo
423	58.2	5.9	89376	1	AJ632270	Actinopla	AJ632270	496	57	5.8	11219	6	AR049367	Saccharopol
424	58.2	5.9	91839	2	AC098688	Bos tauru	AC098688	497	57	5.8	11219	6	AR095528	Sequence
c 425	58.2	5.9	197805	2	AC105307	Bos tauru	AC105307	498	57	5.8	36602	6	CQ878999	Sequence
c 426	58.2	5.9	295150	1	SC0939125	Streptomy	AL939125	c 499	57	5.8	38494	6	AR345349	Sequence
c 427	58.2	5.9	299925	1	AP005039	Streptomy	AP005039	c 500	57	5.8	38503	1	MSGB1912CS	Sequence
428	58	5.9	897	6	AX654732	Sequence	AX654732	c 501	57	5.8	38675	1	MLU15180	Mycobacteri
c 429	58	5.9	2329	1	SGHRDT	S. griseus h	X79979	c 502	57	5.8	38675	6	AR345367	Sequence
430	58	5.9	2396	1	AF425994	Streptomy	AF425994	c 503	57	5.8	281450	1	AP005032	Streptomy
431	58	5.9	10444	14	PVI422133	Suid herp	AJ422133	c 504	57	5.8	348450	1	MLEPRTNA	Mycobacte
c 432	58	5.9	88421	6	AX417445	Sequence	AX417445	505	56.8	5.7	990	6	BD179631	Nicotiana t
c 433	58	5.9	110000	1	AP006840_20	Continuation (21 o	Continuation (21 o	506	56.8	5.7	1003	6	NTU62735	Sequence
434	58	5.9	186752	9	AC111200_20	Hom sapi	AC111200	507	56.8	5.7	1182	6	AR151710	Sequence
c 435	58	5.9	290850	1	SC0939127	Streptomy	AL939127	508	56.8	5.7	1182	6	AR352531	Sequence
c 436	58	5.9	308050	1	SC0939124	Streptomy	AL939124	509	56.8	5.7	1306	6	AR352338	Sequence
437	57.8	5.8	9678	1	AB110645	Streptomy	AB110645	510	56.8	5.7	1306	8	AY323240	Zea mays
438	57.8	5.8	110000	1	AP006618_38	Continuation (39 o	Continuation (39 o	511	56.8	5.7	1306	8	AY323262	Zea mays
439	57.8	5.8	110000	1	AP006618_39	Continuation (40 o	Continuation (40 o	512	56.8	5.7	1306	8	AY323270	Zea mays
c 440	57.8	5.8	110000	1	AP006840_27	Continuation (28 o	Continuation (28 o	513	56.8	5.7	1308	8	AY323269	Zea mays
441	57.8	5.8	245210	2	AC137771	Hom sapi	AC137771	514	56.8	5.7	1309	8	AY323239	Zea mays
c 442	57.8	5.8	299550	1	AP005031	Streptomy	AP005031	515	56.8	5.7	1309	8	AY323256	Zea mays
c 443	57.8	5.8	347894	1	BX640431	Bordetell	BX640431	516	56.8	5.7	1309	8	AY323266	Zea mays
444	57.6	5.8	2358	8	AJ635325	Spermatoz	AJ635325	517	56.8	5.7	1311	8	AY323267	Zea mays
445	57.6	5.8	3297	6	BD180129	Highly th	BD180129	518	56.8	5.7	1314	8	AY323253	Zea mays
c 446	57.6	5.8	106873	14	AB096160	Cercopith	AB096160	519	56.8	5.7	1314	8	AY323268	Zea mays
c 447	57.6	5.8	110000	1	AP006618_19	Continuation (20 o	Continuation (20 o	520	56.8	5.7	1320	8	AY323271	Zea mays
c 448	57.6	5.8	156789	14	AF533768	Cercopith	AF533768	521	56.8	5.7	1544	8	AY323246	Zea mays
449	57.6	5.8	166036	2	AC145332	Felis cat	AC145332	522	56.8	5.7	1546	8	AY323244	Zea mays
c 450	57.6	5.8	299050	1	SC0939119	Streptomy	AL939119	523	56.8	5.7	2000	6	AX655393	Sequence
451	57.6	5.8	321250	1	SC0939111	Streptomy	AL939111	524	56.8	5.7	3900	1	AF262754	Amicolato
452	57.4	5.8	1029	6	BD174410	DNA resto	BD174410	c 525	56.8	5.7	5269	1	AB001610	Deinococc
453	57.4	5.8	1298	8	AY323254	Zea mays	AY323254	526	56.8	5.7	6584	1	SCPACAS	Streptomyes
454	57.4	5.8	1298	8	AY323255	Zea mays	AY323255	527	56.8	5.7	11604	6	AR151704	Sequence
455	57.4	5.8	1298	8	AY323256	Zea mays	AY323256	528	56.8	5.7	11604	6	AR352525	Sequence
456	57.4	5.8	1298	8	AY323259	Zea mays	AY323259	529	56.8	5.7	15079	6	AR151702	Sequence
457	57.4	5.8	1298	8	AY323260	Zea mays	AY323260	530	56.8	5.7	15120	1	SCU87786	Streptomyce

531	56.8	5.7	15120	6	AR352523	Sequence	604	5.7	2109	6	AX321622	Sequence
532	56.8	5.7	22976	6	AR410057	Sequence	605	5.7	2142	6	BD157246	Primer fo
533	56.8	5.7	22976	6	AX000035	Sequence	606	5.7	2142	6	AX878471	Sequence
534	56.8	5.7	22976	6	AX969142	Sequence	607	5.7	2142	9	AK021532	Homo sapi
535	56.8	5.7	22976	6	BD062419	LSR recep	608	5.7	2198	6	BD156336	Primer fo
536	56.8	5.7	29870	6	AX763606	Sequence	609	5.7	2198	6	AX876825	Sequence
537	56.8	5.7	36401	1	AX763398	Sequence	610	5.7	2198	9	AK001474	Homo sapi
538	56.8	5.7	41936	6	AX335752	Sequence	611	5.7	2347	9	BC009372	Homo sapi
539	56.8	5.7	41936	9	CH19R30879	Sequence	612	5.7	2360	9	BC043619	Homo sapi
540	56.8	5.7	55972	1	AF386507	Streptomy	613	5.7	2392	6	AX003881	Sequence
541	56.8	5.7	65351	2	AC139773	Homo sapi	614	5.7	2392	9	BD086467	DNA demet
542	56.8	5.7	102230	8	AP004045	Oryza sat	615	5.7	2392	9	AF072247	Homo sapi
543	56.8	5.7	110000	1	AP006840_04	Continuation (5 of	616	5.7	2885	9	HUMHBA3	Homo sapien
544	56.8	5.7	110000	1	AP006840_10	Continuation (11 of	617	5.7	4257	6	ARI44708	Sequence
545	56.8	5.7	110000	1	AP006840_34	Continuation (35 of	618	5.7	4257	6	ARI45616	Sequence
546	56.8	5.7	138289	2	AP004873	Oryza sat	619	5.7	4257	6	AR526866	Sequence
547	56.8	5.7	188050	1	AL646072	Ralstonia	620	5.7	4943	6	BD188749	Novel tyr
548	56.8	5.7	299925	1	AP005048	Streptomy	621	5.7	4943	9	AB067470	Homo sapi
549	56.8	5.7	300800	1	AP005036	Streptomy	622	5.7	4988	6	AX766352	Sequence
550	56.8	5.7	303550	1	SC0339131	Streptomy	623	5.7	6633	14	HEH5VIG3	Herpes simp
551	56.8	5.7	313800	1	SC0339114	Streptomy	624	5.7	12001	6	AR048721	Sequence
552	56.6	5.7	976	8	AK073885	Oryza sat	625	5.7	12561	1	AE004557	Pseudomon
553	56.6	5.7	2450	6	AX654813	Sequence	626	5.7	15559	1	AF074603	Streptomy
554	56.6	5.7	25085	6	AX598627	Sequence	627	5.7	26245	14	HSIUS	Human herpe
555	56.6	5.7	50543	6	AX598617	Sequence	628	5.7	26245	14	HSIUS	Human herpe
556	56.6	5.7	92392	8	AC128647	Oryza sat	629	5.7	32668	1	MPU575934	Micromono
557	56.6	5.7	110000	1	AP006618_51	Continuation (52 of	630	5.7	33676	1	SCARDIGN	Saccharothr
558	56.6	5.7	110000	1	AP006840_08	Continuation (9 of	631	5.7	38146	1	AY524043	Micromono
559	56.6	5.7	110000	1	AP006840_17	Continuation (18 of	632	5.7	43058	6	AX332810	Sequence
560	56.6	5.7	110000	1	AP006840_19	Continuation (20 of	633	5.7	43058	6	AX333047	Sequence
561	56.6	5.7	110000	2	BX284653_2	Continuation (3 of	634	5.7	43058	6	AX411306	Sequence
562	56.6	5.7	110000	8	AC145127_06	Continuation (7 of	635	5.7	43058	9	HSGGI	Human DNA s
563	56.6	5.7	114184	8	AP003984	Oryza sat	636	5.7	107955	2	AP005551	Oryza sat
564	56.6	5.7	150336	9	HSJ395C13	Human DNA	637	5.7	110000	2	LMFLCHR36_13	Continuation (14 o
565	56.6	5.7	154082	8	AC108756	Oryza sat	638	5.7	121849	8	AC092779	Oryza sat
566	56.6	5.7	189349	8	AC068654	Genomic S	639	5.7	150155	8	AC097277	Oryza sat
567	56.6	5.7	216050	1	AL646076	Ralstonia	640	5.7	152261	14	HEICG	Human herpe
568	56.6	5.7	245210	2	AC137771	Homo sapi	641	5.7	152261	14	HEICG	Human herpe
569	56.6	5.7	304564	8	AE017049	Oryza sat	642	5.7	170020	8	AC138001	Oryza sat
570	56.4	5.7	1013	8	SLASADN	Stellaria l	643	5.7	172238	8	AC145381	Oryza sat
571	56.4	5.7	1230	8	AK105901	Oryza sat	644	5.7	190076	9	AC008403	Homo sapi
572	56.4	5.7	1392	6	BD180195	Highly th	645	5.7	258002	9	AE006462	Homo sapi
573	56.4	5.7	3957	6	AX5258	Sequence 2	646	5.7	276800	1	SC0939115	Streptomy
574	56.4	5.7	9450	1	AF190463	Comamonas	647	5.7	299925	1	AP005043	Streptomy
575	56.4	5.7	15738	6	AX803762	Sequence	648	5.7	300100	1	SC0939123	Streptomy
576	56.4	5.7	110000	1	AP006618_16	Continuation (17 of	649	5.7	302898	1	AE017238	Mycobacte
577	56.4	5.7	150715	14	AY714813	Cercopith	650	5.6	890	8	NTU38612	Nicotiana t
578	56.4	5.7	154746	14	HSV2HG52	Herpes simp	651	5.6	1150	14	HSALIR3	epstein-bar
579	56.4	5.7	154746	14	HSV2HG52	Herpes simp	652	5.6	1152	6	AX653506	Sequence
580	56.4	5.7	172368	2	CR450819	Danio rer	653	5.6	1393	11	PM11HI2G	Penicilli
581	56.4	5.7	187829	2	AC025388	Homo sapi	654	5.6	1427	8	AK109606	Oryza sat
582	56.4	5.7	289308	1	AE017242	Mycobacte	655	5.6	1926	6	AR217866	Sequence
583	56.4	5.7	348866	1	BE640426	Bordetell	656	5.6	1926	6	AR254714	Sequence
584	56.2	5.7	1143	6	AX574142	Sequence	657	5.6	1926	6	AR107940	Sequence
585	56.2	5.7	2793	6	AR009990	Sequence	658	5.6	2580	6	AR108994	Sequence
586	56.2	5.7	2793	6	195876	Sequence 1	659	5.6	2651	10	MMU08210	Mus musculu
587	56.2	5.7	3060	3	AF027735	Nephila c	660	5.6	2810	1	STWTCR3	Streptomyce
588	56.2	5.7	13513	1	AY423269	Streptomy	661	5.6	3281	3	LMA243459	Leishmani
589	56.2	5.7	14186	6	AX204987	Sequence	662	5.6	3643	10	BC051649	Mus muscu
590	56.2	5.7	48221	6	AX574200	Sequence	663	5.6	5452	6	AR083151	Sequence
591	56.2	5.7	58996	1	AB034704	Rubriviva	664	5.6	5452	12	U02454	Cloning vec
592	56.2	5.7	110000	1	AP006618_14	Continuation (15 of	665	5.6	8705	6	BD225380	Targeting
593	56.2	5.7	226251	10	AL833803	Mouse DNA	666	5.6	8705	6	BD225380	Targeting
594	56.2	5.7	300425	1	AP005038	Streptomy	667	5.6	9482	6	AR349578	Sequence
595	56.2	5.7	339650	1	SC0939108	Streptomy	668	5.6	9551	6	CQ829527	Sequence
596	56.2	5.7	343243	1	EX640414	Bordetell	669	5.6	9551	6	AR076233	Sequence
597	56.2	5.7	349260	1	EX572595	Rhodopsu	670	5.6	9551	9	HUMHYAL	Human trich
598	56.2	5.7	1104	5	AF364329	Coturnix	671	5.6	9600	6	AR2665	Sequence 1
599	56	5.7	1302	8	AK070743	Oryza sat	672	5.6	9600	6	AR158345	Sequence
600	56	5.7	2043	9	BC032443	Homo sapi	673	5.6	9600	6	AR241207	Sequence
601	56	5.7	2109	6	BD237101	Compounds	674	5.6	10285	6	AX551315	Sequence
602	56	5.7	2109	6	AR225501	Sequence	675	5.6	10285	6	AX552015	Sequence
603	56	5.7	2109	6	AR562924	Sequence	676	5.6	10330	6	CQ789661	Sequence

C 677	55.8	5.6	10477	6	CQ789659	Sequence	750	55.2	5.6	66669	1	AME16952	Y16952 Amycolatops
C 678	55.8	5.6	10516	6	CQ789657	Sequence	751	55.2	5.6	85163	1	AY048670	AY048670 Streptomy
C 679	55.8	5.6	10561	6	CQ789655	Sequence	752	55.2	5.6	95209	2	AP004323	AP004323 Oryza sat
C 680	55.8	5.6	10596	6	I25041	Sequence 15	753	55.2	5.6	110000	1	AP006618_53	Continuation (54 o
C 681	55.8	5.6	10596	6	I25041	Sequence 15	754	55.2	5.6	110000	1	AP006618_17	Continuation (18 o
C 682	55.8	5.6	10615	6	CQ789682	Sequence	755	55.2	5.6	110000	1	EX571966_06	Continuation (7 of
C 683	55.8	5.6	10737	12	XXU02428	U02428 Cloning vec	756	55.2	5.6	110000	2	LMFLCHR16_02	Continuation (3 of
C 684	55.8	5.6	10774	6	CQ789660	Sequence	757	55.2	5.6	110000	2	LMFLCHR16_03	Continuation (4 of
C 685	55.8	5.6	10850	12	U02455	U02455 Cloning vec	758	55.2	5.6	110000	8	AE016815_4	Continuation (5 of
C 686	55.8	5.6	10921	6	CQ789658	Sequence	759	55.2	5.6	137860	10	AC122407	AC122407 Mus muscu
C 687	55.8	5.6	10961	6	CQ789656	Sequence	760	55.2	5.6	145796	8	AC130598	AC130598 Oryza sat
C 688	55.8	5.6	11006	6	CQ789654	Sequence	761	55.2	5.6	146408	8	AC130610	AC130610 Oryza sat
C 689	55.8	5.6	11059	6	CQ789683	Sequence	762	55.2	5.6	154728	9	AC018730	AC018730 Homo sapi
C 690	55.8	5.6	13750	1	AY260903	AY260903 Rhodospir	763	55.2	5.6	187956	8	AC135425	AC135425 Oryza sat
C 691	55.8	5.6	16080	6	AR404205	Sequence	764	55.2	5.6	299300	1	AP005026	AP005026 Streptomy
C 692	55.8	5.6	17753	6	CQ790449	Sequence	765	55.2	5.6	348257	1	BX640425	BX640425 Bordetell
C 693	55.8	5.6	22960	12	AV192024	AV192024 BAC cloni	766	55.2	5.6	349497	1	BX640440	BX640440 Bordetell
C 694	55.8	5.6	115245	8	AP005682	AP005682 Oryza sat	767	55	5.6	2205	9	BC009438	BC009438 Homo sapi
C 695	55.8	5.6	128525	8	AP003118	AP003118 Oryza sat	768	55	5.6	2490	8	AK100050	AK100050 Oryza sat
C 696	55.8	5.6	132733	8	CNS08CA4	AL772426 Oryza sat	769	55	5.6	2559	6	AR488839	AR488839 Sequence
C 697	55.8	5.6	135793	8	CNS08CA5	AL772427 Oryza sat	770	55	5.6	2562	6	CQ720385	CQ720385 Sequence
C 698	55.8	5.6	141983	8	AP003047	AP003047 Oryza sat	771	55	5.6	28890	1	AF512431	AF512431 Saccharot
C 699	55.8	5.6	151578	9	AL589986	AL589986 Human DNA	772	55	5.6	30943	6	CQ801140	CQ801140 Sequence
C 700	55.8	5.6	171823	14	HBV	AJ507799 Human her	773	55	5.6	53784	1	AMM223012	AJ223012 Sequence
C 701	55.8	5.6	172281	14	EBV	VO1555 Epstein-Bar	774	55	5.6	53789	6	A69720	A69720 Sequence 3
C 702	55.8	5.6	184113	14	HS4B958RAJ	M80517 Epstein-Bar	775	55	5.6	66280	1	AF195122	AF195122 Rhodobact
C 703	55.8	5.6	196950	2	CRS89874	CRS89874 Danio rer	776	55	5.6	103576	8	YUP8H12	AC000098 Arabidops
C 704	55.8	5.6	232605	1	AE017222	AE017222 Thermus t	777	55	5.6	109528	1	AF040570	AF040570 Amycolato
C 705	55.8	5.6	251872	2	AE012598	AE012598 Rattus no	778	55	5.6	110000	1	AP006618_08	Continuation (9 of
C 706	55.8	5.6	270418	1	AE017303	AE017303 Thermus t	779	55	5.6	110000	2	BX255276_15	Continuation (16 o
C 707	55.8	5.6	280558	1	AE017301	AE017301 Thermus t	780	55	5.6	188050	1	AL646072	AL646072 Ralstonia
C 708	55.8	5.6	313800	1	SC0939114	AL939114 Streptomy	781	55	5.6	292200	1	SC0939129	AL939129 Streptomy
C 709	55.6	5.6	726	6	BD145399	BD145399 Primer fo	782	55	5.6	295150	1	SC0939126	AL939126 Streptomy
C 710	55.6	5.6	726	6	AX865337	AX865337 Sequence	783	54.8	5.5	594	6	BD224381	BD224381 Materials
C 711	55.6	5.6	74542	1	BX571965_40	Continuation (41 o	784	54.8	5.5	594	6	AR216431	AR216431 Sequence
C 712	55.6	5.6	110000	1	AP006618_43	Continuation (44 o	785	54.8	5.5	594	6	AR432833	AR432833 Sequence
C 713	55.6	5.6	110000	1	AP006840_33	Continuation (34 o	786	54.8	5.5	607	6	AR074114	AR074114 Sequence
C 714	55.6	5.6	110000	1	AP006840_34	Continuation (35 o	787	54.8	5.5	607	6	BD224299	BD224299 Materials
C 715	55.6	5.6	110000	1	CP00010_30	Continuation (31 o	788	54.8	5.5	607	6	BD273001	BD273001 Materials
C 716	55.6	5.6	110000	8	AE016819_05	Continuation (6 of	789	54.8	5.5	607	6	AR216349	AR216349 Sequence
C 717	55.6	5.6	150200	8	AP004459	AP004459 Oryza sat	790	54.8	5.5	607	6	AR432751	AR432751 Sequence
C 718	55.6	5.6	155069	8	AP004396	AP004396 Oryza sat	791	54.8	5.5	607	6	BD005662	BD005662 Materials
C 719	55.6	5.6	301443	1	AE017239	AE017239 Mycobacte	792	54.8	5.5	1795	1	AF118856	AF118856 Streptomy
C 720	55.4	5.6	657	12	AY657485	AY657485 Synthetic	793	54.8	5.5	2142	1	CCU42203	U42203 Caulobacter
C 721	55.4	5.6	1251	6	BD180575	BD180575 Highly th	794	54.8	5.5	2365	8	AK102809	AK102809 Oryza sat
C 722	55.4	5.6	1726	8	AK064395	AK064395 Oryza sat	795	54.8	5.5	2783	1	STMENBT	D13170 Streptomyce
C 723	55.4	5.6	3033	6	AR534432	AR534432 Sequence	796	54.8	5.5	2030	8	VCA429230	AJ429230 Volvox ca
C 724	55.4	5.6	3033	6	AX573728	AX573728 Sequence	797	54.8	5.5	5500	8	ATGLYRP	AX5838 A.thaliana
C 725	55.4	5.6	11873	1	AE004710	AE004710 Pseudomon	798	54.8	5.5	10894	1	AE005785	AE005785 Caulobact
C 726	55.4	5.6	95209	2	AP004323	AP004323 Oryza sat	799	54.8	5.5	12528	1	AE005826	AE005826 Caulobact
C 727	55.4	5.6	110000	1	AP006618_57	Continuation (58 o	800	54.8	5.5	58638	7	AY576796	AY576796 Actinopla
C 728	55.4	5.6	110000	1	AP006840_14	Continuation (15 o	801	54.8	5.5	92620	8	AB026636	AB026636 Arabidops
C 729	55.4	5.6	110000	1	AP006840_26	Continuation (27 o	802	54.8	5.5	110000	2	BX255276_07	Continuation (8 of
C 730	55.4	5.6	128136	1	AF440524	AF440524 Pseudomon	803	54.8	5.5	156789	14	AF533768	AF533768 Cercopith
C 731	55.4	5.6	133534	10	AL929233	AL929233 Mouse DNA	804	54.8	5.5	166182	10	AC084391	AC084391 Mus muscu
C 732	55.4	5.6	158230	1	AF440523	AF440523 Pseudomon	805	54.8	5.5	218310	10	AC034265	AC034265 Mus muscu
C 733	55.4	5.6	172081	10	AC137124	AC137124 Mus muscu	806	54.8	5.5	231001	2	AC130981	AC130981 Rattus no
C 734	55.4	5.6	197050	1	AL646081	AL646081 Ralstonia	807	54.8	5.5	258319	2	AC127770	AC127770 Rattus no
C 735	55.4	5.6	299050	1	SC0939119	AL939119 Streptomy	808	54.8	5.5	292100	1	SC0939121	AL939121 Streptomy
C 736	55.4	5.6	299800	1	AP005028	AP005028 Streptomy	809	54.6	5.5	955	8	NTU62736	U62736 Nicotiana t
C 737	55.4	5.6	314100	1	SC0939106	AL939106 Streptomy	810	54.6	5.5	980	6	AX652989	AX652989 Sequence
C 738	55.2	5.6	986	8	AF377753	AF377753 Zea mays	811	54.6	5.5	1261	8	AK112011	AK112011 Oryza sat
C 739	55.2	5.6	1182	8	AK105138	AK105138 Oryza sat	812	54.6	5.5	1308	6	BD217906	BD217906 Gene fami
C 740	55.2	5.6	1324	8	OSLIIP19	XS7325 Rice lip19	813	54.6	5.5	2830	3	AF027972	AF027972 Nephila c
C 741	55.2	5.6	1344	8	AK104844	AK104844 Oryza sat	814	54.6	5.5	3866	1	D31792	D31792 Streptomyce
C 742	55.2	5.6	1375	8	AK065180	AK065180 Oryza sat	815	54.6	5.5	3866	1	D31792	D31792 Streptomyce
C 743	55.2	5.6	1679	9	AB001835	AB001835 Homo sapi	816	54.6	5.5	4761	1	SC0244019	AJ244019 Streptomy
C 744	55.2	5.6	2208	1	STWLRWMT	M74717 Streptomyce	817	54.6	5.5	5520	3	AC084329	AC084329 Leishmani
C 745	55.2	5.6	9589	1	SC0001205	AJ001205 Streptomy	818	54.6	5.5	9811	14	AF449714	AF449714 Cercopith
C 746	55.2	5.6	13508	1	AE005037	AE005037 Halobacte	819	54.6	5.5	12277	1	AF340166	AF340166 Streptomy
C 747	55.2	5.6	14219	1	AB0070957	AB0070957 Streptomy	820	54.6	5.5	22449	1	SPSNBCDE	Y11548 S.pristinae
C 748	55.2	5.6	21481	2	CR847893	CR847893 Danio rer	821	54.6	5.5	22449	1	SPSNBCGN	X98690 S.pristinae
C 749	55.2	5.6	65351	2	AC139773	AC139773 Homo sapi	822	54.6	5.5	110086	8	AP003373	AP003373 Oryza sat





969	53.4	5.4	110000	1	AP006618_07	Continuation (8 of	1042	52.8	5.3	3157	1	MSGPOLA	L11920 Mycobacteri
c 970	53.4	5.4	110000	1	CP0006840_22	Continuation (23 of	c1043	52.8	5.3	4423	10	MMUSEF217	X77602 M.musculus
c 971	53.4	5.4	110000	1	CP000011_01	Continuation (2 of	1044	52.8	5.3	11842	1	AE005053	AE005053 Halobac
c 972	53.4	5.4	136254	8	CNS079P9	AL713941 Oryza sat	c1045	52.8	5.3	66135	1	AP006840_35	Continuation (36 o
c 973	53.4	5.4	136551	2	AC048354	AC048354 Homo sapi	c1046	52.8	5.3	92509	1	AL646086	AL646086 Ralstonia
c 974	53.4	5.4	141066	8	AP005188	AP005188 Oryza sat	1047	52.8	5.3	110000	1	AE000516_18	Continuation (19 o
c 975	53.4	5.4	151699	8	AP003916	AP003916 Oryza sat	1048	52.8	5.3	110000	1	AE000516_18	Continuation (19 o
c 976	53.4	5.4	155337	2	AC116408	Mus muscu	c1049	52.8	5.3	114996	8	AY485643	AY485643 Burkholde
c 977	53.4	5.4	163778	9	AL391005	AL391005 Human DNA	c1050	52.8	5.3	172647	8	AC130732	AC130732 Oryza sat
c 978	53.4	5.4	181214	2	AC110907	AC110907 Mus muscu	1051	52.8	5.3	189010	2	AC150509	AC150509 Bos tauru
c 979	53.4	5.4	187410	8	AP005579	AP005579 Oryza sat	c1052	52.8	5.3	299925	1	AP005039	AP005039 Streptomy
c 980	53.4	5.4	233405	2	AC126733	AC126733 Rattus no	1053	52.8	5.3	300050	1	BE248339	BE248339 Mycobacte
c 981	53.4	5.4	236502	2	AC098186	AC098186 Rattus no	c1054	52.8	5.3	305584	1	AE016920	AE016920 Chromobac
982	53.4	5.4	272101	1	AE017302	AE017302 Thermus t	1055	52.8	5.3	341000	1	SCO93106	AL939106 Streptomy
983	53.4	5.4	296500	1	SC0939128	AL939128 Streptomy	1056	52.8	5.3	343071	2	AC150933	AC150933 Bos tauru
984	53.4	5.4	308050	1	SC0939124	AL939124 Streptomy	1057	52.8	5.3	347137	1	BE840448	BE840448 Bordetell
985	53.4	5.4	344805	1	BE640434	BE640434 Bordetell	1058	52.8	5.3	347496	1	BE840448	BE840448 Mycobacte
986	53.4	5.4	348074	1	BE640449	BE640449 Bordetell	c1059	52.8	5.3	348934	1	BE640417	BE640417 Bordetell
987	53.2	5.4	1183	8	AK109116	AK109116 Oryza sat	c1060	52.8	5.3	349028	1	BE640413	BE640413 Bordetell
988	53.2	5.4	1283	8	AK058442	AK058442 Oryza sat	1061	52.8	5.3	349497	1	BE640440	BE640440 Bordetell
989	53.2	5.4	1341	1	AY337515	AY337515 Myxococcu	c1062	52.8	5.3	349726	1	BE640421	BE640421 Bordetell
990	53.2	5.4	1405	8	AK108620	AK108620 Oryza sat	1063	52.6	5.3	948	6	BD180185	BD180185 Highly th
991	53.2	5.4	1509	6	BD180173	BD180173 Highly th	1064	52.6	5.3	1569	5	AY518690	AY518690 Gallus ga
992	53.2	5.4	2672	1	AF159692	AF159692 Myxococcu	1065	52.6	5.3	2466	6	CQ759736	CQ759736 Sequence
993	53.2	5.4	2767	8	SSI224970	AJ224970 Spermatoz	c1066	52.6	5.3	2560	4	AY453841	AY453841 Oryctolag
994	53.2	5.4	10161	1	AF546153	AF546153 Micromono	c1067	52.6	5.3	2561	6	AR409339	AR409339 Sequence
995	53.2	5.4	13325	1	AE005016	AE005016 Halobacte	c1068	52.6	5.3	2561	6	AX239605	AX239605 Sequence
996	53.2	5.4	110000	1	AP006618_24	Continuation (25 o	1069	52.6	5.3	2619	6	CQ759734	CQ759734 Sequence
c 997	53.2	5.4	110000	1	AP006618_36	Continuation (37 o	1070	52.6	5.3	2778	6	CQ850770	CQ850770 Sequence
c 998	53.2	5.4	110000	1	AP006618_43	Continuation (44 o	1071	52.6	5.3	2778	9	AK128815	AK128815 Homo sapi
999	53.2	5.4	110000	1	AP006840_28	Continuation (29 o	1072	52.6	5.3	3342	1	AF200819	AF200819 Streptomy
1000	53.2	5.4	110400	8	AP005919	AP005919 Oryza sat	1073	52.6	5.3	3705	6	CQ759732	CQ759732 Sequence
1001	53.2	5.4	116887	10	AL929153	AL929153 Mouse DNA	1074	52.6	5.3	4881	1	AME318385	AJ318385 Amycolati
c1002	53.2	5.4	135838	1	AF484556	AF484556 Streptomy	1075	52.6	5.3	7985	14	AB096202	AB096202 Cercopit
c1003	53.2	5.4	137468	8	AP003269	AP003269 Oryza sat	1076	52.6	5.3	11064	1	D63799	D63799 Thermus the
c1004	53.2	5.4	181676	10	AC124194	AC124194 Mus muscu	1077	52.6	5.3	12162	1	AY034175	AY034175 Streptomy
1005	53.2	5.4	197411	10	AC135961	AC135961 Mus muscu	1078	52.6	5.3	13803	1	AE011784	AE011784 Xanthomon
c1006	53.2	5.4	232605	1	AE017222	AE017222 Thermus t	1079	52.6	5.3	13901	1	AY258009	AY258009 Streptomy
c1007	53.2	5.4	309267	1	AE017235	AE017235 Mycobacte	1080	52.6	5.3	29132	1	STH575648	AJ575648 Streptomy
1008	53.2	5.4	348525	1	BE640428	BE640428 Bordetell	1081	52.6	5.3	47090	9	AC092310	AC092310 Homo sapi
1009	53.2	5.4	349354	1	BE640416	BE640416 Bordetell	1082	52.6	5.3	47090	9	AC093233	AC093233 Homo sapi
1010	53.2	5.4	349672	1	BE640419	BE640419 Bordetell	c1083	52.6	5.3	81767	2	AC021929	AC021929 Homo sapi
c1011	53	5.4	632	6	AR227195	AR227195 Sequence	c1084	52.6	5.3	110000	1	AE00516_27	Continuation (28 o
1012	53	5.4	765	6	BD180096	BD180096 Highly th	1085	52.6	5.3	110000	1	AE016822_21	Continuation (22 o
1013	53	5.4	1929	6	AX811491	AX811491 Sequence	c1086	52.6	5.3	110000	1	AP006618_02	Continuation (3 of
1014	53	5.4	2304	6	BD179527	BD179527 Highly th	c1087	52.6	5.3	110000	1	AP006618_03	Continuation (4 of
1015	53	5.4	2953	10	BC054782	BC054782 Mus muscu	c1088	52.6	5.3	110000	1	AP006618_28	Continuation (25 o
1016	53	5.4	3518	10	MUSHSP7A2	M35021 Mouse heat	c1089	52.6	5.3	110000	1	AP006618_28	Continuation (29 o
1017	53	5.4	3701	1	AF172724	AF172724 Caulobact	c1090	52.6	5.3	110000	2	LMFLCHR34_13	Continuation (14 o
c1018	53	5.4	8113	14	HSBBTCP4A	L14320 Bovine herp	1091	52.6	5.3	135357	8	AP003896	AP003896 Oryza sat
c1019	53	5.4	10029	1	AE012236	AE012236 Xanthomon	c1092	52.6	5.3	138390	14	AY261359	AY261359 Bovine he
c1020	53	5.4	10513	1	AE004792	AE004792 Pseudomon	c1093	52.6	5.3	163328	8	AP004865	AP004865 Oryza sat
c1021	53	5.4	11283	1	AE005710	AE005710 Caulobact	1094	52.6	5.3	183495	8	AP005620	AP005620 Oryza sat
c1022	53	5.4	11923	1	AE005972	AE005972 Caulobact	1095	52.6	5.3	230362	2	AC009942	AC009942 Rattus no
1023	53	5.4	32668	1	MPU575934	AJ575934 Micromono	1096	52.6	5.3	277363	2	AC134745	AC134745 Rattus no
c1024	53	5.4	38146	1	AY524043	AY524043 Micromono	c1097	52.6	5.3	299425	1	AP005049	AP005049 Streptomy
c1025	53	5.4	100773	8	AF466201	AF466201 Sorghum b	1098	52.6	5.3	303550	1	SCO939118	AL939118 Streptomy
c1026	53	5.4	102591	9	AC002978	AC002978 Homo sapi	c1099	52.6	5.3	308550	1	BE248342	BE248342 Mycobacte
c1027	53	5.4	110000	1	AP006618_39	Continuation (40 o	c1100	52.6	5.3	346051	1	BE842580	BE842580 Mycobacte
c1028	53	5.4	110000	1	AP006618_54	Continuation (55 o	1101	52.4	5.3	1175	5	CMHISH5	X01065 Duck (c. mo
1029	53	5.4	110000	1	AP006840_03	Continuation (4 of	1102	52.4	5.3	1227	6	AX467205	AX467205 Sequence
1030	53	5.4	110000	2	LMFLCHR12_13	Continuation (14 o	1103	52.4	5.3	1485	8	AX107516	AX107516 Oryza sat
1031	53	5.4	135301	14	BHV1CGEN	Continuation (14 o	1104	52.4	5.3	1891	6	AX337108	AX337108 Sequence
c1032	53	5.4	135301	14	BHV1CGEN	AJ004801 Bovine he	1105	52.4	5.3	1891	6	AX587764	AX587764 Sequence
c1033	53	5.4	144093	10	AC109193	AJ004801 Bovine he	1106	52.4	5.3	1891	9	HSJUNDR	AX587764 Sequence
1034	53	5.4	178620	10	AC121865	AC109193 Mus muscu	1107	52.4	5.3	2796	3	AF043944	AF043944 Mytilus e
c1035	53	5.4	194387	10	AC105989	AC121865 Mus muscu	1108	52.4	5.3	3139	8	D63955	D63955 Oryza sativ
1036	53	5.4	301925	1	AP005046	AC105989 Mus muscu	1109	52.4	5.3	3978	4	BOVADC	D63955 Oryza sativ
1037	53	5.4	303842	1	AE016923	AP005046 Streptomy	1110	52.4	5.3	3978	6	AR106654	AR106654 Sequence
c1038	53	5.4	347071	1	BE640415	BE016923 Chromobac	1111	52.4	5.3	3980	1	AF546147	AF546147 Streptomy
1039	53	5.4	348706	1	BE640415	BE640415 Bordetell	1112	52.4	5.3	5117	6	AX818240	AX818240 Sequence
1040	52.8	5.3	1094	11	PM7G11B	BE640445 Bordetell	1113	52.4	5.3	5117	9	AB011105	AB011105 Homo sapi
1041	52.8	5.3	1236	6	AR007558	AL685196 Penicilli	1114	52.4	5.3	5204	6	AX512251	AX512251 Sequence



1115	52.4	5.3	5640	6	AR338550	Sequence	1188	52	5.3	2800	1	PSNOSZR	Z13988 P. stutzeri
1116	52.4	5.3	8296	6	AX463772	Sequence	1189	52	5.3	3113	8	SS95BASAL	AJ001438 Spermatoz
1117	52.4	5.3	10911	6	CQ730457	Sequence	1190	52	5.3	3114	12	AY192356	AY192356 Synthetic
1118	52.4	5.3	11238	6	AX697991	Sequence	1191	52	5.3	3135	12	AV192357	AV192357 Synthetic
1119	52.4	5.3	11329	9	AF443072	Homo sapi	1192	52	5.3	3150	12	AV192358	AV192358 Synthetic
1120	52.4	5.3	11350	6	AX463738	Sequence	1193	52	5.3	10352	1	AF546152	AF546152 Streptomy
1121	52.4	5.3	11367	6	AX704754	Sequence	1194	52	5.3	10854	1	AE001886	AE001886 Deinococc
1122	52.4	5.3	16197	1	AE020272	Sequence	1195	52	5.3	11506	1	AE004793	AE004793 Pseudomon
1123	52.4	5.3	60196	6	AX697977	Sequence	1196	52	5.3	49269	8	AC135499	AC135499 Oryza sat
1124	52.4	5.3	79568	2	AC151725	Medicago	1197	52	5.3	110000	1	AE016822_22	Continuation (23 o
1125	52.4	5.3	85434	2	AC066610	Homo sapi	1198	52	5.3	110000	1	AP006840_22	Continuation (23 o
1126	52.4	5.3	101075	8	CNS08CRU	Oryza sat	1199	52	5.3	142081	8	AP004572	AP004572 Oryza sat
1127	52.4	5.3	104326	1	AB070940	Streptomy	1200	52	5.3	152374	8	AP004572	AP004572 Oryza sat
1128	52.4	5.3	110000	1	AP006618_13	Continuation (14 o	1201	52	5.3	186090	2	AC097352	AC097352 Canis fam
1129	52.4	5.3	110000	1	AP006618_15	Continuation (16 o	1202	52	5.3	191916	2	AC095027	AC095027 Canis fam
1130	52.4	5.3	110000	1	BX571965_02	Continuation (35 o	1203	52	5.3	191996	9	AC092275	AC092275 Homo sapi
1131	52.4	5.3	110000	1	CP000010_34	Continuation (35 o	1204	52	5.3	193119	8	AC025907	AC025907 Oryza sat
1132	52.4	5.3	138203	1	AY310323	Streptomy	1205	52	5.3	200968	8	AP005516	AP005516 Oryza sat
1133	52.4	5.3	149098	8	AP003296	Oryza sat	1206	52	5.3	211857	10	AL732564	AL732564 Mouse DNA
1134	52.4	5.3	157302	9	AL445209	AP003296 Oryza sat	1207	52	5.3	299925	1	AP005045	AP005045 Streptomy
1135	52.4	5.3	168861	2	AC130786	Human DNA	1208	52	5.3	300029	8	AE017099	AE017099 Streptomy
1136	52.4	5.3	169162	8	AP004267	AP004267 Oryza sat	1209	52	5.3	301846	1	AE016913	AE016913 Chromobac
1137	52.4	5.3	176647	2	AC130188	AP004267 Oryza sat	1210	52	5.3	307435	1	AE016914	AE016914 Chromobac
1138	52.4	5.3	196558	10	AC073946	AC073946 Mus muscu	1211	51.8	5.2	974	8	AF377768	AF377768 Zea mays
1139	52.4	5.3	202270	10	AC102341	AC102341 Mus muscu	1212	51.8	5.2	975	8	AF377745	AF377745 Zea mays
1140	52.4	5.3	242662	2	AC080020	AC080020 Mus muscu	1213	51.8	5.2	980	8	AF377759	AF377759 Zea mays
1141	52.4	5.3	247910	1	AE017307	AE017307 Thermus t	1214	51.8	5.2	980	8	AF377761	AF377761 Zea mays
1142	52.4	5.3	300550	1	AP005030	AP005030 Streptomy	1215	51.8	5.2	981	8	AY513914	AY513914 Zea luxur
1143	52.4	5.3	320150	1	AP005033	AP005033 Streptomy	1216	51.8	5.2	981	8	AY513920	AY513920 Zea luxur
1144	52.2	5.3	705	6	BD179549	BD179549 Highly th	1217	51.8	5.2	981	8	AY513928	AY513928 Zea mays
1145	52.2	5.3	833	8	AY088274	AY088274 Arabidops	1218	51.8	5.2	982	8	AF377767	AF377767 Zea mays
1146	52.2	5.3	936	6	BD179727	BD179727 Highly th	1219	51.8	5.2	983	8	AY513929	AY513929 Zea mays
1147	52.2	5.3	996	6	PM12CAG	PM12CAG Penicilli	1220	51.8	5.2	989	8	AY513923	AY513923 Zea mays
1148	52.2	5.3	1611	8	AK071964	AK071964 Oryza sat	1221	51.8	5.2	995	8	AY513927	AY513927 Zea mays
1149	52.2	5.3	1719	6	BD180543	BD180543 Highly th	1222	51.8	5.2	1255	10	AE076156	AE076156 Mus muscu
1150	52.2	5.3	1766	8	AF325915	AF325915 Euglena g	1223	51.8	5.2	1262	10	BC010402	BC010402 Mus muscu
1151	52.2	5.3	2085	8	AK119580	AK119580 Oryza sat	1224	51.8	5.2	1673	8	AY600140	AY600140 Broussone
1152	52.2	5.3	2529	1	AE005536	AE005536 Streptomy	1225	51.8	5.2	1705	8	AK069785	AK069785 Oryza sat
1153	52.2	5.3	2760	1	SRSENRS	Y14336 Streptomyce	1226	51.8	5.2	1926	6	AR217867	AR217867 Sequence
1154	52.2	5.3	6297	6	AX598629	AX598629 Sequence	1227	51.8	5.2	1931	6	AR083152	AR083152 Sequence
1155	52.2	5.3	7155	1	RCU64519	U64519 Rhodospiril	1228	51.8	5.2	2036	8	AF050631	AF050631 Zea mays
1156	52.2	5.3	9353	14	BHV1UUX	Z49078 Bovine herp	1229	51.8	5.2	2075	6	AR253206	AR253206 Sequence
1157	52.2	5.3	10460	1	AE011791	AE011791 Xanthomon	1230	51.8	5.2	2075	6	AR361924	AR361924 Sequence
1158	52.2	5.3	10696	1	AE012103	AE012103 Xanthomon	1231	51.8	5.2	2075	6	AR433000	AR433000 Sequence
1159	52.2	5.3	14355	3	AF218623S1	AF218623 Nephtila m	1232	51.8	5.2	2075	6	AX482567	AX482567 Sequence
1160	52.2	5.3	31444	14	BVHLLFT31	Z54206 Bovine herp	1233	51.8	5.2	2075	6	AX565707	AX565707 Sequence
1161	52.2	5.3	66808	1	SAU421825	AJ421825 Stigmatel	1234	51.8	5.2	2075	6	AX597107	AX597107 Sequence
1162	52.2	5.3	76396	1	AY354515	AY354515 Streptomy	1235	51.8	5.2	2075	6	AX701365	AX701365 Sequence
1163	52.2	5.3	82868	1	AJ620477	AJ620477 Angiococc	1236	51.8	5.2	2075	9	AF001900	AF001900 Homo sapi
1164	52.2	5.3	82868	6	CQ792587	CQ792587 Sequence	1237	51.8	5.2	2525	6	CQ782831	CQ782831 Sequence
1165	52.2	5.3	82868	6	CQ792587	CQ792587 Sequence	1238	51.8	5.2	2525	6	BD127336	BD127336 Primer fo
1166	52.2	5.3	110000	1	AP006618_58	Continuation (59 o	1239	51.8	5.2	2525	9	AK074866	AK074866 Homo sapi
1167	52.2	5.3	128098	8	AP004309	AP004309 Oryza sat	1240	51.8	5.2	2597	6	AK0700203	AK0700203 Sequence
1168	52.2	5.3	133387	2	AP004061	AP004061 Oryza sat	1241	51.8	5.2	2714	9	AF327056	AF327056 Homo sapi
1169	52.2	5.3	143200	8	AP004380	AP004380 Oryza sat	1242	51.8	5.2	2725	9	BC069227	BC069227 Homo sapi
1170	52.2	5.3	159860	8	AP005647	AP005647 Oryza sat	1243	51.8	5.2	4469	6	AX236302	AX236302 Sequence
1171	52.2	5.3	190050	1	AL646080	AL646080 Ralstonia	1244	51.8	5.2	4469	6	AX578081	AX578081 Sequence
1172	52.2	5.3	205144	4	AY495827	AY495827 Oryctolag	1245	51.8	5.2	4469	9	AF056087	AF056087 Homo sapi
1173	52.2	5.3	273285	1	AE017304	AE017304 Thermus t	1246	51.8	5.2	4612	1	AF317284	AF317284 Burkholde
1174	52.2	5.3	276800	1	SC0939115	AL939115 Streptomy	1247	51.8	5.2	10732	6	E32986	E32986 Gene encodi
1175	52.2	5.3	300327	1	AE017228	AE017228 Mycobacte	1248	51.8	5.2	11462	8	AF327876	AF327876 Chlamydom
1176	52.2	5.3	300425	1	AP005038	AP005038 Streptomy	1249	51.8	5.2	15231	1	AY026598	AY026598 Burkholde
1177	52.2	5.3	305584	1	AE016920	AE016920 Chromobac	1250	51.8	5.2	34600	1	AV028431	AV028431 Burkholde
1178	52.2	5.3	309501	1	SC0939117	AL939117 Streptomy	1251	51.8	5.2	40343	2	AC099831	AC099831 Homo sapi
1179	52	5.3	391	11	PM12H12B	AL684455 Penicilli	1252	51.8	5.2	76521	2	AC148294	AC148294 Zea mays
1180	52	5.3	992	8	AF377751	AF377751 Zea mays	1253	51.8	5.2	104190	8	AP004257	AP004257 Oryza sat
1181	52	5.3	1000	8	AY513932	AY513932 Zea mays	1254	51.8	5.2	110000	1	AP006618_21	Continuation (22 o
1182	52	5.3	1155	8	AB028182	AB028182 Oryza sat	1255	51.8	5.2	110000	1	AP006618_28	Continuation (29 o
1183	52	5.3	1255	8	AK073667	AK073667 Oryza sat	1256	51.8	5.2	110000	1	AP006840_09	Continuation (10 o
1184	52	5.3	1410	1	AME277083	AJ277083 Amycolato	1257	51.8	5.2	110000	1	AP006840_10	Continuation (11 o
1185	52	5.3	1491	6	AX455983	AX455983 Sequence	1258	51.8	5.2	110000	1	AP006840_26	Continuation (27 o
1186	52	5.3	1703	8	AK120673	AK120673 Oryza sat	1259	51.8	5.2	110000	2	BX25276_03	Continuation (4 of
1187	52	5.3	1711	1	AF347026	AF347026 Streptomy	1260	51.8	5.2	110000	2	LMFLCHR36_22	Continuation (23 o

1261	51.8	5.2	113193	1	AF357202	Streptomy	1334	51.4	5.2	110000	1	AP006618_44	Continuation (45 o
1262	51.8	5.2	113193	6	AX703543	Sequence	1335	51.4	5.2	110000	1	AP006618_45	Continuation (46 o
1263	51.8	5.2	123149	9	AC008655	AC008655 Homo sapi	1336	51.4	5.2	110000	1	AP006840_01	Continuation (2 of
1264	51.8	5.2	185539	2	AC018349	AC018349 Homo sapi	1337	51.4	5.2	110000	1	AY305378_0	AY305378 Ralstonia
1265	51.8	5.2	190590	2	AC135045	AC135045 Homo sapi	1338	51.4	5.2	110000	1	CP000011_04	Continuation (5 of
1266	51.8	5.2	202050	1	AL646065	Ralstonia	1339	51.4	5.2	110000	2	LMFLCHR15_5	Continuation (6 of
1267	51.8	5.2	203050	1	AL646071	AL646071 Ralstonia	1340	51.4	5.2	110000	2	LMFLCHR15_6	Continuation (7 of
1268	51.8	5.2	217514	2	AC145779	Sus scrofa	1341	51.4	5.2	110000	2	LMFLCHR34_00	AL499623 Leishmani
1269	51.8	5.2	298300	1	AP005025	Streptomy	1342	51.4	5.2	130273	8	OSJN00011_	AL606447 Oryza sat
1270	51.8	5.2	298450	1	SC0939107	Streptomy	1343	51.4	5.2	152828	8	AC133859	AC133859 Oryza sat
1271	51.8	5.2	298550	1	AP005047	Streptomy	1344	51.4	5.2	163945	2	AC116727	AC116727 Mus muscu
1272	51.8	5.2	298900	1	AP005937	Bradyrhiz	1345	51.4	5.2	205054	10	AE016925	AE016925 Mus muscu
1273	51.8	5.2	299325	1	AP005042	Streptomy	1346	51.4	5.2	208524	1	AE016925	AE016925 Chromobac
1274	51.8	5.2	300550	1	AP005030	Streptomy	1347	51.4	5.2	301332	1	AE017237	AE017237 Streptomy
1275	51.8	5.2	301875	1	AP005027	Streptomy	1348	51.4	5.2	302300	1	AP005034	AP005034 Streptomy
1276	51.8	5.2	305520	1	AE016780	Pseudomon	1349	51.4	5.2	343473	1	BX640451	BX640451 Bordetell
1277	51.8	5.2	349008	1	BX640444	Bordetell	1350	51.2	5.2	699	6	AX412281	AX412281 Sequence
1278	51.8	5.2	349841	1	BX572606	Rhodosphe	1351	51.2	5.2	699	6	AX412282	AX412282 Sequence
1279	51.6	5.2	486	1	AF071792	Micromono	1352	51.2	5.2	699	6	AX507044	AX507044 Sequence
1280	51.6	5.2	730	8	AF060180	Nicotiana	1353	51.2	5.2	699	6	AX651360	AX651360 Sequence
1281	51.6	5.2	1394	8	AY551433	Hordeum v	1354	51.2	5.2	993	6	BD179823	BD179823 Highly th
1282	51.6	5.2	1584	6	BD180289	Highly th	1355	51.2	5.2	1182	12	AY659409	AY659409 Synthetic
1283	51.6	5.2	2595	6	BD179554	Highly th	1356	51.2	5.2	1220	8	MZETASSELS	L20621 Zea mays al
1284	51.6	5.2	2865	8	AF019296	Zea mays	1357	51.2	5.2	1683	6	AX697979	AX697979 Sequence
1285	51.6	5.2	4523	14	MMULGNES	X95710 Pseudorabie	1358	51.2	5.2	2181	8	AK100401	AK100401 Oryza sat
1286	51.6	5.2	4548	8	AY499410	Zea mays	1359	51.2	5.2	2277	6	AR004983	AR004983 Sequence
1287	51.6	5.2	29148	14	AY486470S04	Human her	1360	51.2	5.2	2815	1	SLCUTRS	X58793 S.lividans
1288	51.6	5.2	39576	3	AC008054	AC008054 Leishmani	1361	51.2	5.2	3480	1	CFICEND	L02544 Cellulomona
1289	51.6	5.2	93821	2	AC021596	AC021596 Homo sapi	1362	51.2	5.2	3993	6	AB017481	AB017481 Heterosig
1290	51.6	5.2	110000	1	AE017282_22	Continuation (23 o	1363	51.2	5.2	4467	8	E33370	E33370 NA+-ATPase
1291	51.6	5.2	110000	1	AP006618_30	Continuation (31 o	1364	51.2	5.2	6125	1	PSRSTD	D45195 Pseudomonas
1292	51.6	5.2	110000	1	AP006840_09	Continuation (10 o	1365	51.2	5.2	10375	1	AE004549	AE004549 Pseudomon
1293	51.6	5.2	110000	1	AP006840_32	Continuation (33 o	1366	51.2	5.2	11334	1	AE004948	AE004948 Pseudomon
1294	51.6	5.2	110000	1	CP000010_31	Continuation (6 of	1367	51.2	5.2	12357	1	AE004471	AE004471 Pseudomon
1295	51.6	5.2	110000	1	AE017233	Continuation (32 o	1368	51.2	5.2	13802	1	STES79650	AEJ579650 Streptomy
1296	51.6	5.2	113193	1	AF357202	Streptomy	1369	51.2	5.2	22437	1	AF027524	AF027524 Frankia s
1297	51.6	5.2	113193	6	AX703543	Sequence	1370	51.2	5.2	77457	1	AF210249	AF210249 Streptomy
1298	51.6	5.2	14051	8	OSJN00036	AL606598 Oryza sat	1371	51.2	5.2	103458	8	AC108502	AC108502 Oryza sat
1299	51.6	5.2	150715	14	AX714813	AL714813 Cercopith	1372	51.2	5.2	110000	1	BX571965_11	Continuation (12 o
1300	51.6	5.2	169003	10	AC115699	AC115699 Mus muscu	1373	51.2	5.2	110000	1	BX571966_07	Continuation (8 of
1301	51.6	5.2	174139	2	AC116700	AC116700 Mus muscu	1374	51.2	5.2	110000	1	CP000010_07	Continuation (8 of
1302	51.6	5.2	192857	8	AP005605	AP005605 Oryza sat	1375	51.2	5.2	118018	8	AP005675	AP005675 Oryza sat
1303	51.6	5.2	213050	1	AL646067	AL646067 Ralstonia	1376	51.2	5.2	137650	8	AC130600	AC130600 Oryza sat
1304	51.6	5.2	226889	14	AC146905	AC146905 Human Her	1377	51.2	5.2	165634	2	CR354375	CR354375 Danio rer
1305	51.6	5.2	229483	14	AC148951	AC148951 Human Her	1378	51.2	5.2	185437	8	AP005422	AP005422 Oryza sat
1306	51.6	5.2	231236	14	AX315197	AX315197 Human her	1379	51.2	5.2	189370	1	AF010496	AF010496 Rhodobact
1307	51.6	5.2	234881	14	AC146906	AC146906 Human Her	1380	51.2	5.2	267320	2	AC106562	AC106562 Rattus no
1308	51.6	5.2	290850	1	SC0939127	AL939127 Streptomy	1381	51.2	5.2	293050	1	SC0939116	AL939116 Streptomy
1309	51.6	5.2	291000	1	SC0939105	AL939105 Streptomy	1382	51.2	5.2	298550	1	AP005029	AP005029 Streptomy
1310	51.6	5.2	299050	1	SC0939104	AL939104 Streptomy	1383	51.2	5.2	300425	1	AP005022	AP005022 Streptomy
1311	51.6	5.2	299425	1	AP005037	AP005037 Streptomy	1384	51.2	5.2	301925	1	AP005046	AP005046 Streptomy
1312	51.6	5.2	299550	1	AP005031	AP005031 Streptomy	1385	51.2	5.2	313200	1	AP005214	AP005214 Corynebac
1313	51.6	5.2	301399	1	BX640417	AE017233 Mycobacte	1386	51.2	5.2	348997	1	BX640427	BX640427 Bordetell
1314	51.6	5.2	348934	1	BX640417	BX640417 Bordetell	1387	51.2	5.2	349028	1	BX640413	BX640413 Bordetell
1315	51.6	5.2	348997	1	BX640427	BX640427 Bordetell	1388	51.2	5.2	349305	1	BX640433	BX640433 Bordetell
1316	51.6	5.2	349008	1	BX640444	BX640444 Bordetell	1389	51.2	5.2	473	1	AB066368	AB066368 Streptomy
1317	51.6	5.2	349016	1	AP003003	AP003003 Mesorhizo	1390	51.2	5.2	473	1	AB066369	AB066369 Streptomy
1318	51.6	5.2	349640	1	BX572600	BX572600 Rhodosphe	1391	51.2	5.2	591	12	AY658503	AY658503 Synthetic
1319	51.4	5.2	985	8	AK058890	AK058890 Oryza sat	1392	51.2	5.2	846	6	BD179798	BD179798 Highly th
1320	51.4	5.2	1746	6	AF425992	AF425992 Streptomy	1393	51.2	5.2	959	8	AY513924	AY513924 Zea mays
1321	51.4	5.2	1926	6	AX811493	AX811493 Sequence	1394	51.2	5.2	1004	8	AY513936	AY513936 Zea mays
1322	51.4	5.2	2454	8	AF022816	AF022816 Chlamydom	1395	51.2	5.2	1007	8	AF377762	AF377762 Zea mays
1323	51.4	5.2	2826	9	HSCBFA	Y11525 H.sapiens m	1396	51.2	5.2	1008	8	AF377752	AF377752 Zea mays
1324	51.4	5.2	3292	10	MUSHPTA2	M76613 Mouse heat	1397	51.2	5.2	1008	8	AF377755	AF377755 Zea mays
1325	51.4	5.2	3520	5	AY008272	AY008272 Gallus ga	1398	51.2	5.2	1008	8	AF377763	AF377763 Zea mays
1326	51.4	5.2	4725	6	AX697993	AX697993 Sequence	1399	51.2	5.2	1008	8	AF377764	AF377764 Zea mays
1327	51.4	5.2	7916	1	ASV18523	Y18523 Actinoplane	1400	51.2	5.2	1012	8	AF377748	AF377748 Zea mays
1328	51.4	5.2	10968	1	AY204471	AY204471 Myxococcu	1401	51.2	5.2	1012	8	AF377749	AF377749 Zea mays
1329	51.4	5.2	12855	1	AF533985	AF533985 Streptomy	1402	51.2	5.2	1012	8	AF377754	AF377754 Zea mays
1330	51.4	5.2	14999	3	AF218621S1	AF218621 Nephila c	1403	51.2	5.2	1012	8	AF377756	AF377756 Zea mays
1331	51.4	5.2	30000	6	AX250262	AX250262 Sequence	1404	51.2	5.2	1012	8	AF377765	AF377765 Zea mays
1332	51.4	5.2	35138	9	AL353799	Human DNA	1405	51.2	5.2	1012	8	AF377766	AF377766 Zea mays
1333	51.4	5.2	103450	1	AF440781	AF440781 Streptomy	1406	51.2	5.2	1014	8	AF377746	AF377746 Zea mays





```

QY 961 GCTGGGACACAAAAA 989
Db 961 GCTGGGACACAAAAA 989

RESULT 3
AY358476 989 bp mRNA linear PRI 03-OCT-2003
LOCUS Homo sapiens clone DNA71282 methyltransferase (UNQ766) mRNA,
DEFINITION complete cds.
ACCESSION AY358476
VERSION AY358476.1 GI:37182074
KEYWORDS FL1_CDNA
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 989)
AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
Stinson,J., Vagts,A., Vanden,R., Watanabe,C., Wieand,D., Woods,K.,
Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
Goddard,A., Wood,W.I. and Godowski,P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)
JOURNAL 12975309
PUBMED 2 (bases 1 to 989).
REFERENCE Clark,H.F.
AUTHORS Direct Submission
TITLE Department of Bioinformatics, Genentech,
JOURNAL Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES
source
location/Qualifiers
1..989
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DNA71282"
1..989
/locus_tag="UNQ766"
84..872
/locus_tag="UNQ766"
/note="PRO1558"
/codon_start=1
/product="methyltransferase"
/protein_id="AAQ8840.1"
/db_xref="GI:37182075"
/tranlation="MTQPVRLSVPAALGSAALGAAPATGLFLGRCPWRGRREQ
CLLPEDSLRWYLLSRMREPALRSLLLEQPGDSMTCEQAQLIANLIQ
AKKALDGTFTGYSAALALPADRVVTCVDAPQELGPLMRQAEHKLRL
KPALETDLLEAGAEATDVADAKENCASAYRRCIQLLRPGSILAVLVLWRGK
VLQPPKGVAAECVRLNERIRRDVRVYISLLPLGDLTAFKI"

Query Match 100.0%; Score 989; DB 9; Length 989;
Best Local Similarity 100.0%; Pred. No. 7.7e-125;
Matches 989; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGGCCCGGAGCTCGAGACCTGTCCAGGAGCTCCAGTCACTACGACCTGTCACTGCC 60
Db 1 GCGGGCCCGGAGCTCGAGACCTGTCCAGGAGCTCCAGTCACTACGACCTGTCACTGCC 60
KEYWORDS

QY 61 TCCCGCGGCTCTCTGCGCGGCATGACCCAGCGGTCGCCGCTCTCCGTGCGCGCG 120
Db 61 TCCCGCGGCTCTCTGCGCGGCATGACCCAGCGGTCGCCGCTCTCCGTGCGCGCG 120
QY 121 CGCTGGCCCTCGGCTCAGCGGCACTGGGCGCGCCTTCGCCACTGSCCTCTTCTGGGGA 180

```

JOURNAL	thereof
Patent:	WO 0183719-A 1 08-NOV-2001;
Millennium Pharmaceuticals, Inc. (US)	
Location/Qualifiers	
source	1. .1037
	/organism="Homo sapiens"
	/mol_type="unassigned DNA"
	/db_xref="taxon:9606"
	113. .901
CDS	/note="unnamed protein product"
	/codon_start=1
	/protein_id="CAD20539.1"
	/db_xref="GI:1812894"
	/translation="MTQPVRLSVPAALAGSAAAGAAATGFLGRCPWRGREG
	CLLPDRLMQVLLSRMREHPALRSLLLEQPGDSMMTCQAQLLANLARLIQ
	AKKALDGTFTGSALALALAPALRVVTCEVDAPQBELGPLMRQAEAEKHIDLRL
	KPALETLLAAGAEAGTDFVAVDADKENCAYSAYERCILQLLRPGGILAVLRVLRGK
	VLQPPKGDVAACEVRNLNERIRRDVRVYISLLPLGDLTLAFKI"
ORIGIN	
Query Match	99.7%; Score 985.8; DB 6; Length 1037;
Best Local Similarity	99.8%; Pred. No. 2.1e-124;
Matches 987; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
QY	1 GCGGGCCCGCGAGTCCGAGACCTGTCGCCAGGAGCTCCAGCTACGCTGACCTGTCACTGCC 60
DB	
QY	30 GCGGGCCCGCGAGTCCGAGACCTGTCGCCAGGAGCTCCAGCTACGCTGACCTGTCACTGCC 89
DB	
QY	61 TCCCGCGGCTCTCTGCTCCGCGCATGACCCAGCCGGTGCCTCCGCTCTCTCCGTGCCGCG 120
DB	
QY	90 TCCCGCGGCTCTCTGCTCCGCGCATGACCCAGCCGGTGCCTCCGCTCTCTCCGTGCCGCG 149
DB	
QY	121 CGTGGCCCTCGGCTCAGCGGCTGCGGCGCGCTTCGCGCATGCGCTCTCTCTCGGGA 180
DB	
QY	150 CGTGGCCCTCGGCTCAGCGGCTGCGGCGCGCTTCGCGCATGCGCTCTCTCTCGGGA 209
DB	
QY	181 GCGGTGCCCCCATGCGGAGCGCGGAGAGCAGTCTGCTTCCCGCGGAGCAGCC 240
DB	
QY	210 GCGGTGCCCCCATGCGGAGCGCGGAGAGCAGTCTGCTTCCCGCGGAGCAGCC 269
DB	
QY	241 GCGTGGCAGTATCTTCTGAGCGCTTCCATGCGGAGCAGCCGGCGCTGCGAAGCCTGA 300
DB	
QY	270 GCGTGGCAGTATCTTCTGAGCGCTTCCATGCGGAGCAGCCGGCGCTGCGAAGCCTGA 329
DB	
QY	301 GCGTGGTACCTGGAGCGCGCAGCGGAGTCTATGATGACCTGCGAGCGGCCCGC 360
DB	
QY	330 GCGTGGTACCTGGAGCGCGCAGCGGAGTCTATGATGACCTGCGAGCGGCCCGC 389
DB	
QY	361 TCTTGGCCAACTGGCGCGCTCATCCAGGCCAAGAGCGCTGGACCTGGGCACCTTCA 420
DB	
QY	390 TCTTGGCCAACTGGCGCGCTCATCCAGGCCAAGAGCGCTGGACCTGGGCACCTTCA 449
DB	
QY	421 CGGGCTACTCCGCTTGGCCCTTGGCCCTTGGCCCTTGGCCCTTGGCCCTTGGCCCTT 480
DB	
QY	450 CGGGCTACTCCGCTTGGCCCTTGGCCCTTGGCCCTTGGCCCTTGGCCCTTGGCCCT 509
DB	
QY	481 GCGAGTGACGCGCGCGCGCGAGCTGGGACGCGCCCTTGTGGAGCGAGCGCGCGG 540
DB	
QY	510 GCGAGTGACGCGCGCGCGCGAGCTGGGACGCGCCCTTGTGGAGCGAGCGCGCGG 569
DB	
QY	541 AGCACAAGATGACCTTCCGGCTGAAGCCCGCTTGGAGACCTTGGAGAGCTTGGCGG 600
DB	
QY	570 AGCACAAGATGACCTTCCGGCTGAAGCCCGCTTGGAGACCTTGGAGAGCTTGGCGG 629
DB	
QY	601 CGGGCGAGCGCGCACCTTTCGAGCTGGCGCTGGTGGATCGGACGAGGAGAACTGCTCCG 660
DB	
QY	630 CGGGCGAGCGCGCACCTTTCGAGCTGGCGCTGGTGGATCGGACGAGGAGAACTGCTCCG 689
DB	
QY	661 CCTACTACGAGCGCTGCTGAGCTGCTCGAGCCCGAGGAGCATCTCGCGCTCTCAGAG 720
DB	
QY	690 CCTACTACGAGCGCTGCTGAGCTGCTCGAGCCCGAGGAGCATCTCGCGCTCTCAGAG 749
DB	
QY	721 TCCTGTGGCGCGGGAAGGTGCTGCAACCTCCGAAAGGGGACGTGGCGGCGGAGTGTGTGC 780

Db	750																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
----	-----	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--



R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>  
 Series: IRAK plate: 98 Row: 9 Column: 5  
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21389376.

## FEATURES

source

1..1041  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="MGC:54273 IMAGE:5761696"  
 /tissue\_type="lung, spleen, fetal, pooled"  
 /clone\_lib="NIH MGC\_122"  
 /lab\_host="DH10B"  
 /note="Vector: pCMV-SPORT6"  
 1..1041  
 /gene="COMT1"  
 /note="synonym: FLJ23841"  
 /db\_xref="LocusID:118881"  
 85..873  
 /gene="COMT1"  
 /codon\_start=1  
 /product="catechol-O-methyltransferase domain containing 1"  
 /protein\_id="AAH47774.1"  
 /db\_xref="GI:28839537"  
 /db\_xref="LocusID:118881"  
 /translation="MTQPVRLSVPAALALGSAALGAAPATGLFLGRCPVWRBREQ  
 CLLPEDSRLLWYLLSRNREHPALRSLLLEQPGDSMMTCQOALLANLRLIQ  
 AKKALDLGFTGYSALALALPADRVVTCEVDQPPELGRPLRQAEKHIDRL  
 KPALSTDELLAAGAGTFDVAVDADKENCASVYERCIQLLRPGILLAVLRWKG  
 VLQPPKGDVAABECVRLNERIRRDVRYVVISLLPLDGLTLAFKI"

## ORIGIN

Query Match 99.7%; Score 985.8; DB 9; Length 1041;  
 Best Local Similarity 99.8%; Pred. No. 2,1e-124;  
 Matches 987; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCGGCGCGGAGTCCGAGACCTGTCACAGGAGCTCCAGCTCAGCTGACCTGCTCACTGCC 60  
 DB |||||  
 QY 2 GCGGCGCGGAGTCCGAGACCTGTCACAGGAGCTCCAGCTCAGCTGACCTGCTCACTGCC 61  
 DB |||||

QY 61 TCCCGCGGCTCTGTCGCGCGCATGACCCAGCCGCTGTCGCGGCTCTCCGTCGCCGCGC 120  
 DB |||||

QY 62 TCCCGCGGCTCTGTCGCGCGCATGACCCAGCCGCTGTCGCGGCTCTCCGTCGCCGCGC 121  
 DB |||||

QY 121 CGCTGGCTTGGCTCAGCCGACCTGGGCGCGCCCTTCCGCTGCTGCTTCTTCTGGGGA 180  
 DB |||||

QY 122 CGCTGGCTTGGCTCAGCCGACCTGGGCGCGCCCTTCCGCTGCTGCTTCTTCTGGGGA 181  
 DB |||||

QY 181 GCGGTGCCCCCATGGCGAGCGCGGAGAGAGTCCGCTTCCCCCGGAGGACAGCC 240  
 DB |||||

QY 182 GCGGTGCCCCCATGGCGAGCGCGGAGAGAGTCCGCTTCCCCCGGAGGACAGCC 241  
 DB |||||

QY 241 GCTGTGGCAGTATCTTCTGAGCGCTTCCATGGCGGAGCACCAGCGCTGCGAAGCTCA 300  
 DB |||||

QY 242 GCTGTGGCAGTATCTTCTGAGCGCTTCCATGGCGGAGCACCAGCGCTGCGAAGCTCA 301  
 DB |||||

QY 301 GCGTGTGACCTGGAGCAGCGCGGAGGATTTCTATGATGACCTGCGAGCAGGCCCCAGC 360  
 DB |||||

QY 302 GCGTGTGACCTGGAGCAGCGCGGAGGATTTCTATGATGACCTGCGAGCAGGCCCCAGC 361  
 DB |||||

QY 361 TCTTGGCCAACTGGCGCGGCTCATCCAGGCCAAGAGCGCTGAGCTGGGCACTTCA 420  
 DB |||||

QY 362 TCTTGGCCAACTGGCGCGGCTCATCCAGGCCAAGAGCGCTGAGCTGGGCACTTCA 421  
 DB |||||

QY 421 CCGGGTACTCCGCGCTTGGCGCTGCGCGCTGCGCGGAGCGCGCTGCTGACCT 480  
 DB |||||

QY 422 CCGGGTACTCCGCGCTTGGCGCTGCGCGCTGCGCGGAGCGCGCTGCTGACCT 481  
 DB |||||

QY 481 GCGAGGTGAGCGCAGCGCCCGCGAGCTGGGACGCGCCCTGTGTGGAGCGCGCGGCGG 540  
 DB |||||

Db 482 GCGAGGTGAGCGCGCAGCGCCCGGAGCTGGGACGCGCCCTGTGGAGCGAGCGCGCGG 541  
 QY 541 AGCACAAAGATGACCTCCGGCTGAAGCCCGCTTGGAGACCTTGGACGAGCTGCTGGCGG 600  
 DB 542 AGCACAAAGATGACCTCCGGCTGAAGCCCGCTTGGAGACCTTGGACGAGCTGCTGGCGG 601  
 QY 601 CGGGGAGCGCGGACCTTTCGACGCTGGCGCTGTGTGATGCGGACAAAGAGAACTGCTCG 660  
 DB 602 CGGGGAGCGCGGACCTTTCGACGCTGGCGCTGTGTGATGCGGACAAAGAGAACTGCTCG 661  
 QY 661 CCTACTAGAGCGCTGCTGACGCTGCTGCGACCGGAGGCACTCTCGCCCTCTCAGAG 720  
 DB 662 CCTACTAGAGCGCTGCTGACGCTGCTGCGACCGGAGGCACTCTCGCCCTCTCAGAG 721  
 QY 721 TCTGTGGCGCGGGAAGTGTCTGCAACCTCCGAAAGGAGCGCTGGCGCGGAGTGTGTC 780  
 DB 722 TCTGTGGCGCGGGAAGTGTCTGCAACCTCCGAAAGGAGCGCTGGCGCGGAGTGTGTC 781  
 QY 781 GAAACCTAAACGAAACGCAATCCGCGCGGAGCTCAGGGTCTACATCAGCTCTCTGCCCTGG 840  
 DB 782 GAAACCTAAACGAAACGCAATCCGCGCGGAGCTCAGGGTCTACATCAGCTCTCTGCCCTGG 841  
 QY 841 GCGATGGACTACCTTGGCGCTTCAAGATCTAGGGCTGCGCCCTAGTGTAGTGGCTCGAG 900  
 DB 842 GCGATGGACTACCTTGGCGCTTCAAGATCTAGGGCTGCGCCCTAGTGTAGTGGCTCGAG 901  
 QY 901 GAGGTTGCTGGGAACCCAGGAATTCACCTGAGTTTAAATTCGAAATAAAGTGGG 960  
 DB 902 GAGGTTGCTGGGAACCCAGGAATTCACCTGAGTTTAAATTCGAAATAAAGTGGG 961  
 QY 961 GCTGGGACACAAAAAAGGCTGCTGCAACCTCCGAAAGGAGCGCTGGCGCGGAGTGTGTC 989  
 DB 962 GCTGGGACACAAAAAAGGCTGCTGCAACCTCCGAAAGGAGCGCTGGCGCGGAGTGTGTC 990

RESULT 6  
 BD222712  
 LOCUS Human signal peptide-containing protein. 985 bp DNA linear PAT 17-JUL-2003  
 DEFINITION  
 ACCESSION BD222712  
 VERSION BD222712.1 GI:33032482  
 KEYWORDS JP 2002519030-A/58.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 LAL,P., Tang,Y.T., Gorgone,G.A., Corley,N.C., Guegler,K.J.,  
 Baughn,M.R., Akersblom,I.E., Young,J.A., Yue,H., Patterson,C.,  
 Reddy,R., Hillman,J.L. and Bandman,O.  
 Human signal peptide-containing protein  
 Patent: JP 2002519030-A 58 02-JUL-2002;  
 INCYTE PHARMACEUTICALS INC  
 OS Homo sapiens (human)  
 PN JP 2002519030-A/58  
 PD 02-JUL-2002  
 PF 25-JUN-1999 JP 2000557363  
 PR 26-JUN-1998 US 60/090762,31-JUL-1998 US 60/094983 PR  
 01-OCT-1998 US 60/102686,11-DEC-1998 US 60/112129 PI PREETI  
 LAL,Y TOM TANG,GINA A GORGONE,NEIL C CORLEY,KARL J PI GUEGLER,  
 PI MARIAH R BAUGHN,INGRID E AKERBLUM,JANICE AU YOUNG,HENRY YUE,  
 PI CHANDRA PATTERSON,ROOPA REDDY,JENNIFER L HILLMAN,OLGA BANDMAN,  
 PC C12N15/09,A61K38/00,A61K39/395,A61K45/00,A61P5/00,A61P15/00,  
 PC A61P25/00,  
 PC A61P29/00,A61P35/00,A61P43/00,C07K14/47,C07K16/18,C12N1/15, PC  
 C12N1/19,  
 PC C12N1/21,C12N5/10,C12P21/02,C12Q1/68,G01N33/68//C12P21/08, PC  
 C12N15/00,  
 PC A61K37/02,C12N5/00  
 CC Incyte Clone No: 2816821  
 FH Key Location/Qualifiers  
 FT source 1..985

FEATURES	Location/Qualifiers		/organism='Homo sapiens (human)'	
	source	1..985		
ORIGIN	Query Match		99.3%; Score 981.8; DB 6; Length 985;	
	Best Local Similarity		99.8%; Pred. No. 7.3e-124; Mismatches 2; Indels 0; Gaps 0;	
QY	1		GCGGGCCGCGAGTCCGAGACCTGTGCCAGAGCTCCAGCTCACGTGACCTGTCACTGCC 60	
	DB			
QY	1		GCGGGCCGCGAGTCCGAGACCTGTGCCAGAGCTCCAGCTCACGTGACCTGTCACTGCC 60	
	DB			
QY	61		TCGCGCGGCTCTGCGCGGCGCATGACCCAGCGGTGCGCGGCTCTCCGTGCGCGCG 120	
	DB			
QY	121		CGCTGGCCTGGGCTCAGCGCACTGGGCGCGCTTGGCCACTGGCCCTCTTCTCGGGGA 180	
	DB			
QY	121		CGCTGGCCTGGGCTCAGCGCACTGGGCGCGCTTGGCCACTGGCCCTCTTCTCGGGGA 180	
	DB			
QY	181		GCGGTGCCCCCATGGCGAGGCGCGGAGAGCAGTGCTGCTTCCCCCGAGGACAGCC 240	
	DB			
QY	181		GCGGTGCCCCCATGGCGAGGCGCGGAGAGCAGTGCTGCTTCCCCCGAGGACAGCC 240	
	DB			
QY	241		GCCTGGCAGTATCTTTCGAGCGGTCTCATCGGGAGACCCGGCGGTGCGAAGCTGA 300	
	DB			
QY	241		GCCTGGCAGTATCTTTCGAGCGGTCTCATCGGGAGACCCGGCGGTGCGAAGCTGA 300	
	DB			
QY	301		GGCTGCTGACCTGGAGCAGCGCGAGGGGATCTATGATGACCTCGAGCAGGCGCCAGC 360	
	DB			
QY	301		GGCTGCTGACCTGGAGCAGCGCGAGGGGATCTATGATGACCTCGAGCAGGCGCCAGC 360	
	DB			
QY	361		TCTTGGCCAACTGGCGCGCTCATCCAGGCCAAGAAGCGCTGGACCTGGGCACCTTCA 420	
	DB			
QY	361		TCTTGGCCAACTGGCGCGCTCATCCAGGCCAAGAAGCGCTGGACCTGGGCACCTTCA 420	
	DB			
QY	421		CGGGCTACTCGGCCCTGGCCCTGGCCCTGGCCCTGGCCCTGGCCCTGGCCCTGGCCCT 480	
	DB			
QY	421		CGGGCTACTCGGCCCTGGCCCTGGCCCTGGCCCTGGCCCTGGCCCTGGCCCTGGCCCT 480	
	DB			
QY	481		GCGAGTGAACCGCAGCCCGCGAGCTGGGACGCGCCCTGTGGAGGAGCGCGAGGCGG 540	
	DB			
QY	481		GCGAGTGAACCGCAGCCCGCGAGCTGGGACGCGCCCTGTGGAGGAGCGCGAGGCGG 540	
	DB			
QY	541		AGCAAGATGACCTCCGGCTGAAGCCCGCTTGGAGACCTTGGAGACCTTGGAGCTGTGCGG 600	
	DB			
QY	541		AGCAAGATGACCTCCGGCTGAAGCCCGCTTGGAGACCTTGGAGACCTTGGAGCTGTGCGG 600	
	DB			
QY	601		CGGGCAGCGCGGACCTTTCGAGCTGGCGCTGGTGGATGCGGACCAAGAGAACTGCTCG 660	
	DB			
QY	601		CGGGCAGCGCGGACCTTTCGAGCTGGCGCTGGTGGATGCGGACCAAGAGAACTGCTCG 660	
	DB			
QY	661		CCTACTAGAGCGCTGCTGAGCTGCTGCGACCGGAGGCACTCTCCCGCTCTCAGAG 720	
	DB			
QY	661		CCTACTAGAGCGCTGCTGAGCTGCTGCGACCGGAGGCACTCTCCCGCTCTCAGAG 720	
	DB			
QY	721		TCCTGTGGCGGGGAAGTGTCTGCAACCTCCGAAAGGGGACGTGGCGGCGGAGTGTGTC 780	
	DB			
QY	721		TCCTGTGGCGGGGAAGTGTCTGCAACCTCCGAAAGGGGACGTGGCGGCGGAGTGTGTC 780	
	DB			
QY	781		GAAACCTAAACGAAACGATCCGGCGGGAGCTCAGGGTCTACATAGCTCTTCCGCCCTGG 840	
	DB			
QY	781		GAAACCTAAACGAAACGATCCGGCGGGAGCTCAGGGTCTACATAGCTCTTCCGCCCTGG 840	
	DB			
QY	841		GCGATGGACTACCTTGGCTTCAAGATCTAGGGCTGGCCCTCTAGTGGTGGCTCGAGG 900	
	DB			
QY	841		GCGATGGACTACCTTGGCTTCAAGATCTAGGGCTGGCCCTCTAGTGGTGGCTCGAGG 900	
	DB			
QY	901		GAGGGTTGCTGGGAACCCAGGAATTGACCTGAGTTTTAAATTCGAAATAAAGTGGG 960	
	DB			

FEATURES	Location/Qualifiers		/organism='Homo sapiens (human)'	
	source	1..985		
ORIGIN	Query Match		94.9%; Score 938.2; DB 9; Length 988;	
	Best Local Similarity		99.7%; Pred. No. 5.9e-118;	
QY	47		GACCTGTCACTCCCTCCCGCGCTTCTCTCCCGCGCCATGACCCAGCGGTGCCCGGCT 106	
	DB			
QY	1		GACCTGTCACTCCCTCCCGCGCTTCTCTCCCGCGCCATGACCCAGCGGTGCCCGGCT 60	
	DB			
QY	107		CTCGTGGCGCGCGCTGGCGCTTGGCGCTTGGCGCTTGGCGCTTGGCGCTTGGCGCT 166	
	DB			
QY	61		CTCGTGGCGCGCGCTTGGCGCTTGGCGCTTGGCGCTTGGCGCTTGGCGCTTGGCGCT 120	
	DB			

FEATURES	Location/Qualifiers		/organism='Homo sapiens'	
	source	1..988		
CDS	1		/mol_type="mRNA"	
			/db_xref="taxon:9606"	
			/clone="KAT04516"	
			/cell_lines="KATO III"	
			/cell_type="signet-ring cell carcinoma"	
			/clone_lib="KAT"	
			/note="cloning vector: pME18SFL3"	
			38..826	
			/note="unnamed protein product"	
			/codon_start=1	
			/protein_id="BAB85077.1"	
			/db_xref="GI:18677020"	
			/translation="MTQPVRLSVPAALGSAALGAATGATGLFLGRRCPPWRGRREQ	
			CLLPEDSRIMQVLLSRSMREHPALRLTLTPOQDYMWTCTQAOALLANLRLIQ	
			AKKALDGLTFTGYSALALALADPADRVVTCVDAQPELGRPLWRQAEAHKIDRL	
			KPALETDELLAAGEAGTFDVAVVDADKENCAYSERCLQLIRPGILAVLRLVRGK	
			VLQPFKGDVAACVRNLNLRIRDRVRYISLLPLGDDGLTAFKI"	

FEATURES	Location/Qualifiers		/organism='Homo sapiens'	
	source	1..988		
CDS	1		/mol_type="mRNA"	
			/db_xref="taxon:9606"	
			/clone="KAT04516"	
			/cell_lines="KATO III"	
			/cell_type="signet-ring cell carcinoma"	
			/clone_lib="KAT"	
			/note="cloning vector: pME18SFL3"	
			38..826	
			/note="unnamed protein product"	
			/codon_start=1	
			/protein_id="BAB85077.1"	
			/db_xref="GI:18677020"	
			/translation="MTQPVRLSVPAALGSAALGAATGATGLFLGRRCPPWRGRREQ	
			CLLPEDSRIMQVLLSRSMREHPALRLTLTPOQDYMWTCTQAOALLANLRLIQ	
			AKKALDGLTFTGYSALALALADPADRVVTCVDAQPELGRPLWRQAEAHKIDRL	
			KPALETDELLAAGEAGTFDVAVVDADKENCAYSERCLQLIRPGILAVLRLVRGK	
			VLQPFKGDVAACVRNLNLRIRDRVRYISLLPLGDDGLTAFKI"	

FEATURES	Location/Qualifiers		/organism='Homo sapiens'	
	source	1..988		
CDS	1		/mol_type="mRNA"	
			/db_xref="taxon:9606"	
			/clone="KAT04516"	
			/cell_lines="KATO III"	
			/cell_type="signet-ring cell carcinoma"	
			/clone_lib="KAT"	
			/note="cloning vector: pME18SFL3"	
			38..826	
			/note="unnamed protein product"	
			/codon_start=1	
			/protein_id="BAB85077.1"	
			/db_xref="GI:18677020"	
			/translation="MTQPVRLSVPAALGSAALGAATGATGLFLGRRCPPWRGRREQ	
			CLLPEDSRIMQVLLSRSMREHPALRLTLTPOQDYMWTCTQAOALLANLRLIQ	
			AKKALDGLTFTGYSALALALADPADRVVTCVDAQPELGRPLWRQAEAHKIDRL	
			KPALETDELLAAGEAGTFDVAVVDADKENCAYSERCLQLIRPGILAVLRLVRGK	
			VLQPFKGDVAACVRNLNLRIRDRVRYISLLPLGDDGLTAFKI"	

Db	901	GAGGGTGGCTGGGAACCCAGAAATGACCCCTGAGTTTAAATTCGAAATAAAGTGGG	960	
Qy	961	GCTGGGACACAAAAA	985	
Db	961	GCTGGGACACAAAAA	985	
RESULT 7				
AK074421				
LOCUS				
DEFINITION Homo sapiens cDNA FLJ23841 fis, clone KAT04516.				
ACCESSION AK074421				
VERSION AK074421.1 GI:18677019				
KEYWORDS oligo capping; fis (full insert sequence).				
SOURCE Homo sapiens (human)				
ORGANISM Homo sapiens				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
1				
Watanabe,K., Kumagai,A., Itakura,S., Yamazaki,M., Tashiro,H.,				
Ota,T., Suzuki,Y., Ohbayashi,M., Nishi,T., Shibahara,T., Tanaka,T.,				
Nakamura,Y., Isogai,T. and Sugano,S.				
NEDO human cDNA sequencing project				
Unpublished				
2 (bases 1 to 988)				
Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,				
Shibahara,T., Tanaka,T. and Nakamura,Y.				
Direct Submission				
Submitted (14-FEB-2002) Sumio Sugano, Institute of Medical Science,				
University of Tokyo, Laboratory of Genome Structure, Human Genome				
Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan				
(E-mail:flcdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,				
Fax:81-3-5449-5416)				
NEDO human cDNA sequencing project supported by Ministry of				
Economy, Trade and Industry of Japan; cDNA full insert sequencing:				
Research Association for Biotechnology; cDNA library construction,				
5'- and 3'-end one pass sequencing: Department of Virology and Human				
Genome Center, Institute of Medical Science, University of Tokyo				
(partly supported by Science and Technology Agency).				
FEATURES				
source				
1..988				
/organism="Homo sapiens"				
/mol_type="mRNA"				
/db_xref="taxon:9606"				
/clone="KAT04516"				
/cell_line="KATO III"				
/cell_type="signet-ring cell carcinoma"				
/clone_lib="KAT"				
/note="cloning vector: pME18SFL3"				
38..826				
/note="unnamed protein product"				
/codon_start=1				
/protein_id="BAB85077.1"				
/db_xref="GI:18677020"				
/translation="MTQPVRLSVPAALGSAALGAATGATGLFLGRRCPPWRGRREQ				
CLLPEDSLWYLLSRSMREHPALRLTLTPOQDYMWTCTQAOALLANLRLIQ				
AKKALDGLTFTGYSALALALADPADRVVTCVDAQPELGRPLWRQAEAHKIDRL				
KPALETDELLAAGEAGTFDVAVVDADKENCAYSERCLQLIRPGILAVLRLVRGK				
VLQPFKGDVAACVRNLNLRIRDRVRYISLLPLGDDGLTAFKI"				
CDS				
38..826				
/note="unnamed protein product"				
/codon_start=1				
/protein_id="BAB85077.1"				
/db_xref="GI:18677020"				
/translation="MTQPVRLSVPAALGSAALGAATGATGLFLGRRCPPWRGRREQ				
CLLPEDSLWYLLSRSMREHPALRLTLTPOQDYMWTCTQAOALLANLRLIQ				
AKKALDGLTFTGYSALALALADPADRVVTCVDAQPELGRPLWRQAEAHKIDRL				
KPALETDELLAAGEAGTFDVAVVDADKENCAYSERCLQLIRPGILAVLRLVRGK				
VLQPFKGDVAACVRNLNLRIRDRVRYISLLPLGDDGLTAFKI"				
ORIGIN				
Query Match 94.9%; Score 938.2; DB 9; Length 988;				
Best Local Similarity 99.7%; Pred. No. 5.9e-118;				
Matches 940; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
Qy	47	GACCTGTCACTGCTCCCGCGGCTCTCGCGCGGCATGACCCAGCGGTGCCCGGCT	106	
Db	1	GACCTGTCACTGCTCCCGCGGCTCTCGCGCGGCATGACCCAGCGGTGCCCGGCT	60	
Qy	107	CTCCGTGCCCCGGCGCTCGGCTCGACCGGCTCGGGCGCGCCCTTCGCCACTGG	166	
Db	61	CTCCGTGCCCCGGCGCTCGGCTCGACCGGCTCGGGCGCGCCCTTCGCCACTGG	120	











```
Best Local Similarity 99.7%; Pred. No. 5.9e-33;
Matches 323; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 649 AGAAGTGTCTCCGCC-TACTACGAGGCTGCTGAGCTGCTGCGACCCGAGGATCTCTC 707
Db 326 AGAAGTGTCTCCGCC-TACTACGAGGCTGCTGAGCTGCTGCGACCCGAGGATCTCTC 267

QY 708 GCCGTCTCTCAGAGTCTGTGGGCGGAGGAGTGTGCAACCTCCGAAAGGGACGTGGCG 767
Db 266 GCCGTCTCTCAGAGTCTGTGGGCGGAGGAGTGTGCAACCTCCGAAAGGGACGTGGCG 207

QY 768 GCCGAGTGTGCGAAACCTAAACGACGATCCGCGGAGCTCAGGCTCTACATCAGC 827
Db 206 GCCGAGTGTGCGAAACCTAAACGACGATCCGCGGAGCTCAGGCTCTACATCAGC 147

QY 828 CTCCTGCCCTGGCGATGACCTTGGCTTCAAGATCTAGGCTGGCCCTTAGTG 887
Db 146 CTCCTGCCCTGGCGATGACCTTGGCTTCAAGATCTAGGCTGGCCCTTAGTG 87

QY 888 AGTGGGCTCGAGGAGGTTGGCTGGGAACCCAGGAATGACCCCTGAGTTTAAATTCG 947
Db 86 AGTGGGCTCGAGGAGGTTGGCTGGGAACCCAGGAATGACCCCTGAGTTTAAATTCG 27

QY 948 AAAATAAGTGGGCTGGGACACA 971
Db 26 AAAATAAGTGGGCTGGGACACA 3

RESULT 13
AC120475 237829 bp DNA linear HTG 20-NOV-2002
LOCUS Rattus norvegicus clone CH230-34D17, WORKING DRAFT SEQUENCE, 2
DEFINITION AC120475
ACCESSION AC120475
VERSION 7 GI:25137871
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 237829)
Muzny,D.Marie., Metzker,M.Lee., Abramson,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswal,K., Blair,J., Blankenburg,K., Blych,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Caesar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.Lis., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Gebregorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
Gunaratne,P., Haaland,W., Hamill,C., Hamilton,C., Hamilton,K.,
Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,J.,
Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
Kowals,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
Lorensuhewa,L., Loulseghe,H., Lozado,R.J., Lu,X., Ma,J.,
Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
Mawhney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
```

TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

COMMENT

Nwaekemele, O., Okwuonu, G., Olarpunsgoon, A., Pal, S., Parks, K.,  
Pasternak, S., Paul, H., Perez, A., Perez, L., Pfankuch, C.,  
Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L.,  
Puzo, M., Quirio, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R.,  
Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,  
Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J.,  
Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,  
Shetty, J., Shvartsbeyn, A., Sison, I., Sitter, C.D., Smajs, D.,  
Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,  
Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,  
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,  
Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J.,  
Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,  
Williams, G., Willson, R., Wlezyk, R., Wooden, H., Worley, K.,  
Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,  
Yu, F., Zhang, J., Zhou, X., Zhou, X., Zhao, S., Dunn, D., von  
Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,  
Weinstock, G. and Gibbs, R.A.  
Direct Submission  
Unpublished  
2 (bases 1 to 237829)  
Worley, K.C.  
Direct Submission  
Submitted (07-MAY-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 237829)  
Rat Genome Sequencing Consortium.  
Direct Submission  
Submitted (20-NOV-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA  
On Nov 20, 2002 this sequence version replaced gi:23267656.  
The sequence in this assembly is a combination of BAC based reads  
and whole genome shotgun sequencing reads assembled using Atlas  
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described  
in the feature table below represents a scaffold in the Atlas  
assembly (a 'contig-scaffold'). Within each contig-scaffold,  
individual sequence contigs are ordered and oriented, and separated  
by sized gaps filled with Ns to the estimated size. The sequence  
may extend beyond the ends of the clone and there may be sequence  
contigs within a contig-scaffold that consist entirely of whole  
genome shotgun sequence reads. Both end sequences and whole genome  
shotgun sequence only contigs will be indicated in the feature  
table.  
----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: http://www.hgsc.bcm.tmc.edu/  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: GXLH  
Center clone name: CH230-34D17  
----- Summary Statistics  
Assembly program: Phrap; version 0.990329  
Consensus quality: 218320 bases at least Q40  
Consensus quality: 223359 bases at least Q30  
Consensus quality: 225092 bases at least Q20  
Estimated insert size: 222440; sum-of-contigs estimation  
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation  
-----  
\* NOTE: Estimated insert size may differ from sequence length  
\* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank\_draft\_data.html).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 2 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
\* 1 236267: contig of 236267 bp in length  
\* 236268 236367: gap of unknown length

FEATURES	* 236368 237829: contig of 1462 bp in length.	
	source	Location/Qualifiers
misc_feature	1..237829	/organism="Rattus norvegicus"
		/mol_type="genomic DNA"
misc_feature	1..1400	/db_xref="taxon:10116"
		/clone="CH230-34D17"
misc_feature	2227..3684	/note="wgs end extension"
		/clone_end:Sp6"
misc_feature	7112..7990	/note="clone boundary"
		/clone_end:Sp6"
misc_feature	end:sequence:BH35953"	site:
	complement(233022..233942)	end:sequence:BH35953"
misc_feature	note="clone boundary"	site:
	clone_end:T7	end:sequence:BH358581"
ORIGIN	31.3%; Score 309.2; DB 2; Length 237829;	
	Query Match	Best Local Similarity 69.6%; Pred. No. 2.6e-33;
	Matches 433; Conservative 0; Mismatches 188; Indels 1; Gaps 1;	
	QY 53 TCACGTCTCCCGCCGCTCTCTCCCGCCGACCCAGCCAGCGGTGCCCGCTCTCCGT 112	
	Db 81826 TTACTGGTCCCACTCTGTCCTCTACTCCAGCACACGTGACCTCTGCTTGTCTAACT 81885	
	QY 113 GCCCGCGCGCTGGCGCTGGCTCAGCCACACTGGCGCGCTTGGCCACTGGGCTCTT 172	
	Db 81886 CGCACATGGCCAGCCGCTGCTGGCTGTCTATTCCACCGCGCTGGCCCTTCGCTCT 81945	
	QY 173 CTTGGGAGCGGTGCCCCCCTGAGCGAGCGCGGAGAGTGTCTGCTTCCCCCGCA 232	
	Db 81946 CTTGGGAAATGGTGGCTCGTGGGGTTCAGATGGCATGACACTGCTGCCCTTCA 82005	
	QY 233 GGACAGCCGCTGTGGCAGTATCTTGTAGCGCTCCATCGGGAGCACCCGCGCTGGG 292	
	Db 82006 GGACAATCCCTGTGGCAGTATCTGTAGCTGCTCCATGAGGGAACACCCAGCGCTGG 82065	
	QY 293 AAGCCTGAGCTGTGACCTGAGCAGCGCAGGGGATTTCTATGATGACCTGCGAGCA 352	
	Db 82066 GAGCCTGGACTGCTGACCTGGAGCAGCGCAGGGGGATTCATGATGACCTGTGAACA 82125	
	QY 353 GGCCCAAGCTCTTGGCCAACTGGCGCGGCTCATCCAGGCCAAGAGCGGCTGGACTGGG 412	
	Db 82126 GGCCCAACTTCTGGTCACTGGCGCGGCTCATCAAGCCAGAAAGCTCTGGATCTGGG 82185	
	QY 413 CACCTTCAAGGCTA-CTCCGCTGGCCCTGGCCCTGGCGTGGCGGACGCGCGCG 471	
	Db 82186 TACTTTTACGGGCTACTTCGGCCCTGGCCCTAGCCTTGGCGCTTCCGAGGCTGGCGCG 82245	
	QY 472 TGGTCACTTGGAGGTGAGCGCGAGCCCGGAGCTGGGACGGCCCTTGGAGCGAGG 531	
	Db 82246 TGGTCACTTGGAGGTGAGCGAGCGAGCCCGGAGCTGGGAGGGCCCTTGTGGAAGCAGA 82305	
	QY 532 CGAGCGGAGCACAAGATCGACTCCGCTCAAGCCCGCTTGGAGACCTTGGACGAGC 591	
	Db 82306 CAGAGTGGAGCAGAAGATCGAACTTGGCTGCACCCCGCTTGGATGAGT 82365	
	QY 592 TGTGGCGCGGCGAGCGCCGACCTTTCGAGTGGCCGCTGGTGGATGGGACAAAGGAGA 651	
	Db 82366 TCCTGGCGCGGCTGAGCGACATAGCAGTGGTGGAGCGCAGCAAGCTTACTACGAGCA 82425	
	QY 652 ACTGCTCCGCTACTACGAGCG 673	
	Db 82426 CTGCTGCAACTCTTACGCCCG 82447	

RESULT 14	AL390034	38679 bp	DNA	linear	PRI 01-JAN-2002
LOCUS	AL390034/c				
DEFINITION	Human DNA sequence from clone RP11-375G3 on chromosome 10, complete sequence.				
ACCESSION	AL390034				
VERSION	AL390034.23	GI:18041549			
KEYWORDS	HTG.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 38679)				
AUTHORS	Wray, P.				
TITLE	Direct Submission				
JOURNAL	Submitted (01-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk				
COMMENT	On Jan 2, 2002 this sequence version replaced gi:18032099. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em.; EMBL; SW.; SWISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr10 RP11-375G3 is from the library RPI1-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: pBAC3.6 IMPORTANT: This sequence is not the entire insert of clone RP11-375G3 It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true left end of clone RP11-399K21 is at 36680 in this sequence. The true right end of clone RP11-487I5 is at 2000 in this sequence.				
FEATURES	Location/Qualifiers				
source	1..38679				
	/organism="Homo sapiens"				
	/mol_type="genomic DNA"				
	/db_xref="taxon:9606"				
	/chromosome="10"				
	/clone="RP11-375G3"				
	/clone_lib="RPI1-11.2"				
misc_feature	29061..29121				
	/note="Sequence from uni-directional dGTP big dye terminator reads only."				
ORIGIN					
Query Match	26.0%; Score 256.8; DB 9; Length 38679;				
Best Local Similarity	97.4%; Pred. NO. 5.3e-26;				
Matches 261; Conservative 0; Mismatches 7; Indels 0; Gaps 0;					
QY 704 CTTGGCCCTCTCAGATCTCTGTGGCGGGAGGTGCTGCAACTCCGAAGGGAGCT 763					
Db 7761 CCCGCCCTCCCGAGGTCCTGTGGCGGGAGAGTGTCTGCAACTCCGAAGGGAGCT 7702					



QY 764 GCGCGCGAGTGTGTGCGAAGCTTAAACGACGATCCGCGGCGAGCTCAGGCTCTACAT 823  
 DB 7701 GCGCGCGAGTGTGTGCGAAGCTTAAACGACGATCCGCGGCGAGCTCAGGCTCTACAT 7642  
 QY 824 CAGCCTCTCTGCGCCCTGCGCGATCGAGTCACTTGGCTTCAAGATCTTAGGGCTGGCCCT 883  
 DB 7641 CAGCCTCTCTGCGCCCTGCGCGATCGAGTCACTTGGCTTCAAGATCTTAGGGCTGGCCCT 7582  
 QY 884 AGTGAAGTGGCTCGAGGGAGGTTGCTGGGAACCCAGGAATTGACCTTGAATTTTAA 943  
 DB 7581 AGTGAAGTGGCTCGAGGGAGGTTGCTGGGAACCCAGGAATTGACCTTGAATTTTAA 7522  
 QY 944 TTCGAAATAAAGTGGGCTGGGACACA 971  
 DB 7521 TTCGAAATAAAGTGGGCTGGGACACA 7494

RESULT 15  
 AC027393/c  
 LOCUS  
 DEFINITION Homo sapiens chromosome 10, clone RP11-770D23 map 10, WORKING DRAFT  
 AC027393  
 VERSION 3 GI:8076860  
 KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 169612)  
 Birren,B., Linton,L., Nusbaum,C. and Lander,E.  
 Homo sapiens chromosome 10, clone RP11-770D23  
 Unpublished  
 2 (bases 1 to 169612)  
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,  
 Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,  
 Boguslavsky,L., Bouckagter,B., Brown,A., Burkett,G.,  
 Campopiano,A., Castelle,A., Choepel,Y., Colangelo,M., Collins,S.,  
 Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,  
 Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,  
 Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,  
 Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,  
 Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,  
 Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J.,  
 Levine,R., Lie,C., Liu,C., Locke,K., Macdonald,P., Marquis,N.,  
 McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,  
 Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mienga,V., Morrow,J.,  
 Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,  
 O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,  
 Pisanic,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,  
 Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,  
 Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,  
 Testaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,  
 Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,  
 Young,G., Zainoun,J., Zimmer,A. and Zody,M.

Direct Submission  
 Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 3 (bases 1 to 169612)  
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,  
 Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,  
 Boguslavsky,L., Bouckagter,B., Brown,A., Burkett,G.,  
 Campopiano,A., Castelle,A., Choepel,Y., Colangelo,M., Collins,S.,  
 Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,  
 Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,  
 Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,  
 Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,  
 Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,  
 Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J.,  
 Levine,R., Lie,C., Liu,C., Locke,K., Macdonald,P., Marquis,N.,  
 McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,  
 Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mienga,V., Morrow,J.,  
 Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,  
 O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,  
 Pisanic,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,  
 Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,  
 Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,  
 Testaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,  
 Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,  
 Young,G., Zainoun,J., Zimmer,A. and Zody,M.

TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS

O'Neill,D., Oliver,T.M., Oliver,J., Peterson,K., Pierre,N.,  
 Pisanic,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,  
 Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,  
 Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,  
 Testaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,  
 Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,  
 Young,G., Zainoun,J., Zimmer,A. and Zody,M.

Direct Submission  
 Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On May 25, 2000 this sequence version replaced gi:7652066.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RW/RepeatMasker.html  
 ----- Genome Center  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIBR  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu  
 ----- Project Information  
 Center project name: L6572  
 Center clone name: 770\_D\_23  
 ----- Summary Statistics  
 Sequencing vector: M13; M7815; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.960731  
 Consensus quality: 155213 bases at least Q40  
 Consensus quality: 162022 bases at least Q30  
 Consensus quality: 164973 bases at least Q20  
 Insert size: 179000; agarose-fp  
 Insert size: 166912; sum-of-coverage  
 Quality coverage: 4.1 in Q20 bases; agarose-fp  
 Quality coverage: 4.4 in Q20 bases; sum-of-coverage  
 -----  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 28 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
 \*  
 \* 1 1191: contig of 1191 bp in length  
 \* 1192 1291: gap of 100 bp  
 \* 1292 2404: contig of 1113 bp in length  
 \* 2405 2504: gap of 100 bp  
 \* 2505 3705: contig of 1201 bp in length  
 \* 3706 3805: gap of 100 bp  
 \* 3806 4734: contig of 929 bp in length  
 \* 4735 4834: gap of 100 bp  
 \* 4835 6570: contig of 1736 bp in length  
 \* 6571 6670: gap of 100 bp  
 \* 6671 8583: contig of 1913 bp in length  
 \* 8584 8683: gap of 100 bp  
 \* 8684 10290: contig of 1607 bp in length  
 \* 10291 10390: gap of 100 bp  
 \* 10391 11939: contig of 1548 bp in length  
 \* 11939 12038: gap of 100 bp  
 \* 12039 15839: contig of 3801 bp in length  
 \* 15840 19203: contig of 3264 bp in length  
 \* 19204 19303: gap of 100 bp  
 \* 19304 22581: contig of 3278 bp in length  
 \* 22582 22681: gap of 100 bp  
 \* 22682 25947: contig of 2266 bp in length  
 \* 25948 28167: contig of 3120 bp in length  
 \* 28168 28267: gap of 100 bp  
 \* 28268 32083: contig of 3816 bp in length  
 \* 32084 32183: gap of 100 bp  
 \* 32184 35533: contig of 3350 bp in length  
 \* 35534 35634: gap of 100 bp  
 \* 41517: contig of 5884 bp in length

```
* 41518 41617: gap of 100 bp
* 41618 47143: contig of 5526 bp in length
* 47144 47243: gap of 100 bp
* 47244 51694: contig of 4451 bp in length
* 51695 51794: gap of 100 bp
* 51795 57570: contig of 5776 bp in length
* 57571 57670: gap of 100 bp
* 57671 63190: contig of 5520 bp in length
* 63191 63290: gap of 100 bp
* 63291 70708: contig of 7418 bp in length
* 70709 70808: gap of 100 bp
* 70809 78988: contig of 8180 bp in length
* 78989 79089: gap of 100 bp
* 79089 86527: contig of 7439 bp in length
* 86528 86628: gap of 100 bp
* 86629 99114: contig of 12487 bp in length
* 99115 99214: gap of 100 bp
* 99215 110221: contig of 11007 bp in length
* 110222 110321: gap of 100 bp
* 110322 123287: contig of 12966 bp in length
* 123288 123387: gap of 100 bp
* 123388 147877: contig of 24490 bp in length
* 147878 147977: gap of 100 bp
* 147978 169612: contig of 21635 bp in length.
FEATURES
    source
        1..169612
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            /chromosome="10"
            /map="10"
            /clone="RP11-770D23"
            /clone_lib="RPC1-11 Human Male BAC"
        1..1191
            /note="assembly_fragment"
            1292..2404
                /note="assembly_fragment"
            2505..3705
                /note="assembly_fragment"
            3806..4734
                /note="assembly_fragment"
            clone_end:T7
            vector_side:right
            4835..6570
                /note="assembly_fragment"
            6671..8583
                /note="assembly_fragment"
            8684..10290
                /note="assembly_fragment"
            clone_end:SP6
            vector_side:left
            10391..11938
                /note="assembly_fragment"
            12039..15839
                /note="assembly_fragment"
            15940..19203
                /note="assembly_fragment"
            19304..22581
                /note="assembly_fragment"
            22682..24947
                /note="assembly_fragment"
            25048..28167
                /note="assembly_fragment"
            28268..32083
                /note="assembly_fragment"
            32184..35533
                /note="assembly_fragment"
            35634..41517
                /note="assembly_fragment"
            41618..47143
                /note="assembly_fragment"
            47244..51694
                /note="assembly_fragment"
```

```
Query Match      26.0%; Score 256.8; DB 2; Length 169612;
Best Local Similarity 97.4%; Pred No. 3.6e-26;
Matches 261; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 704 CCTCGCCGTCCTCAGAGTCCTGTGCGCGGGGAAGGTGCTGCAACCTCCGAAAGGGGACGT 763
    |||||
DB 140411 CCGCGCCCTCCCGCAGGTCTCTGTGCGGGGAAGGTGCTGCAACCTCCGAAAGGGGACGT 140352
    |||||

QY 764 GCGGCGCAGTGTGTGCGAAACCTAAACGACGATCCGGCGGGAGCTCAGGGTCTACAT 823
    |||||
DB 140351 GCGGCGCAGTGTGTGCGAAACCTAAACGACGATCCGGCGGGAGCTCAGGGTCTACAT 140292
    |||||

QY 824 CAGCCTCTGCCCCCTGGGCGATGGACTCACCTTGCCCTTCAAGATCTAGGGCTGGCCCT 883
    |||||
DB 140291 CAGCCTCTGCCCCCTGGGCGATGGACTCACCTTGCCCTTCAAGATCTAGGGCTGGCCCT 140232
    |||||

QY 884 AGTGAGTGGGCTCGAGGGAGGGTTGCTTGGGAACCCAGGAATTGACCTTGAGTTTAAA 943
    |||||
DB 140231 AGTGAGTGGGCTCGAGGGAGGGTTGCTTGGGAACCCAGGAATTGACCTTGAGTTTAAA 140172
    |||||

QY 944 TTCGAAAATAAAGTGGGCTGGGACACA 971
    |||||
DB 140171 TTCGAAAATAAAGTGGGCTGGGACACA 140144

Search completed: April 19, 2005, 20:52:18
Job time : 7565 secs
```